



# STIC Search Report

## Biotech-Chem Library

STIC Database Tracking Number: 122860

TO: Terra Gibbs  
Location: rem/2d10/2c18  
Art Unit: 1635  
Friday, May 28, 2004  
Case Serial Number: 09/121239

From: Paul Schulwitz  
Location: Biotech-Chem Library  
REM-1A65  
Phone: (571)272-2527

[paul.schulwitz@uspto.gov](mailto:paul.schulwitz@uspto.gov)

### Search Notes

Examiner Gibbs,

See attached results.

If you have any questions about this search feel free to contact me at any time.

Thank you for using STIC search services!

Paul Schulwitz  
Technical Information Specialist  
STIC Biotech/Chem Library  
(571)272-2527

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TIC-Biotech/ChemLib

122860

From: Fredman, Jeffrey  
Sent: Tuesday, May 25, 2004 6:38 AM  
To: STIC-Biotech/ChemLib  
Cc: Gibbs, Terra  
Subject: FW: Sequence search request...

Please RUSH!

I Approve the search.

Jeff Fredman

-----Original Message-----

From: Gibbs, Terra  
Sent: Monday, May 24, 2004 10:29 AM  
To: Fredman, Jeffrey  
Subject: Sequence search request...

Jeff, can you please approve a RUSH on this sequence search request?

This is an older case, before we began restricting to less than 10 sequences. The sequences that need to be searched are all less than 25 nucleobases in length, as they are all either primers or probes.

Can you please search SEQ ID NOs: 1-4, 6-23, 26, and 27 of USSN 09/121,239?

The claims read on consisting of language, so all hits must be the exact, not comprising. Also, can you perform an interference search?

Terra Cotta Gibbs, Ph.D.  
Art Unit 1635  
Remsen Building 2D10  
571-272-0758

Searcher: \_\_\_\_\_  
Phone: \_\_\_\_\_  
Location: \_\_\_\_\_  
Date Picked Up: \_\_\_\_\_  
Date Completed: 5/28  
Searcher Prep/Review: \_\_\_\_\_  
Clerical: \_\_\_\_\_  
Online time: \_\_\_\_\_

TYPE OF SEARCH:  
NA Sequences: \_\_\_\_\_  
AA Sequences: \_\_\_\_\_  
Structures: \_\_\_\_\_  
Bibliographic: \_\_\_\_\_  
Litigation: \_\_\_\_\_  
Full text: \_\_\_\_\_  
Patent Family: \_\_\_\_\_  
Other: \_\_\_\_\_

VENDOR/COST (where applic.)  
STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
Questel/Orbit: \_\_\_\_\_  
DRLink: \_\_\_\_\_  
Lexis/Nexis: \_\_\_\_\_  
Sequence Sys.: \_\_\_\_\_  
WWW/Internet: \_\_\_\_\_  
Other (specify): \_\_\_\_\_

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 26, 2004, 16:00:31 ; Search time 1149.26 Seconds  
(without alignments)  
2036.547 Million cell updates/sec

Title: US-09-121-239-1

Perfect score: 54

Sequence: 1 TAAATTAATACGACTCACTA.....CCCTGAGGCTCAAAAGTCAGA 54

Scoring table: OLIGO\_NUC

Gapop 60.0 , Gapext 60.0

Searched: 3470272 seqs, 21671516995 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

GenEmbl.\*

1: gb\_ba.\*

2: gb\_htg.\*

3: gb\_in.\*

4: gb\_om.\*

5: gb\_ov.\*

6: gb\_pat.\*

7: gb\_ph.\*

8: gb\_pl.\*

9: gb\_pr.\*

10: gb\_ro.\*

11: gb\_sts.\*

12: gb\_sy.\*

13: gb\_un.\*

14: gb\_vi.\*

15: em\_ba.\*

16: em\_fun.\*

17: em\_hum.\*

18: em\_in.\*

19: em\_mu.\*

20: em\_om.\*

21: em\_or.\*

22: em\_ov.\*

23: em\_pat.\*

24: em\_ph.\*

25: em\_pl.\*

26: em\_ro.\*

27: em\_sts.\*

28: em\_un.\*

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31: em\_htg\_inv.\*

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33: em\_htg\_mus.\*

34: em\_htg\_pln.\*

35: em\_htg\_rod.\*

36: em\_htg\_mam.\*

37: em\_htg\_vrt.\*

38: em\_sy.\*

39: em\_htgo\_hum.\*

40: em\_htgo\_mus.\*

41: em\_htgo\_other.\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	54	100.0	54	6	BD222523	BD222523 Methods f
2	54	100.0	54	6	BD222524	BD222524 Methods f
C 3	54	100.0	54	6	BD222525	BD222525 Methods f
C 4	54	100.0	54	6	BD222526	BD222526 Methods f
5	49	90.7	50	6	AR352057	AR352057 Sequence
6	32	59.3	54	6	BD236957	BD236957 Nucleic a
7	32	59.3	54	6	AR307443	AR307443 Nucleic a
8	30	55.6	49	6	BD236963	BD236963 Nucleic a
9	30	55.6	49	6	AR307449	AR307449 Sequence
10	30	55.6	50	6	BD236956	BD236956 Nucleic a
11	30	55.6	50	6	AR307442	AR307442 Sequence
12	30	55.6	52	6	BD236968	BD236968 Nucleic a
13	30	55.6	52	6	AR307454	AR307454 Sequence
14	29	53.7	37	6	I25071	I25071 Sequence 5
15	29	53.7	45	6	AX575411	AX575411 Sequence
16	29	53.7	50	6	AR102985	AR102985 Sequence
17	29	53.7	51	6	AR344851	AR344851 Sequence
18	29	53.7	51	6	AX397806	AX397806 Sequence
19	29	53.7	52	6	BD236961	BD236961 Nucleic a
20	29	53.7	52	6	BD236967	BD236967 Nucleic a
21	29	53.7	52	6	AR307447	AR307447 Sequence
22	29	53.7	52	6	AR307453	AR307453 Sequence
23	29	53.7	54	6	BD236955	BD236955 Nucleic a
24	29	53.7	54	6	BD236974	BD236974 Nucleic a
25	29	53.7	54	6	AR307441	AR307441 Sequence
26	29	53.7	54	6	AR307460	AR307460 Sequence
27	29	53.7	55	6	BD236972	BD236972 Nucleic a
28	29	53.7	55	6	AR307458	AR307458 Sequence
29	29	53.7	60	6	I25073	I25073 Sequence 7
30	29	53.7	79	6	I25069	I25069 Sequence 3
31	29	53.7	180	6	I25067	I25067 Sequence 1
32	29	53.7	586	6	AX701716	AX701716 Sequence
33	29	53.7	1440	6	AX701737	AX701737 Sequence
34	29	53.7	3073	12	CVU02284	U02284 Cloning vec
35	29	53.7	6306	6	AX286493	AX286493 Sequence
36	29	53.7	7201	6	AX800664	AX800664 Sequence
37	29	53.7	7231	6	AX806466	AX806466 Sequence
38	29	53.7	7297	6	AX806467	AX806467 Sequence
39	29	53.7	7429	6	AX839727	AX839727 Sequence
40	29	53.7	7456	6	AX806465	AX806465 Sequence
41	28	51.9	28	6	BD236969	BD236969 Nucleic a
42	28	51.9	28	6	AR307455	AR307455 Sequence
43	28	51.9	30	6	AR369578	AR369578 Sequence
44	28	51.9	30	6	AR404157	AR404157 Sequence
45	28	51.9	33	6	AR344815	AR344815 Sequence

ALIGNMENTS

RESULT 1	BD222523	54 bp	DNA	linear	PAT 17-JUL-2003
LOCUS	BD222523				
DEFINITION	Methods for detecting and measuring spliced nucleic acids.				
ACCESSION	BD222523				
VERSION	BD222523.1	GI:33032293			
KEYWORDS	JP 2002521037-A/1.				
SOURCE	synthetic construct				
ORGANISM	artificial sequences				
REFERENCE	1 (bases 1 to 54)				
AUTHORS	Harvey, R.C. and Eastman, P.S.				
TITLE	Methods for detecting and measuring spliced nucleic acids				
JOURNAL	Patent: JP 2002521037-A 1 16-JUL-2002;				
	GEN PROBE INC				

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COMMENT OS Artificial Sequence
PN JP 2002521037-A/1
PD 16-JUL-2002
PF 23-JUL-1999 JP 2000561364
PI RICHARD C HARVEY, PAUL S EASTMAN
PC C12Q1/68, C12N15/09, C12N15/00
CC Description of Artificial Sequence: Synthetic promoter primer
CC promoter sequence at residues 1-27
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Location/Qualifiers
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BD222524
LOCUS 54 bp RNA linear PAT 17-JUL-2003
DEFINITION Methods for detecting and measuring spliced nucleic acids.
ACCESSION BD222524
VERSION BD222524.1 GI:33032294
KEYWORDS JP 2002521037-A/2.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 54)
HARVEY, R.C. and EASTMAN, P.S.
METHODS FOR DETECTING AND MEASURING SPLICED NUCLEIC ACIDS
TITLE Patent: JP 2002521037-A 2 16-JUL-2002;
JOURNAL GEN PROBE INC
COMMENT OS Artificial Sequence
PN JP 2002521037-A/2
PD 16-JUL-2002
PF 23-JUL-1999 JP 2000561364
PI RICHARD C HARVEY, PAUL S EASTMAN
PC C12Q1/68, C12N15/09, C12N15/00
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DB 1 TAAATTAAATACGACTCACTATAGGGAGACTCAGACCCCTGAGGCTCAAAGTCAGA 54
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RESULT 3
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LOCUS 54 bp DNA linear PAT 17-JUL-2003
DEFINITION Methods for detecting and measuring spliced nucleic acids.
ACCESSION BD222525
VERSION BD222525.1 GI:33032295
KEYWORDS JP 2002521037-A/3.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 54)
HARVEY, R.C. and EASTMAN, P.S.
METHODS FOR DETECTING AND MEASURING SPLICED NUCLEIC ACIDS
TITLE Patent: JP 2002521037-A 3 16-JUL-2002;
JOURNAL GEN PROBE INC
COMMENT OS Artificial Sequence
PN JP 2002521037-A/3
PD 16-JUL-2002
PF 23-JUL-1999 JP 2000561364
PI RICHARD C HARVEY, PAUL S EASTMAN
PC C12Q1/68, C12N15/09, C12N15/00
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Location/Qualifiers
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DB 54 TAAATTAAATACGACTCACTATAGGGAGACTCAGACCCCTGAGGCTCAAAGTCAGA 1
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RESULT 4
BD222526/c
LOCUS 54 bp RNA linear PAT 17-JUL-2003
DEFINITION Methods for detecting and measuring spliced nucleic acids.
ACCESSION BD222526
VERSION BD222526.1 GI:33032296
KEYWORDS JP 2002521037-A/4.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 54)
HARVEY, R.C. and EASTMAN, P.S.
METHODS FOR DETECTING AND MEASURING SPLICED NUCLEIC ACIDS
TITLE Patent: JP 2002521037-A 4 16-JUL-2002;
JOURNAL GEN PROBE INC
COMMENT OS Artificial Sequence
PN JP 2002521037-A/4
PD 16-JUL-2002
PF 23-JUL-1999 JP 2000561364
PI RICHARD C HARVEY, PAUL S EASTMAN
PC C12Q1/68, C12N15/09, C12N15/00
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FH Key Location/Qualifiers
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RESULT 5  
 AR352057  
 LOCUS AR352057 50 bp DNA linear PAT 17-AUG-2003  
 DEFINITION Sequence 45 from patent US 6589734.  
 ACCESSION AR352057  
 VERSION AR352057.1 GI:33757020  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unclassified.  
 REFERENCE 1 (bases 1 to 50)  
 AUTHORS Kacian,D.L., Fultz,T.J. and McDonough,S.H.  
 TITLE Detection of HIV  
 JOURNAL Patent: US 6589734-A 45 08-JUL-2003;  
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ORIGIN

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RESULT 6  
 BD236957  
 LOCUS BD236957 54 bp DNA linear PAT 17-JUL-2003  
 DEFINITION Nucleic acid sequence for detecting genetic marker for cancer in biological samples.  
 ACCESSION BD236957  
 VERSION BD236957.1 GI:33046727  
 KEYWORDS JP 2002535014-A/32.  
 SOURCE synthetic construct  
 ORGANISM artificial sequences.  
 REFERENCE 1 (bases 1 to 54)  
 AUTHORS Harvey,R.C. and Jr,T.J.C.  
 TITLE Nucleic acid sequence for detecting genetic marker for cancer in biological samples  
 JOURNAL Patent: JP 2002535014-A 32 22-OCT-2002;  
 GEN PROBE INC  
 COMMENT OS Artificial Sequence  
 PN JP 2002535014-A/32  
 PD 22-OCT-2002  
 PF 28-JAN-2000 JP 2000596180  
 PR 28-JAN-1999 US 60/117640  
 PI RICHARD C HARVEY,THOMAS J CLARK JR  
 PC C12N15/09,C12Q1/68,C12N15/00  
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 LOCUS AR307443 54 bp DNA linear PAT 12-JUN-2003  
 DEFINITION Sequence 32 from patent US 6551778.  
 ACCESSION AR307443  
 VERSION AR307443.1 GI:31697982  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unclassified.  
 REFERENCE 1 (bases 1 to 54)  
 AUTHORS Harvey,R.C. and Clark,T.J. Jr.  
 TITLE Nucleic acid sequences for detecting genetic markers for cancer in a biological sample  
 JOURNAL Patent: US 6551778-A 32 22-APR-2003;  
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 BD236963  
 LOCUS BD236963 49 bp DNA linear PAT 17-JUL-2003  
 DEFINITION Nucleic acid sequence for detecting genetic marker for cancer in biological samples.  
 ACCESSION BD236963  
 VERSION BD236963.1 GI:33046733  
 KEYWORDS JP 2002535014-A/38.  
 SOURCE synthetic construct  
 ORGANISM artificial sequences.  
 REFERENCE 1 (bases 1 to 49)  
 AUTHORS Harvey,R.C. and Jr,T.J.C.  
 TITLE Nucleic acid sequence for detecting genetic marker for cancer in biological samples  
 JOURNAL Patent: JP 2002535014-A 38 22-OCT-2002;  
 GEN PROBE INC  
 COMMENT OS Artificial Sequence  
 PN JP 2002535014-A/38  
 PD 22-OCT-2002  
 PF 28-JAN-2000 JP 2000596180  
 PR 28-JAN-1999 US 60/117640  
 PI RICHARD C HARVEY,THOMAS J CLARK JR  
 PC C12N15/09,C12Q1/68,C12N15/00  
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ORIGIN

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LOCUS  
DEFINITION Sequence 38 from patent US 6551778. PAT 12-JUN-2003  
ACCESSION AR307449  
VERSION AR307449.1 GI:31697988  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 49)  
AUTHORS Harvey,R.C. and Clark,T.J. Jr.  
TITLE Nucleic acid sequences for detecting genetic markers for cancer in a biological sample  
JOURNAL Patent: US 6551778-A 38 22-APR-2003;  
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ORIGIN

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RESULT 10  
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LOCUS  
DEFINITION Nucleic acid sequence for detecting genetic marker for cancer in biological samples. PAT 17-JUL-2003  
ACCESSION BD236956  
VERSION BD236956.1 GI:33046726  
KEYWORDS JP 2002535014-A/31.  
SOURCE synthetic construct  
ORGANISM artificial sequences.  
REFERENCE 1 (bases 1 to 50)  
AUTHORS Harvey,R.C. and Jr,T.J.C.  
TITLE Nucleic acid sequence for detecting genetic marker for cancer in biological samples  
JOURNAL Patent: JP 2002535014-A 31 22-OCT-2002;  
COMMENT GEN PROBE INC  
OS Artificial Sequence  
PN JP 2002535014-A/31  
PD 22-OCT-2002  
PF 28-JAN-2000 JP 2000596180  
PR 28-JAN-1999 US 60/117640  
PI RICHARD C HARVEY,THOMAS J CLARK JR  
PC C12N15/09.C12Q1/68.C12N15/00  
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FEATURES  
source

ORIGIN

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Db 1 TAAATTAAATACGACTCACTATAGGGAGACT 30  
|||||

RESULT 11  
AR307442  
LOCUS  
DEFINITION Sequence 31 from patent US 6551778. PAT 12-JUN-2003  
ACCESSION AR307442  
VERSION AR307442.1 GI:31697981  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 50)  
AUTHORS Harvey,R.C. and Clark,T.J. Jr.  
TITLE Nucleic acid sequences for detecting genetic markers for cancer in a biological sample  
JOURNAL Patent: US 6551778-A 31 22-APR-2003;  
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LOCUS  
DEFINITION Nucleic acid sequence for detecting genetic marker for cancer in biological samples. PAT 17-JUL-2003  
ACCESSION BD236968  
VERSION BD236968.1 GI:33046738  
KEYWORDS JP 2002535014-A/43.  
SOURCE synthetic construct  
ORGANISM artificial sequences.  
REFERENCE 1 (bases 1 to 52)  
AUTHORS Harvey,R.C. and Jr,T.J.C.  
TITLE Nucleic acid sequence for detecting genetic marker for cancer in biological samples  
JOURNAL Patent: JP 2002535014-A 43 22-OCT-2002;  
COMMENT GEN PROBE INC  
OS Artificial Sequence  
PN JP 2002535014-A/43  
PD 22-OCT-2002  
PF 28-JAN-2000 JP 2000596180  
PR 28-JAN-1999 US 60/117640  
PI RICHARD C HARVEY,THOMAS J CLARK JR  
PC C12N15/09.C12Q1/68.C12N15/00  
CC Description of Artificial Sequence: synthetic construct FH  
Key promoter Location/Qualifiers  
FT (1)..(28).  
1..52  
/organism="synthetic construct"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"

FEATURES  
source

ORIGIN

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Query Match      55.6%; Score 30; DB 6; Length 52;
Best Local Similarity 100.0%; Pred. No. 1.5e-06;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TAAATTAAATACGACTCACTATAGGGAGACT 30
Db 1 TAAATTAAATACGACTCACTATAGGGAGACT 30

RESULT 13
LOCUS AR307454 52 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 43 from patent US 6551778.
ACCESSION AR307454
VERSION AR307454.1 GI:31697993
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 52)
AUTHORS Harvey,R.C. and Clark,T.J. Jr.
TITLE Nucleic acid sequences for detecting genetic markers for cancer in
a biological sample
JOURNAL Patent: US 6551778-A 43 22-APR-2003;
FEATURES
source Location/Qualifiers
1..52
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match      55.6%; Score 30; DB 6; Length 52;
Best Local Similarity 100.0%; Pred. No. 1.5e-06;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TAAATTAAATACGACTCACTATAGGGAGACT 30
Db 1 TAAATTAAATACGACTCACTATAGGGAGACT 30

RESULT 14
LOCUS I25071 37 bp DNA linear PAT 07-OCT-1996
DEFINITION Sequence 5 from patent US 5547862.
ACCESSION I25071
VERSION I25071.1 GI:1604941
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 37)
AUTHORS Meador,J., McElroy,H.E., Herrmann,M.L. and Winkler,M.
TITLE Vectors containing multiple promoters in the same orientation
JOURNAL Patent: US 5547862-A 5 20-AUG-1996;
FEATURES
source Location/Qualifiers
1..37
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match      53.7%; Score 29; DB 6; Length 37;
Best Local Similarity 100.0%; Pred. No. 6.3e-06;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AATTATACGACTCACTATAGGGAGACTC 31
Db 1 AATTATACGACTCACTATAGGGAGACTC 29

RESULT 15
LOCUS AX575411 45 bp DNA linear PAT 07-JAN-2003
DEFINITION Sequence 4 from Patent WO02068635.
ACCESSION AX575411
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---

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VERSION AX575411.1 GI:27552050
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Billy E., Filipowicz, W. and Mueller U.
TITLE Methods of inhibiting expression of a target gene in mammalian
cells
JOURNAL Patent: WO 02068635-A 4 06-SEP-2002;
Novartis Forschungsstiftung Zweigniederlassung (CH)
FEATURES
source Location/Qualifiers
1..45
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="oligonucleotide"

ORIGIN
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Best Local Similarity 100.0%; Pred. No. 6.1e-06;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TTAATACGACTCACTATAGGGAGACTCAG 33
Db 1 TTAATACGACTCACTATAGGGAGACTCAG 29

Search completed: May 27, 2004, 02:16:34
Job time : 1151.26 secs
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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: May 26, 2004, 14:55:11 ; Search time 240.833 Seconds  
(without alignments)  
952.539 Million cell updates/sec

Title: US-09-121-239-1

Perfect score: 54

Sequence: 1 TAAATAATACGACTCACTA.....CCCTGAGGCTCAAGTCAGA 54

Scoring table: OLIGO NUC

Gapop 60.0 , Gapext 60.0

Searched: 3373863 seqs, 2124099041 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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- 2: Geneseqn1990s.\*
- 3: Geneseqn2000s.\*
- 4: Geneseqn2001as.\*
- 5: Geneseqn2001bs.\*
- 6: Geneseqn2002s.\*
- 7: Geneseqn2003as.\*
- 8: Geneseqn2003bs.\*
- 9: Geneseqn2003cs.\*
- 10: Geneseqn2004s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	54	100.0	54	AAZ60843	Aaz60843 Oligonucleotide
2	54	100.0	54	AAZ60841	Aaz60841 Oligonucleotide
3	54	100.0	54	AAZ60840	Aaz60840 Oligonucleotide
4	54	100.0	54	AAZ60842	Aaz60842 Oligonucleotide
5	49	90.7	50	AAQ86626	AAQ86626 CML chrom
6	49	90.7	50	AAT15571	Aat15571 CML-2 chr
7	49	90.7	50	AAT42417	Aat42417 CML chrom
8	49	90.7	50	AAV66349	Aav66349 CML-2 chr
9	49	90.7	50	AAZ23191	Aaz23191 CML chrom
10	49	90.7	50	AAZ62600	Aaz62600 CML chrom
11	32	59.3	54	AAA76067	Aaa76067 Human pro
12	30	55.6	49	AAA76206	Aaa76206 Human pro
13	30	55.6	50	AAA76066	Aaa76066 Human pro
14	30	55.6	52	AAA76211	Aaa76211 Human pro
15	29	53.7	45	ABZ59191	Abz59191 LacZ RNA
16	29	53.7	50	AAT07445	Aat07445 T7 gene 1
17	29	53.7	51	ABK53140	Abk53140 HIV-1 rev
18	29	53.7	51	AAI45502	Aai45502 HIV-1 pol
19	29	53.7	52	AAA76210	Aaa76210 Human pro
20	29	53.7	52	AAA76204	Aaa76204 Human pro
21	29	53.7	54	AAA76220	Aaa76220 Human pro
22	29	53.7	54	AAA76065	Aaa76065 Human pro
23	29	53.7	55	AAA76218	Aaa76218 Human pro

24	29	53.7	180	2	AAT41733	Aat41733 Promoter
25	29	53.7	1442	7	ABZ70392	Abz70392 Autofluor
26	29	53.7	6306	6	ABA03923	Aba03923 Human NHP
27	29	53.7	7201	8	ACF05731	Acf05731 Plasmid p
28	29	53.7	7231	8	ACF06299	Acf06299 Plasmid p
29	29	53.7	7297	8	ACF06300	Acf06300 Sigpcdipa
30	29	53.7	7429	8	ACF05558	Acf05558 Plasmid p
31	29	53.7	7456	8	ACF06298	Acf06298 Plasmid p
32	28	51.9	28	3	AA76212	Aaa76212 Human pro
33	28	51.9	30	2	AAT95233	Aat95233 Macaque s
34	28	51.9	33	4	AAD11020	Aad11020 Bacteriop
35	28	51.9	33	4	ABD11286	Abd11286 Bacteriop
36	28	51.9	33	6	ABK53104	Abk53104 T7 promot
37	28	51.9	33	6	ABK93905	Abk93905 Human imm
38	28	51.9	33	6	AAI45466	Aai45466 Bacteriop
39	28	51.9	35	2	AAV05796	Aav05796 Primer fo
40	28	51.9	35	2	AAV05794	Aav05794 3-frame H
41	28	51.9	35	6	AAI50495	Aai50495 3-frame H
42	28	51.9	35	8	ADA24416	Ada24416 His-tag v
43	28	51.9	36	4	AAC64735	Aac64735 Human pro
44	28	51.9	36	6	ABQ81381	Abq81381 Human pro
45	28	51.9	36	9	ADB71188	Adb71188 Human pro

## ALIGNMENTS

RESULT 1  
AAZ60843/c  
ID AAZ60843 standard; RNA; 54 BP.  
XX  
AC AAZ60843;  
XX  
DT 16-MAY-2000 (first entry)  
XX  
DE Oligonucleotide used to detect bcr b3-abl fusion transcripts.  
XX  
KW Fusion transcript; translocation; bcr b3 region; abl gene;  
KW amplification assay; detection assay; medical diagnosis;  
KW clinical monitoring; chimeric RNA; fusion RNA; condition marker;  
KW disease marker; cancer; leukemia; ss.  
XX  
OS Synthetic.  
XX  
PN WO200005418-A1.  
XX  
PD 03-FEB-2000.  
XX  
PF 23-JUL-1999; 99WO-US016832.  
XX  
PR 23-JUL-1998; 98US-00121239.  
XX  
PA (GENP-) GEN-PROBE INC.  
XX  
PI Harvey RC, Eastman PS;  
XX  
DR WPI; 2000-182730/16.  
XX  
PT Novel methods for preparing RNA from biological samples, used for the  
XX detection and measurement of nucleic acids and fusion nucleic acids.  
XX  
PS Claim 19; Page 40; 49pp; English.  
XX  
CC Oligonucleotides AAZ60840-62 and AAZ60865-66 are used in the method of  
CC the invention to detect fusion transcripts produced from a translocation  
CC between the bcr b3 region and the abl gene. The specification describes a  
CC method for detecting a fusion nucleic acid (particularly chimeric mRNA  
CC species), in a biological sample. The method comprises contacting a  
CC sample of fusion nucleic acid with primers, amplifying the hybridized  
CC fusion nucleic acid, and detecting the target hybrid. The method is used  
CC for the sample and rapid preparation of RNA from a biological sample,  
CC particularly from the cytoplasm of eukaryotic cells, which is suitable  
CC for use in an amplification and detection assay. The methods are used for

CC the analysis and detection of nucleic acids in biological samples. The  
 CC methods are useful in the human medical and veterinary fields, for  
 CC medical diagnoses and clinical monitoring of a patient's response to  
 CC therapy where a disease or medical condition is associated with a  
 CC particular type and/or level of mRNA present in the sample. The methods  
 CC are also useful for detecting or quantifying fusion or chimeric RNA  
 CC species, and for detecting a translocation as a marker for a given  
 CC condition or disease, e.g. translocations associate with cancers,  
 CC particularly forms of leukemia

XX Sequence 54 BP; 11 A; 11 C; 12 G; 0 T; 20 U; 0 Other;  
 SQ Query Match 100.0%; Score 54; DB 3; Length 54;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-19;  
 Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TAAATTATACGACTCACTATAGGAGACTCAGACCTGAGGCTCAAAGTCAGA 54  
 Db 54 TAAATTATACGACTCACTATAGGAGACTCAGACCTGAGGCTCAAAGTCAGA 1

RESULT 2  
 AAZ60841  
 ID AAZ60841 standard; RNA; 54 BP.  
 AC AAZ60841;  
 XX  
 XX  
 DT 16-MAY-2000 (first entry)  
 DE Oligonucleotide used to detect bcr b3-abl fusion transcripts.  
 XX  
 XX Fusion transcript; translocation; bcr b3 region; abl gene;  
 KW amplification assay; detection assay; medical diagnosis;  
 KW clinical monitoring; chimeric RNA; fusion RNA; condition marker;  
 KW disease marker; cancer; leukemia; ss.  
 XX  
 OS Synthetic.  
 XX  
 XX WO200005418-A1.  
 XX  
 PD 03-FEB-2000.  
 XX  
 XX 23-JUL-1999; 99WO-US016832.  
 PF  
 XX 23-JUL-1998; 98US-00121239.  
 PR  
 XX (GENP-) GEN-PROBE INC.  
 PA  
 XX Harvey RC, Eastman PS;  
 PI  
 XX WPI; 2000-182730/16.  
 DR  
 XX Novel methods for preparing RNA from biological samples, used for the  
 PT detection and measurement of nucleic acids and fusion nucleic acids.  
 PT  
 XX Claim 19; Page 40; 49pp; English.  
 PS  
 XX Oligonucleotides AAZ60840-62 and AAZ60865-66 are used in the method of  
 CC the invention to detect fusion transcripts produced from a translocation  
 CC between the bcr b3 region and the abl gene. The specification describes a  
 CC method for detecting a fusion nucleic acid (particularly chimeric mRNA  
 CC species), in a biological sample. The method comprises contacting a  
 CC sample of fusion nucleic acid with primers, amplifying the hybridized  
 CC fusion nucleic acid, and detecting the target hybrid. The method is used  
 CC for the simple and rapid preparation of RNA from a biological sample,  
 CC particularly from the cytoplasm of eukaryotic cells, which is suitable  
 CC for use in an amplification and detection assay. The methods are used for  
 CC the analysis and detection of nucleic acids in biological samples. The  
 CC methods are useful in the human medical and veterinary fields, for  
 CC medical diagnoses and clinical monitoring of a patient's response to  
 CC therapy where a disease or medical condition is associated with a  
 CC particular type and/or level of mRNA present in the sample. The methods  
 CC are also useful for detecting or quantifying fusion or chimeric RNA  
 CC species, and for detecting a translocation as a marker for a given  
 CC condition or disease, e.g. translocations associate with cancers,  
 CC particularly forms of leukemia

CC species, and for detecting a translocation as a marker for a given  
 CC condition or disease, e.g. translocations associate with cancers,  
 CC particularly forms of leukemia

XX Sequence 54 BP; 20 A; 12 C; 11 G; 0 T; 11 U; 0 Other;  
 SQ Query Match 100.0%; Score 54; DB 3; Length 54;  
 Best Local Similarity 79.6%; Pred. No. 1.8e-19;  
 Matches 43; Conservative 11; Mismatches 0; Indels 0; Gaps 0;

QY 1 TAAATTATACGACTCACTATAGGAGACTCAGACCTGAGGCTCAAAGTCAGA 54  
 Db 1 UAAAUUAUACGACUACUUAAGGAGAGACUACAGCCUGAGGCUCAAAGUCAGA 54

RESULT 3  
 AAZ60840  
 ID AAZ60840 standard; DNA; 54 BP.  
 XX  
 AC AAZ60840;  
 XX  
 DT 16-MAY-2000 (first entry)  
 DE Oligonucleotide used to detect bcr b3-abl fusion transcripts.  
 XX  
 XX Fusion transcript; translocation; bcr b3 region; abl gene;  
 KW amplification assay; detection assay; medical diagnosis;  
 KW clinical monitoring; chimeric RNA; fusion RNA; condition marker;  
 KW disease marker; cancer; leukemia; ss.  
 XX  
 OS Synthetic.  
 XX  
 XX WO200005418-A1.  
 XX  
 PD 03-FEB-2000.  
 XX  
 XX 23-JUL-1999; 99WO-US016832.  
 PF  
 XX 23-JUL-1998; 98US-00121239.  
 PR  
 XX (GENP-) GEN-PROBE INC.  
 PA  
 XX Harvey RC, Eastman PS;  
 PI  
 XX WPI; 2000-182730/16.  
 DR  
 XX Novel methods for preparing RNA from biological samples, used for the  
 PT detection and measurement of nucleic acids and fusion nucleic acids.  
 PT  
 XX Claim 19; Page 39; 49pp; English.  
 PS  
 XX Oligonucleotides AAZ60840-62 and AAZ60865-66 are used in the method of  
 CC the invention to detect fusion transcripts produced from a translocation  
 CC between the bcr b3 region and the abl gene. The specification describes a  
 CC method for detecting a fusion nucleic acid (particularly chimeric mRNA  
 CC species), in a biological sample. The method comprises contacting a  
 CC sample of fusion nucleic acid with primers, amplifying the hybridized  
 CC fusion nucleic acid, and detecting the target hybrid. The method is used  
 CC for the simple and rapid preparation of RNA from a biological sample,  
 CC particularly from the cytoplasm of eukaryotic cells, which is suitable  
 CC for use in an amplification and detection assay. The methods are used for  
 CC the analysis and detection of nucleic acids in biological samples. The  
 CC methods are useful in the human medical and veterinary fields, for  
 CC medical diagnoses and clinical monitoring of a patient's response to  
 CC therapy where a disease or medical condition is associated with a  
 CC particular type and/or level of mRNA present in the sample. The methods  
 CC are also useful for detecting or quantifying fusion or chimeric RNA  
 CC species, and for detecting a translocation as a marker for a given  
 CC condition or disease, e.g. translocations associate with cancers,  
 CC particularly forms of leukemia

XX Sequence 54 BP; 20 A; 12 C; 11 G; 11 T; 0 U; 0 Other;  
 SQ

Query Match 100.0%; Score 54; DB 3; Length 54;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-19;  
 Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TAAATTAATACGACTCACTATAGGAGAGACTAGAGGAGCTCAGACCTGAGGCTCAAAGTCAGA 54  
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 DB 1 TAAATTAATACGACTCACTATAGGAGAGACTAGAGGAGCTCAGACCTGAGGCTCAAAGTCAGA 54  
 |||||||

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 XX AAZ60842 standard; DNA; 54 BP.  
 AC AAZ60842;  
 DT 16-MAY-2000 (first entry)  
 DE Oligonucleotide used to detect bcr b3-abl fusion transcripts.  
 KW Fusion transcript; translocation; bcr b3 region; abl gene;  
 KW amplification assay; detection assay; medical diagnosis;  
 KW clinical monitoring; chimeric RNA; fusion RNA; condition marker;  
 KW disease marker; cancer; leukemia; ss.  
 OS Synthetic.  
 XX WO200005418-A1.  
 PN 03-FEB-2000.  
 PD 23-JUL-1999; 99WO-US016832.  
 XX 23-JUL-1998; 98US-00121239.  
 PR (GENP-) GEN-PROBE INC.  
 PA Harvey RC, Eastman PS;  
 XX WPI; 2000-182730/16.  
 CC Novel methods for preparing RNA from biological samples, used for the  
 CC detection and measurement of nucleic acids and fusion nucleic acids.  
 PT Claim 19; Page 40; 49pp; English.  
 CC Oligonucleotides AAZ60840-62 and AAZ60865-66 are used in the method of  
 CC the invention to detect fusion transcripts produced from a translocation  
 CC between the bcr b3 region and the abl gene. The specification describes a  
 CC method for detecting a fusion nucleic acid (particularly chimeric mRNA  
 CC species), in a biological sample. The method comprises contacting a  
 CC sample of fusion nucleic acid with primers, amplifying the hybridized  
 CC fusion nucleic acid, and detecting the target hybrid. The method is used  
 CC for the simple and rapid preparation of RNA from a biological sample,  
 CC particularly from the cytoplasm of eukaryotic cells, which is suitable  
 CC for use in an amplification and detection assay. The methods are used for  
 CC the analysis and detection of nucleic acids in biological samples. The  
 CC methods are useful in the human medical and veterinary fields, for  
 CC medical diagnoses and clinical monitoring of a patient's response to  
 CC therapy where a disease or medical condition is associated with a  
 CC particular type and/or level of mRNA present in the sample. The methods  
 CC are also useful for detecting or quantifying fusion or chimeric RNA  
 CC species, and for detecting a translocation as a marker for a given  
 CC condition or disease, e.g. translocations associate with cancers,  
 CC particularly forms of leukemia  
 CC Sequence 54 BP; 11 A; 11 C; 12 G; 20 T; 0 U; 0 Other;

Query Match 100.0%; Score 54; DB 3; Length 54;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-19;  
 Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TAAATTAATACGACTCACTATAGGAGAGACTAGAGGAGCTCAGACCTGAGGCTCAAAGTCAGA 54  
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DB 54 TAAATTAATACGACTCACTATAGGAGAGACTAGAGGAGCTCAGACCTGAGGCTCAAAGTCAGA 1  
 |||||||

RESULT 5  
 ID AAQ86626  
 XX AAQ86626 standard; DNA; 50 BP.  
 AC AAQ86626;  
 DT 25-MAR-2003 (revised)  
 DT 15-NOV-1995 (first entry)  
 DE CML chromosomal translocation minus strand primer.  
 KW Primer; autocatalytic; target; CML; translocation; ss.  
 XX Synthetic.  
 OS US5399491-A.  
 PN 21-MAR-1995.  
 PD 19-MAR-1992; 92US-00855732.  
 XX 11-JUL-1989; 89US-00379501.  
 PR 10-JUL-1990; 90US-00550837.  
 XX (GENP-) GEN-PROBE INC.  
 PA Fultz TJ, Kacian DL;  
 PI WPI; 1995-130686/17.  
 DR Amplification of nucleic acid targets - using a reverse transcriptase  
 PT with RNase H activity and a RNA polymerase at constant temp.  
 PS Disclosure; Col 9; 58pp; English.  
 XX AAQ86626-28 are primers and a probe for the CML chromosomal  
 CC translocation. They are used to produce autocatalytic oligonucleotides  
 CC which require no change in the experimental conditions i.e. constant  
 CC temperature, pH and ionic strength. These sequences are useful in  
 CC generating multiple copies of specific nucleic acid target sequences.  
 CC (Updated on 25-MAR-2003 to correct PF field.)  
 XX Sequence 50 BP; 17 A; 12 C; 11 G; 10 T; 0 U; 0 Other;  
 SQ Query Match 90.7%; Score 49; DB 2; Length 50;  
 Best Local Similarity 100.0%; Pred. No. 8.8e-17;  
 Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AATTAATACGACTCACTATAGGAGAGACTCAGACCTGAGGCTCAAAGTC 51  
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 DB 2 AATTAATACGACTCACTATAGGAGAGACTCAGACCTGAGGCTCAAAGTC 50  
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RESULT 6  
 ID AAT15571  
 XX AAT15571 standard; DNA; 50 BP.  
 AC AAT15571;  
 DT 25-MAR-2003 (revised)  
 DT 17-JUL-1996 (first entry)  
 DE CML-2 chromosomal translocation major breakpoint t(9;22) (-) primer.  
 KW CML-2 chromosomal translocation major breakpoint; t(9; 22); primer;  
 KW auto-catalytic; synthesis; RNA target sequence; assay; detection;  
 KW quantification; ss.  
 XX Synthetic.  
 OS

PN US5480784-A.  
 XX  
 PD 02-JAN-1996.  
 XX  
 XX 10-JUL-1990; 90US-00550837.  
 PF  
 XX 11-JUL-1989; 89US-00379501.  
 PR  
 XX (GENP-) GEN-PROBE INC.  
 PA  
 XX Fultz TU, Kacian DL;  
 PI  
 XX WPI; 1996-068248/07.  
 DR  
 XX Auto-catalytic synthesis of multiple copies of an RNA target sequence -  
 PT uses cooperative action of a DNA and RNA polymerase in presence of RNase  
 PT H, useful for detection of target sequence e.g. in clinical or  
 PT environmental sample.  
 PT  
 XX Example; Col 9-10; 51pp; English.  
 PS  
 XX The present sequence is a primer for the CML-2 chromosomal translocation  
 CC major breakpoint t(9;22), which was used to demonstrate an improved  
 CC method for synthesising multiple copies of a RNA target sequence. The  
 CC method comprises combining the target with a primer which hybridises to  
 CC the 3'-terminal portion of the target, a promoter primer which hybridises  
 CC with a portion of the DNA primer extension prod., reverse transcriptase,  
 CC RNase H and transcriptase. It can be used as a component of an assay to  
 CC detect and/or quantitate specific target sequences in clinical,  
 CC environmental or forensic samples. It also has the advantages of being  
 CC autocatalytic, using the cooperative action of a DNA polymerase, e.g. a  
 CC reverse transcriptase and avoids repetitive manipulations of reaction  
 CC conditions, e.g. temp., ionic strength and pH. (Updated on 25-MAR-2003 to  
 CC correct PF field.)  
 XX  
 SQ Sequence 50 BP; 17 A; 12 C; 11 G; 10 T; 0 U; 0 Other;  
 Query Match 90.7%; Score 49; DB 2; Length 50;  
 Best Local Similarity 100.0%; Pred. No. 8.8e-17;  
 Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 AATTAATACGACTCTACTATAGGAGACTCAGACCCCTGAGGCTCAAAGTC 51  
 Db 2 AATTAATACGACTCTACTATAGGAGACTCAGACCCCTGAGGCTCAAAGTC 50  
 RESULT 7  
 AAT42417  
 ID AAT42417 standard; DNA; 50 BP.  
 XX  
 AC AAT42417;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 28-APR-1997 (first entry)  
 XX  
 DE CML chromosomal translocation primer #1.  
 XX  
 XX HIV; probe; primer; amplify; polymerase chain reaction; microorganism;  
 KW BCL-2; PCR; hepatitis B virus; HBV; CML; ss.  
 XX  
 XX Synthetic.  
 OS  
 XX EP731175-A2.  
 PN  
 XX 11-SEP-1996.  
 PD  
 XX 10-JUL-1990; 96EP-00101621.  
 PF  
 XX 11-JUL-1989; 89US-00379501.  
 PR  
 XX 10-JUL-1990; 90EP-00307503.  
 PR  
 XX (GENP-) GEN-PROBE INC.  
 PA  
 XX

PI Mcdonough S;  
 XX  
 DR WPI; 1996-403995/41.  
 XX  
 PT Detection of HIV nucleic acids in samples - using new specific oligo-  
 PT nucleotide(s) for the amplification and detection of target sequences.  
 XX  
 XX Disclosure; Page 8; 66pp; English.  
 PS  
 XX AAT42417-T42419 represent primers and a probe for the CML chromosomal  
 CC translocation t(9;22). These sequences can be used in modified versions  
 CC of the kits of the invention. The kits of the invention, are for  
 CC detecting the presence of HIV nucleic acid sequences in a sample. The  
 CC kits comprise two amplification primers (such as AAT40182 and AAT40183),  
 CC and a probe (such as AAT42404) for detection of the amplified sequence.  
 CC By using these sequences, the amplification of HIV nucleic acid sequences  
 CC is improved. The kits can also be used for the detection of other  
 CC microorganisms, by using different probe sequences. Other sequences that  
 CC can be detected using this method include those from HBV (using the  
 CC sequences shown in AAT42410-T42412), and BCL-2 (using AAT42413-T42416).  
 CC The samples can be clinical, environmental or forensic samples, and the  
 CC method produces large amounts of the target sequence for a variety of  
 CC uses. The method can also be used to produce multiple copies of a target  
 CC sequence for use in cloning, and sequencing, and to produce probes for  
 CC the target sequence. (Updated on 25-MAR-2003 to correct PF field.)  
 CC (Updated on 25-MAR-2003 to correct PR field.)  
 XX  
 SQ Sequence 50 BP; 17 A; 12 C; 11 G; 10 T; 0 U; 0 Other;  
 Query Match 90.7%; Score 49; DB 2; Length 50;  
 Best Local Similarity 100.0%; Pred. No. 8.8e-17;  
 Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 AATTAATACGACTCTACTATAGGAGACTCAGACCCCTGAGGCTCAAAGTC 51  
 Db 2 AATTAATACGACTCTACTATAGGAGACTCAGACCCCTGAGGCTCAAAGTC 50  
 RESULT 8  
 AAV66349  
 ID AAV66349 standard; DNA; 50 BP.  
 XX  
 AC AAV66349;  
 XX  
 DT 06-JAN-1999 (first entry)  
 DT  
 XX  
 DE CML-2 chromosomal translocation t(9;22) primer.  
 XX  
 KW CML-2 chromosomal translocation t(9;22); block splice template;  
 KW autocatalytic RNA amplification; primer; ss.  
 XX  
 OS Synthetic.  
 OS  
 XX US5824518-A.  
 PN  
 XX 20-OCT-1998.  
 PD  
 XX 06-JUN-1995; 95US-00469067.  
 PF  
 XX 11-JUL-1989; 89US-00379501.  
 PR  
 XX 10-JUL-1990; 90US-00550837.  
 PR  
 XX (GENP-) GEN-PROBE INC.  
 PA  
 XX Fultz TU, Kacian DL;  
 PI  
 XX WPI; 1998-582557/49.  
 DR  
 XX Block splice template useful for amplification of nucleic acids -  
 PT comprises two nucleic acid regions, the first region located 3' of the  
 PT second region and blocked at its 3' terminus to inhibit primer extension  
 PT by a DNA polymerase.  
 XX



```

XX 25-JAN-2001 (first entry)
XX Human prostate specific antigen PCR primer SEQ ID NO: 29.
DE Prostate specific antigen; PSA; prostate-specific membrane antigen; PSMA;
XX glandular kallikrein-2; hK2; prostate cancer; breast cancer; probe;
KW PCR primer; ss.
XX Homo sapiens.
XX WO200044940-A2.
XX 03-AUG-2000.
XX 28-JAN-2000; 2000WO-US002270.
XX 28-JAN-1999; 99US-0117640P.
XX (GENP-) GEN-PROBE INC.
XX Harvey RC, Clark TJ;
XX WPI; 2000-505986/45.
XX Detecting prostate-specific antigen (PSA), prostate specific membrane
XX antigen (PSMA) or human kallikrein 2 (hK2) nucleic acids in samples using
XX probe molecules, useful for the diagnosis of prostate and breast cancers.
XX Claim 1; Page 12; 77pp; English.
XX The present invention is concerned with the detection of nucleic acid
XX markers for prostate and breast cancer, and PCR primers and probes which
XX are able to detect and quantify these markers. Prostate specific antigen
XX (PSA), prostate-specific membrane antigen (PSMA) and glandular kallikrein
XX -2 (hK2) have all been linked to prostate and breast cancers, and the
XX primers and probes of the invention are able to detect the abnormal
XX presence of mRNA expressed by their coding sequences in tissues other
XX than the prostate. This enables the presence of cancer to be perceived
XX and aids in the detection of metastases
XX Sequence 54 BP; 16 A; 13 C; 11 G; 14 T; 0 U; 0 Other;
Query Match 59.3%; Score 32; DB 3; Length 54;
Best Local Similarity 100.0%; Pred. No. 1.3e-07;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TAAATTAAATACGACTCACTATAGGGAGACTCA 32
DB 1 TAAATTAAATACGACTCACTATAGGGAGACTCA 32
RESULT 12
AAA76206
ID AAA76206 standard; DNA; 49 BP.
XX
XX AAA76206;
AC
XX 25-JAN-2001 (first entry)
DE Human prostate specific antigen PCR primer SEQ ID NO: 35.
XX Prostate specific antigen; PSA; prostate-specific membrane antigen; PSMA;
XX glandular kallikrein-2; hK2; prostate cancer; breast cancer; probe;
KW PCR primer; ss.
XX Homo sapiens.
XX WO200044940-A2.
XX 03-AUG-2000.
XX 28-JAN-2000; 2000WO-US002270.
XX 28-JAN-1999; 99US-0117640P.
XX (GENP-) GEN-PROBE INC.
XX Harvey RC, Clark TJ;
XX WPI; 2000-505986/45.
XX Detecting prostate-specific antigen (PSA), prostate specific membrane
XX antigen (PSMA) or human kallikrein 2 (hK2) nucleic acids in samples using
XX probe molecules, useful for the diagnosis of prostate and breast cancers.
XX Claim 1; Page 12; 77pp; English.
XX The present invention is concerned with the detection of nucleic acid
XX markers for prostate and breast cancer, and PCR primers and probes which
XX are able to detect and quantify these markers. Prostate specific antigen
XX (PSA), prostate-specific membrane antigen (PSMA) and glandular kallikrein
XX -2 (hK2) have all been linked to prostate and breast cancers, and the
XX primers and probes of the invention are able to detect the abnormal
XX presence of mRNA expressed by their coding sequences in tissues other
XX than the prostate. This enables the presence of cancer to be perceived
XX and aids in the detection of metastases
XX Sequence 54 BP; 16 A; 13 C; 11 G; 14 T; 0 U; 0 Other;
Query Match 59.3%; Score 32; DB 3; Length 54;
Best Local Similarity 100.0%; Pred. No. 1.3e-07;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TAAATTAAATACGACTCACTATAGGGAGACTCA 32
DB 1 TAAATTAAATACGACTCACTATAGGGAGACTCA 32

```

```

XX 28-JAN-1999; 99US-0117640P.
XX (GENP-) GEN-PROBE INC.
XX Harvey RC, Clark TJ;
XX WPI; 2000-505986/45.
XX Detecting prostate-specific antigen (PSA), prostate specific membrane
XX antigen (PSMA) or human kallikrein 2 (hK2) nucleic acids in samples using
XX probe molecules, useful for the diagnosis of prostate and breast cancers.
XX Claim 1; Page 13; 77pp; English.
XX The present invention is concerned with the detection of nucleic acid
XX markers for prostate and breast cancer, and PCR primers and probes which
XX are able to detect and quantify these markers. Prostate specific antigen
XX (PSA), prostate-specific membrane antigen (PSMA) and glandular kallikrein
XX -2 (hK2) have all been linked to prostate and breast cancers, and the
XX primers and probes of the invention are able to detect the abnormal
XX presence of mRNA expressed by their coding sequences in tissues other
XX than the prostate. This enables the presence of cancer to be perceived
XX and aids in the detection of metastases
XX Sequence 49 BP; 17 A; 10 C; 10 G; 12 T; 0 U; 0 Other;
Query Match 55.6%; Score 30; DB 3; Length 49;
Best Local Similarity 100.0%; Pred. No. 1.5e-06;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TAAATTAAATACGACTCACTATAGGGAGACT 30
DB 1 TAAATTAAATACGACTCACTATAGGGAGACT 30
RESULT 13
AAA76066
ID AAA76066 standard; DNA; 50 BP.
XX
XX AAA76066;
AC
XX 25-JAN-2001 (first entry)
DE Human prostate specific antigen PCR primer SEQ ID NO: 28.
XX Prostate specific antigen; PSA; prostate-specific membrane antigen; PSMA;
XX glandular kallikrein-2; hK2; prostate cancer; breast cancer; probe;
KW PCR primer; ss.
XX Homo sapiens.
XX WO200044940-A2.
XX 03-AUG-2000.
XX 28-JAN-2000; 2000WO-US002270.
XX 28-JAN-1999; 99US-0117640P.
XX (GENP-) GEN-PROBE INC.
XX Harvey RC, Clark TJ;
XX WPI; 2000-505986/45.
XX Detecting prostate-specific antigen (PSA), prostate specific membrane
XX antigen (PSMA) or human kallikrein 2 (hK2) nucleic acids in samples using
XX probe molecules, useful for the diagnosis of prostate and breast cancers.
XX Claim 1; Page 12; 77pp; English.
XX The present invention is concerned with the detection of nucleic acid

```

CC markers for prostate and breast cancer, and PCR primers and probes which  
CC are able to detect and quantify these markers. Prostate specific antigen  
CC (PSA), prostate-specific membrane antigen (PSMA) and glandular kallikrein  
CC -2 (hk2) have all been linked to prostate and breast cancers, and the  
CC primers and probes of the invention are able to detect the abnormal  
CC presence of mRNA expressed by their coding sequences in tissues other  
CC than the prostate. This enables the presence of cancer to be perceived  
CC and aids in the detection of metastases

XX SQ Sequence 50 BP; 16 A; 11 C; 11 G; 12 T; 0 U; 0 Other;

Query Match 55.6%; Score 30; DB 3; Length 50;  
Best Local Similarity 100.0%; Pred. No. 1.5e-06;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TAAATTAATACGACTCACTATAGGAGACT 30

DB 1 TAAATTAATACGACTCACTATAGGAGACT 30

## RESULT 14

AAA76211

ID AAA76211 standard; DNA; 52 BP.

XX AC AAA76211;

XX DT 25-JAN-2001 (first entry)

XX DE Human prostate specific antigen PCR primer SEQ ID NO: 40.

XX KW Prostate specific antigen; PSA; prostate-specific membrane antigen; PSMA;  
XX glandular kallikrein-2; hk2; prostate cancer; breast cancer; probe;  
XX PCR primer; ss.

XX OS Homo sapiens.

XX FN WO200044940-A2.

XX PD 03-AUG-2000.

XX PF 28-JAN-2000; 2000WO-US002270.

XX PR 28-JAN-1999; 99US-0117640P.

XX PA (GENP-) GEN-PROBE INC.

XX PI Harvey RC, Clark TJ;

XX DR WPI; 2000-505986/45.

XX PT Detecting prostate-specific antigen (PSA), prostate specific membrane  
XX antigen (PSMA) or human kallikrein 2 (hk2) nucleic acids in samples using  
XX probe molecules, useful for the diagnosis of prostate and breast cancers.

XX PS Claim 1; Page 13; 77pp; English.

XX CC The present invention is concerned with the detection of nucleic acid  
XX markers for prostate and breast cancer, and PCR primers and probes which  
XX are able to detect and quantify these markers. Prostate specific antigen  
XX (PSA), prostate-specific membrane antigen (PSMA) and glandular kallikrein  
XX -2 (hk2) have all been linked to prostate and breast cancers, and the  
XX primers and probes of the invention are able to detect the abnormal  
XX presence of mRNA expressed by their coding sequences in tissues other  
XX than the prostate. This enables the presence of cancer to be perceived  
XX and aids in the detection of metastases

XX SQ Sequence 52 BP; 17 A; 11 C; 11 G; 13 T; 0 U; 0 Other;

Query Match 55.6%; Score 30; DB 3; Length 52;  
Best Local Similarity 100.0%; Pred. No. 1.5e-06;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TAAATTAATACGACTCACTATAGGAGACT 30

DB 1 TAAATTAATACGACTCACTATAGGAGACT 30

## RESULT 15

ABZ59191

ID ABZ59191 standard; DNA; 45 BP.

XX AC ABZ59191;

XX DT 15-MAY-2003 (first entry)

XX DE LacZ RNA generating primer.

XX KW LacZ; gene expression; gene function; pharmaceutical; PCR; primer; ss.

XX OS Synthetic.

XX FN WO200268635-A2.

XX PD 06-SEP-2002.

XX PF 27-FEB-2002; 2002WO-EP002098.

XX PR 28-FEB-2001; 2001GB-00004948.

XX PA (NOVS ) NOVARTIS FORSCHUNGSSTIFTUNG ZWEIGNIEDERL.

XX PI Billy E, Filipowicz W, Mueller U;

XX DR WPI; 2002-706992/76.

XX PT Inhibiting expression of a target gene, useful for identifying gene  
XX function in an organism, comprises exposing a mammalian cell to a  
XX partially double-stranded ribonucleic acid with at least 60% sequence  
XX identity to a target gene.

XX PS Example 1; Page 16; 31pp; English.

XX CC The invention relates to inhibiting expression of a target gene. The  
XX method involves exposing a renewable, mammalian cell to a partially  
XX double-stranded ribonucleic acid and with at least 60% sequence identity  
XX to a target gene. The method is useful for identifying gene function in  
XX an organism, in determining potential targets for pharmaceuticals,  
XX and determining normal and pathological events associated with development,  
XX aging. The method may also be used to allow the inhibition of essential  
XX genes which may be required for cell or organism viability at particular  
XX stages of development or cellular compartments, and to allow addition or  
XX expression of RNA at specific times of development and locations in the  
XX organism without introducing permanent mutations into the target genome.  
XX The present sequence represents a PCR primer for generating a lacZ RNA,  
XX used in the preparation of dsRNA

XX SQ Sequence 45 BP; 15 A; 10 C; 10 G; 10 T; 0 U; 0 Other;

Query Match 53.7%; Score 29; DB 6; Length 45;  
Best Local Similarity 100.0%; Pred. No. 5.3e-06;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 TTAATACGACTCACTATAGGAGACTCAG 33

DB 1 TTAATACGACTCACTATAGGAGACTCAG 29

Search completed: May 26, 2004, 16:52:13  
Job time : 244.833 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 26, 2004, 16:02:51 ; Search time 45.5117 Seconds  
(without alignments)  
658.454 Million cell updates/sec

Title: US-09-121-239-1  
Perfect score: 54  
Sequence: 1 TAAATTAATAGACTACTA.....CCCTGAGGCTCAAGTCTAGA 54

Scoring table: OLIGO NUC  
Gapop 60.0 , Gapext 60.0

Searched: 682709 seqs, 277475446 residues

Word size : 0  
Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents NA.\*  
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3: /cgn2\_6/ptodata/2/ina/6A COMB.seq.\*  
4: /cgn2\_6/ptodata/2/ina/6B COMB.seq.\*  
5: /cgn2\_6/ptodata/2/ina/PTUS COMB.seq.\*  
6: /cgn2\_6/ptodata/2/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	49	90.7	50	4	US-09-168-947-45
2	32	59.3	54	4	US-09-493-491-29
3	32	59.3	54	4	US-09-493-491A-32
4	30	55.6	49	4	US-09-493-491-35
5	30	55.6	49	4	US-09-493-491A-38
6	30	55.6	50	4	US-09-493-491-28
7	30	55.6	50	4	US-09-493-491A-31
8	30	55.6	52	4	US-09-493-491-40
9	30	55.6	52	4	US-09-493-491A-43
10	29	53.7	37	1	US-08-099-867-5
11	29	53.7	50	3	US-08-972-799A-25
12	29	53.7	50	3	US-09-506-282-25
13	29	53.7	50	5	PCT-US95-03339-25
14	29	53.7	51	4	US-09-944-036-40
15	29	53.7	52	4	US-09-493-491-33
16	29	53.7	52	4	US-09-493-491-39
17	29	53.7	52	4	US-09-493-491A-36
18	29	53.7	52	4	US-09-493-491A-42
19	29	53.7	54	4	US-09-493-491-27
20	29	53.7	54	4	US-09-493-491-49
21	29	53.7	54	4	US-09-493-491A-30
22	29	53.7	54	4	US-09-493-491A-30
23	29	53.7	55	4	US-09-493-491-47
24	29	53.7	55	4	US-09-493-491A-47
25	29	53.7	60	1	US-08-099-867-7
26	29	53.7	79	1	US-08-099-867-3
27	29	53.7	180	1	US-08-099-867-1

28	51.9	28	4	US-09-493-491-41	Sequence 41, Appl
29	51.9	28	4	US-09-493-491A-44	Sequence 44, Appl
30	51.9	30	4	US-08-811-481-29	Sequence 29, Appl
31	51.9	30	4	US-09-876-527-29	Sequence 29, Appl
32	51.9	33	4	US-09-944-036-4	Sequence 4, Appl
33	51.9	33	4	US-09-738-274-36	Sequence 36, Appl
34	51.9	35	2	US-08-360-051A-22	Sequence 22, Appl
35	51.9	35	2	US-08-360-051A-24	Sequence 24, Appl
36	51.9	35	2	US-08-360-051A-27	Sequence 27, Appl
37	51.9	35	4	US-09-732-990-15	Sequence 15, Appl
38	51.9	35	4	US-09-202-972-15	Sequence 15, Appl
39	51.9	35	4	US-09-202-972-17	Sequence 17, Appl
40	51.9	36	3	US-08-955-636-7	Sequence 7, Appl
41	51.9	37	4	US-09-944-036-2	Sequence 2, Appl
42	51.9	41	4	US-09-425-585-15	Sequence 15, Appl
43	51.9	41	4	US-09-953-321-15	Sequence 15, Appl
44	51.9	47	3	US-08-678-735A-9	Sequence 9, Appl
45	51.9	47	4	US-08-418-992-9	Sequence 9, Appl

ALIGNMENTS

RESULT 1

US-09-168-947-45  
; Sequence 45, Application US/09168947  
; Patent No. 6589734  
; GENERAL INFORMATION:  
; APPLICANT: KACTAN, DANIEL L.  
; APPLICANT: FULTZ, TIMOTHY J.  
; APPLICANT: MCDONOUGH, SHERROL H.  
; TITLE OF INVENTION: DETECTION OF HIV  
; FILE REFERENCE: 218/130  
; CURRENT APPLICATION NUMBER: US/09/168,947  
; CURRENT FILING DATE: 1998-10-08  
; EARLIER APPLICATION NUMBER: 08/469,067  
; EARLIER FILING DATE: 1995-06-06  
; EARLIER APPLICATION NUMBER: 07/550,937  
; EARLIER FILING DATE: 1990-07-10  
; NUMBER OF SEQ ID NOS: 46  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 45  
; LENGTH: 50  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthesized nucleic acid molecule  
US-09-168-947-45

Query Match 90.7%; Score 49; DB 4; Length 50;  
Best Local Similarity 100.0%; Pred. No. 4.1e-18;  
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AATTAATAGACTACTATAGGAGACTCAGACCTGAGGCTCAAGTC 51  
|||||  
DB 2 AATTAATAGACTACTATAGGAGACTCAGACCTGAGGCTCAAGTC 50

RESULT 2

US-09-493-491-29  
; Sequence 29, Application US/09493491  
; Patent No. 6391556  
; GENERAL INFORMATION:  
; APPLICANT: HARVEY, Richard, C.  
; APPLICANT: CLARK, JR., Thomas, J.  
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FOR DETECTING GENETIC MARKERS  
; FILE REFERENCE: GP097-02.UT  
; CURRENT APPLICATION NUMBER: US/09/493,491  
; CURRENT FILING DATE: 2000-01-28  
; EARLIER APPLICATION NUMBER: 60/117,640 US  
; EARLIER FILING DATE: 1999-01-28  
; NUMBER OF SEQ ID NOS: 50

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 29

; LENGTH: 54

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: synthetic

; OTHER INFORMATION: construct

US-09-493-491-29

Query Match

Best Local Similarity 59.3%; Score 32; DB 4; Length 54;

Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

1 TAAATTAAATACGACTCACTATAGGGAGACTCA 32

Db

1 TAAATTAAATACGACTCACTATAGGGAGACTCA 32

RESULT 3

US-09-493-491A-32

; Sequence 32, Application US/09493491A

; Patent No. 6551778

; GENERAL INFORMATION:

; APPLICANT: HARVEY, Richard, C.

; APPLICANT: CLARK, JR., Thomas, J.

; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FOR DETECTING GENETIC MARKERS

; TITLE OF INVENTION: FOR CANCER IN A BIOLOGICAL SAMPLE

; FILE REFERENCE: GP097-02.UT

; CURRENT APPLICATION NUMBER: US/09/493,491A

; PRIOR FILING DATE: 2000-01-28

; PRIOR APPLICATION NUMBER: 60/117,640 US

; PRIOR FILING DATE: 1999-01-28

; NUMBER OF SEQ ID NOS: 50

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 32

; LENGTH: 54

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: synthetic

; OTHER INFORMATION: construct

; FEATURE:

; NAME/KEY: promoter

; LOCATION: (1)..(28)

US-09-493-491A-32

Query Match

Best Local Similarity 59.3%; Score 32; DB 4; Length 54;

Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

1 TAAATTAAATACGACTCACTATAGGGAGACTCA 32

Db

1 TAAATTAAATACGACTCACTATAGGGAGACTCA 32

RESULT 4

US-09-493-491-35

; Sequence 35, Application US/09493491

; Patent No. 6391556

; GENERAL INFORMATION:

; APPLICANT: HARVEY, Richard, C.

; APPLICANT: CLARK, JR., Thomas, J.

; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FOR DETECTING GENETIC MARKERS

; TITLE OF INVENTION: FOR CANCER IN A BIOLOGICAL SAMPLE

; FILE REFERENCE: GP097-02.UT

; CURRENT APPLICATION NUMBER: US/09/493,491

; PRIOR FILING DATE: 2000-01-28

; PRIOR APPLICATION NUMBER: 60/117,640 US

; PRIOR FILING DATE: 1999-01-28

; NUMBER OF SEQ ID NOS: 50

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 35

; LENGTH: 49

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: synthetic

; OTHER INFORMATION: construct

US-09-493-491-35

Query Match

Best Local Similarity 55.6%; Score 30; DB 4; Length 49;

Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

1 TAAATTAAATACGACTCACTATAGGGAGACT 30

Db

1 TAAATTAAATACGACTCACTATAGGGAGACT 30

RESULT 5

US-09-493-491A-38

; Sequence 38, Application US/09493491A

; Patent No. 6551778

; GENERAL INFORMATION:

; APPLICANT: HARVEY, Richard, C.

; APPLICANT: CLARK, JR., Thomas, J.

; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FOR DETECTING GENETIC MARKERS

; TITLE OF INVENTION: FOR CANCER IN A BIOLOGICAL SAMPLE

; FILE REFERENCE: GP097-02.UT

; CURRENT APPLICATION NUMBER: US/09/493,491A

; CURRENT FILING DATE: 2000-01-28

; PRIOR APPLICATION NUMBER: 60/117,640 US

; PRIOR FILING DATE: 1999-01-28

; NUMBER OF SEQ ID NOS: 50

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 38

; LENGTH: 49

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: synthetic

; OTHER INFORMATION: construct

; FEATURE:

; NAME/KEY: promoter

; LOCATION: (1)..(28)

US-09-493-491A-38

Query Match

Best Local Similarity 55.6%; Score 30; DB 4; Length 49;

Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

1 TAAATTAAATACGACTCACTATAGGGAGACT 30

Db

1 TAAATTAAATACGACTCACTATAGGGAGACT 30

RESULT 6

US-09-493-491-28

; Sequence 28, Application US/09493491

; Patent No. 6391556

; GENERAL INFORMATION:

; APPLICANT: HARVEY, Richard, C.

; APPLICANT: CLARK, JR., Thomas, J.

; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FOR DETECTING GENETIC MARKERS

; TITLE OF INVENTION: FOR CANCER IN A BIOLOGICAL SAMPLE

; FILE REFERENCE: GP097-02.UT

; CURRENT APPLICATION NUMBER: US/09/493,491

; CURRENT FILING DATE: 2000-01-28

; EARLIER APPLICATION NUMBER: 60/117,640 US

; EARLIER FILING DATE: 1999-01-28

; NUMBER OF SEQ ID NOS: 50

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 28

; LENGTH: 50

; TYPE: DNA

; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: construct  
US-09-493-491-28

Query Match 55.6%; Score 30; DB 4; Length 50;  
Best Local Similarity 100.0%; Pred. No. 1.2e-07;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TAAATTAATACGACTCACTATAGGAGACT 30  
|||||  
DB 1 TAAATTAATACGACTCACTATAGGAGACT 30

## RESULT 7

US-09-493-491A-31  
; Sequence 31, Application US/09493491A  
; Patent No. 6551778  
; GENERAL INFORMATION:  
; APPLICANT: HARVEY, Richard, C.  
; APPLICANT: CLARK, JR., Thomas, J.  
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FOR DETECTING GENETIC MARKERS  
; FILE REFERENCE: GP097-02.UT  
; CURRENT APPLICATION NUMBER: US/09/493,491A  
; CURRENT FILING DATE: 2000-01-28  
; PRIOR APPLICATION NUMBER: 60/117,640 US  
; PRIOR FILING DATE: 1999-01-28  
; NUMBER OF SEQ ID NOS: 50  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 31  
; LENGTH: 50  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: construct  
; NAME/KEY: promoter  
; LOCATION: (1)...(28)  
US-09-493-491A-31

Query Match 55.6%; Score 30; DB 4; Length 50;  
Best Local Similarity 100.0%; Pred. No. 1.2e-07;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TAAATTAATACGACTCACTATAGGAGACT 30  
|||||  
DB 1 TAAATTAATACGACTCACTATAGGAGACT 30

## RESULT 8

US-09-493-491-40  
; Sequence 40, Application US/09493491  
; Patent No. 6391556  
; GENERAL INFORMATION:  
; APPLICANT: HARVEY, Richard, C.  
; APPLICANT: CLARK, JR., Thomas, J.  
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FOR DETECTING GENETIC MARKERS  
; FILE REFERENCE: GP097-02.UT  
; CURRENT APPLICATION NUMBER: US/09/493,491  
; CURRENT FILING DATE: 2000-01-28  
; EARLIER APPLICATION NUMBER: 60/117,640 US  
; EARLIER FILING DATE: 1999-01-28  
; NUMBER OF SEQ ID NOS: 50  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 40  
; LENGTH: 52  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: construct  
US-09-493-491-40

Query Match 55.6%; Score 30; DB 4; Length 52;  
Best Local Similarity 100.0%; Pred. No. 1.2e-07;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TAAATTAATACGACTCACTATAGGAGACT 30  
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DB 1 TAAATTAATACGACTCACTATAGGAGACT 30

## RESULT 9

US-09-493-491A-43  
; Sequence 43, Application US/09493491A  
; Patent No. 6551778  
; GENERAL INFORMATION:  
; APPLICANT: HARVEY, Richard, C.  
; APPLICANT: CLARK, JR., Thomas, J.  
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FOR DETECTING GENETIC MARKERS  
; FILE REFERENCE: GP097-02.UT  
; CURRENT APPLICATION NUMBER: US/09/493,491A  
; CURRENT FILING DATE: 2000-01-28  
; PRIOR APPLICATION NUMBER: 60/117,640 US  
; PRIOR FILING DATE: 1999-01-28  
; NUMBER OF SEQ ID NOS: 50  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 43  
; LENGTH: 52  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: construct  
; NAME/KEY: promoter  
; LOCATION: (1)...(28)  
US-09-493-491A-43

Query Match 55.6%; Score 30; DB 4; Length 52;  
Best Local Similarity 100.0%; Pred. No. 1.2e-07;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TAAATTAATACGACTCACTATAGGAGACT 30  
|||||  
DB 1 TAAATTAATACGACTCACTATAGGAGACT 30

## RESULT 10

US-08-099-867-5  
; Sequence 5, Application US/08099867  
; Patent No. 5547862  
; GENERAL INFORMATION:  
; APPLICANT: James Meador  
; APPLICANT: Hoyt E. McElroy  
; APPLICANT: Michelle L. Herrmann  
; APPLICANT: Matthew Winkler  
; TITLE OF INVENTION: Vectors Containing Multiple Promoters  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: Arnold, White & Durkee  
; STREET: P. O. Box 4433  
; CITY: Houston  
; STATE: Texas  
; COUNTRY: USA  
; ZIP: 77210  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy Disk  
; COMPUTER: IBM PC Compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS

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/ SOFTWARE: ASCII-DOS
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/099,867
/ FILING DATE: 19930729
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: David L. Parker
/ REGISTRATION NUMBER: 32,165
/ REFERENCE/DOCKET NUMBER: AMB1:009/PAR
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (512) 320-7200
/ TELEFAX: (512) 474-7577
/ INFORMATION FOR SEQ ID NO: 5:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 37 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ US-08-099-867-5

Query Match          53.7%; Score 29; DB 1; Length 37;
Best Local Similarity 100.0%; Pred. No. 4.1e-07;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AATTAATACGACTCACTATAGGAGACTC 31
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Db 1 AATTAATACGACTCACTATAGGAGACTC 29

RESULT 11
US-08-972-799A-25
; Sequence 25, Application US/08972799A
; Patent No. 6087133
; GENERAL INFORMATION:
; APPLICANT: Dattagupta, Nanibhushan
; APPLICANT: Stull, Paul Douglas
; APPLICANT: Spingola, Marc
; APPLICANT: Kacian, Daniel Louis
; TITLE OF INVENTION: ISOTHERMAL STRAND
; TITLE OF INVENTION: DISPLACEMENT NUCLEIC
; TITLE OF INVENTION: ACID AMPLIFICATION
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Gen-Probe Incorporated
; STREET: 9880 Campus Point Drive
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/972,799A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION DATA: including application
; PRIOR APPLICATION DATA: described below:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Fisher, Carlos
; REGISTRATION NUMBER: 36,510
; REFERENCE/DOCKET NUMBER: GP94/001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-2807
; TELEFAX: (619) 452-5848
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 25:
; none
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/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 50
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ US-08-972-799A-25

Query Match          53.7%; Score 29; DB 3; Length 50;
Best Local Similarity 100.0%; Pred. No. 4.1e-07;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AAATTAATACGACTCACTATAGGAGACT 30
    |||||
Db 2 AAATTAATACGACTCACTATAGGAGACT 30

RESULT 12
US-09-506-282-25
; Sequence 25, Application US/09506282
; Patent No. 6214587
; GENERAL INFORMATION:
; APPLICANT: Dattagupta, Nanibhushan
; APPLICANT: Stull, Paul Douglas
; APPLICANT: Spingola, Marc
; APPLICANT: Kacian, Daniel Louis
; TITLE OF INVENTION: ISOTHERMAL STRAND DISPLACEMENT NUCLEIC
; TITLE OF INVENTION: ACID AMPLIFICATION
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Gen-Probe Incorporated
; STREET: 9880 Campus Point Drive
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/506,282
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/215,081
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Fisher, Carlos A.
; REGISTRATION NUMBER: 36,510
; REFERENCE/DOCKET NUMBER: GP94/001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-2807
; TELEFAX: (619) 452-5848
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 50
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
/ US-09-506-282-25

Query Match          53.7%; Score 29; DB 3; Length 50;
Best Local Similarity 100.0%; Pred. No. 4.1e-07;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AAATTAATACGACTCACTATAGGAGACT 30
    |||||
Db 2 AAATTAATACGACTCACTATAGGAGACT 30

RESULT 13
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PCT-US95-03339-25  
; Sequence 25, Application PC/TUS9503339  
; GENERAL INFORMATION:  
; APPLICANT:  
; TITLE OF INVENTION: ISOTHERMAL STRAND DISPLACEMENT NUCLEIC ACID  
; TITLE OF INVENTION: AMPLIFICATION  
; NUMBER OF SEQUENCES: 27  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)  
; CURRENT APPLICATION NUMBER: PCT/US95/03339  
; FILING DATE:  
; CLASSIFICATION:  
; INFORMATION FOR SEQ ID NO: 25:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 50 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
PCT-US95-03339-25

Query Match 53.7%; Score 29; DB 5; Length 50;  
Best Local Similarity 100.0%; Pred. No. 4.1e-07;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AAATTAATACGACTCACTATAGGAGACT 30  
|||||  
DB 2 AAATTAATACGACTCACTATAGGAGACT 30

RESULT 14  
US-09-944-036-40  
; Sequence 40, Application US/09944036  
; Patent No. 6582920  
; GENERAL INFORMATION:  
; APPLICANT: YANG, Yeasing Y.  
; APPLICANT: BRENTANO, Steven T.  
; APPLICANT: BABOLA, Odile  
; APPLICANT: TRAN, Nathalie  
; APPLICANT: VERNET, Guy  
; TITLE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF  
; FILE REFERENCE: GP114-02.UT  
; CURRENT APPLICATION NUMBER: US/09/944,036  
; CURRENT FILING DATE: 2001-08-31  
; PRIOR APPLICATION NUMBER: US 60/229,790  
; PRIOR FILING DATE: 2000-09-01  
; NUMBER OF SEQ ID NOS: 70  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 40  
; LENGTH: 51  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:  
; OTHER INFORMATION: Oligonucleotide primer for Reverse Transcriptase  
; OTHER INFORMATION: target sequence  
; NAME/KEY: promoter  
; LOCATION: (1)..(29)  
US-09-944-036-40

Query Match 53.7%; Score 29; DB 4; Length 51;  
Best Local Similarity 100.0%; Pred. No. 4.1e-07;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AAATTAATACGACTCACTATAGGAGACT 30  
|||||  
DB 1 AAATTAATACGACTCACTATAGGAGACT 29

RESULT 15  
US-09-493-491-33  
; Sequence 33, Application US/09493491  
; Patent No. 6391556  
; GENERAL INFORMATION:  
; APPLICANT: HARVEY, Richard, C.  
; APPLICANT: CLARK, JR., Thomas, J.  
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FOR DETECTING GENETIC MARKERS  
; TITLE OF INVENTION: FOR CANCER IN A BIOLOGICAL SAMPLE  
; FILE REFERENCE: GP097-02.UT  
; CURRENT APPLICATION NUMBER: US/09/493,491  
; CURRENT FILING DATE: 2000-01-28  
; EARLIER APPLICATION NUMBER: 60/117,640 US  
; EARLIER FILING DATE: 1999-01-28  
; NUMBER OF SEQ ID NOS: 50  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 33  
; LENGTH: 52  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: construct  
US-09-493-491-33

Query Match 53.7%; Score 29; DB 4; Length 52;  
Best Local Similarity 100.0%; Pred. No. 4.1e-07;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TAAATTAATACGACTCACTATAGGAGAC 29  
|||||  
DB 1 TAAATTAATACGACTCACTATAGGAGAC 29

Search completed: May 27, 2004, 02:25:08  
Job time : 46.5117 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 27, 2004, 11:30:47 ; Search time 284.177 Seconds  
(without alignments)  
864.392 Million cell updates/sec

Title: US-09-121-239-1

Perfect score: 54

Sequence: 1 TAAATATACGACTCACTA.....CCCTGAGGCTCAAGTCTAGA 54

Scoring table:

OLIGO NUC  
Gapop 60.0 , Gapext 60.0

Searched: 2960401 seqs, 2274450654 residues

Word size : 0

Total number of hits satisfying chosen parameters: 5920802

Minimum DB seq length: 0

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Post-processing: Listing first 45 summaries

Database : Published Applications NA.\*

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- 10: /cgn2\_6/ptodata/2/pubpna/US09B\_PUBCOMB.seq.\*
- 11: /cgn2\_6/ptodata/2/pubpna/US09C\_PUBCOMB.seq.\*
- 12: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq.\*
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- 19: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Length	ID	Description
1	49	90.7	50	15	US-10-244-490-45
2	32	59.3	54	15	US-10-273-707-32
3	30	55.6	49	15	US-10-273-707-38
4	30	55.6	50	15	US-10-273-707-31
5	30	55.6	52	15	US-10-273-707-43
6	29	53.7	51	9	US-09-944-036-40
7	29	53.7	51	16	US-10-425-975-40
8	29	53.7	52	15	US-10-273-707-36
9	29	53.7	52	15	US-10-273-707-42
10	29	53.7	54	15	US-10-273-707-30
11	29	53.7	54	15	US-10-273-707-49
12	29	53.7	55	15	US-10-273-707-47
13	29	53.7	6306	13	US-10-273-782-3
14	28	51.9	28	15	US-10-273-707-44

15	51.9	28	30	9	US-09-876-527-29	Sequence 29, Appl
16	51.9	28	15	33	US-10-124-089-29	Sequence 29, Appl
17	51.9	28	33	9	US-09-738-972-10	Sequence 10, Appl
18	51.9	28	33	9	US-09-944-036-4	Sequence 4, Appl
19	51.9	28	33	10	US-09-738-274-36	Sequence 36, Appl
20	51.9	28	33	14	US-10-001-407-29	Sequence 29, Appl
21	51.9	28	33	16	US-10-425-975-4	Sequence 4, Appl
22	51.9	28	35	9	US-09-202-972-15	Sequence 15, Appl
23	51.9	28	35	9	US-09-202-972-17	Sequence 17, Appl
24	51.9	28	35	10	US-09-897-776A-14	Sequence 14, Appl
25	51.9	28	35	10	US-09-897-776A-19	Sequence 19, Appl
26	51.9	28	36	13	US-09-803-810-7	Sequence 7, Appl
27	51.9	28	36	15	US-10-298-330-7	Sequence 7, Appl
28	51.9	28	37	9	US-09-944-036-2	Sequence 2, Appl
29	51.9	28	37	16	US-10-425-975-2	Sequence 2, Appl
30	51.9	28	39	12	US-10-651-563-9	Sequence 9, Appl
31	51.9	28	41	9	US-09-953-321-15	Sequence 15, Appl
32	51.9	28	49	15	US-10-273-707-37	Sequence 37, Appl
33	51.9	28	49	15	US-10-273-707-39	Sequence 39, Appl
34	51.9	28	50	15	US-10-273-707-40	Sequence 40, Appl
35	51.9	28	51	9	US-09-944-036-41	Sequence 41, Appl
36	51.9	28	51	15	US-10-273-707-41	Sequence 41, Appl
37	51.9	28	51	16	US-10-425-975-41	Sequence 41, Appl
38	51.9	28	52	9	US-09-944-036-39	Sequence 39, Appl
39	51.9	28	52	9	US-09-944-036-43	Sequence 43, Appl
40	51.9	28	52	10	US-09-738-274-12	Sequence 12, Appl
41	51.9	28	52	16	US-10-425-975-39	Sequence 39, Appl
42	51.9	28	52	16	US-10-425-975-43	Sequence 43, Appl
43	51.9	28	53	9	US-09-944-036-34	Sequence 34, Appl
44	51.9	28	53	9	US-09-944-036-35	Sequence 35, Appl
45	51.9	28	53	9	US-09-944-036-36	Sequence 36, Appl

ALIGNMENTS

RESULT 1

US-10-244-490-45  
; Sequence 45, Application US/10244490  
; Publication No. US20030152916A1  
; GENERAL INFORMATION:  
; APPLICANT: KACIAN, DANIEL L.  
; APPLICANT: FULTZ, TIMOTHY J.  
; APPLICANT: MCDONOUGH, SHERROL H.  
; TITLE OF INVENTION: DETECTION OF HIV  
; FILE REFERENCE: 218/130  
; CURRENT APPLICATION NUMBER: US/10/244,490  
; PRIOR FILING DATE: 2002-09-16  
; PRIOR APPLICATION NUMBER: US/09/168,947  
; PRIOR FILING DATE: 1998-10-08  
; PRIOR APPLICATION NUMBER: 08/469,067  
; PRIOR FILING DATE: 1995-06-06  
; PRIOR APPLICATION NUMBER: 07/550,837  
; PRIOR FILING DATE: 1990-07-10  
; NUMBER OF SEQ ID NOS: 46  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 45  
; LENGTH: 50  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthesized nucleic acid molecule  
US-10-244-490-45

Query Match 90.7% ; Score 49; DB 15; Length 50;

Best Local Similarity 100.0%; Pred. No. 3.4e-18; Mismatches 0; Indels 0; Gaps 0;

Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

3 AATTATACGACTCACTATAGGAGACTCAGACCTGAGGCTCAAGTC 51

2 AATTATACGACTCACTATAGGAGACTCAGACCTGAGGCTCAAGTC 50

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RESULT 2
US-10-273-707-32
; Sequence 32, Application US/10273707
; Publication No. US20030104448A1
; GENERAL INFORMATION:
; APPLICANT: HARVEY, Richard, C.
; APPLICANT: CLARK, JR., Thomas, J.
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FOR DETECTING GENETIC MARKERS
; TITLE OF INVENTION: FOR CANCER IN A BIOLOGICAL SAMPLE
; FILE REFERENCE: GP097-03.DV1
; CURRENT APPLICATION NUMBER: US/10/273,707
; CURRENT FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: 09/493,491
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/117,640 US
; PRIOR FILING DATE: 1999-01-28
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 32
; LENGTH: 54
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: construct
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (1)..(28)
US-10-273-707-32

Query Match          59.3%; Score 32; DB 15; Length 54;
Best Local Similarity 100.0%; Pred. No. 2e-08;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TAAATTAAATACGACTCACTATAGGAGACTCA 32
Db 1 TAAATTAAATACGACTCACTATAGGAGACTCA 32

RESULT 3
US-10-273-707-38
; Sequence 38, Application US/10273707
; Publication No. US20030104448A1
; GENERAL INFORMATION:
; APPLICANT: HARVEY, Richard, C.
; APPLICANT: CLARK, JR., Thomas, J.
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FOR DETECTING GENETIC MARKERS
; TITLE OF INVENTION: FOR CANCER IN A BIOLOGICAL SAMPLE
; FILE REFERENCE: GP097-03.DV1
; CURRENT APPLICATION NUMBER: US/10/273,707
; CURRENT FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: 09/493,491
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/117,640 US
; PRIOR FILING DATE: 1999-01-28
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 38
; LENGTH: 49
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: construct
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (1)..(28)
US-10-273-707-38

Query Match          55.6%; Score 30; DB 15; Length 49;
Best Local Similarity 100.0%; Pred. No. 2.8e-07;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 TAAATTAAATACGACTCACTATAGGAGACT 30
Db 1 TAAATTAAATACGACTCACTATAGGAGACT 30

RESULT 4
US-10-273-707-31
; Sequence 31, Application US/10273707
; Publication No. US20030104448A1
; GENERAL INFORMATION:
; APPLICANT: HARVEY, Richard, C.
; APPLICANT: CLARK, JR., Thomas, J.
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FOR DETECTING GENETIC MARKERS
; TITLE OF INVENTION: FOR CANCER IN A BIOLOGICAL SAMPLE
; FILE REFERENCE: GP097-03.DV1
; CURRENT APPLICATION NUMBER: US/10/273,707
; CURRENT FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: 09/493,491
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/117,640 US
; PRIOR FILING DATE: 1999-01-28
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 31
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: construct
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (1)..(28)
US-10-273-707-31

Query Match          55.6%; Score 30; DB 15; Length 50;
Best Local Similarity 100.0%; Pred. No. 2.8e-07;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TAAATTAAATACGACTCACTATAGGAGACT 30
Db 1 TAAATTAAATACGACTCACTATAGGAGACT 30

RESULT 5
US-10-273-707-43
; Sequence 43, Application US/10273707
; Publication No. US20030104448A1
; GENERAL INFORMATION:
; APPLICANT: HARVEY, Richard, C.
; APPLICANT: CLARK, JR., Thomas, J.
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FOR DETECTING GENETIC MARKERS
; TITLE OF INVENTION: FOR CANCER IN A BIOLOGICAL SAMPLE
; FILE REFERENCE: GP097-03.DV1
; CURRENT APPLICATION NUMBER: US/10/273,707
; CURRENT FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: 09/493,491
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/117,640 US
; PRIOR FILING DATE: 1999-01-28
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 43
; LENGTH: 52
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: construct
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (1)..(28)
US-10-273-707-43
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Query Match      55.6%; Score 30; DB 15; Length 52;
Best Local Similarity 100.0%; Pred. No. 2.8e-07;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TAAATTAATACGACTCACTATAGGAGACT 30
   |||||||||||||||||||||||||||||||
DB 1 TAAATTAATACGACTCACTATAGGAGACT 30

RESULT 6
US-09-944-036-40
; Sequence 40, Application US/09944036
; Patent No. US2002005095A1
; GENERAL INFORMATION:
; APPLICANT: YANG, Yeasing Y.
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: BABOLA, Odile
; APPLICANT: TRAN, Nathalie
; APPLICANT: VERNET, Guy
; TITLE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF
; FILE REFERENCE: GP114-02.UT
; CURRENT FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/229,790
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 40
; LENGTH: 51
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Oligonucleotide primer for Reverse Transcriptase
; NAME/KEY: promoter
; LOCATION: (1)..(29)
US-09-944-036-40

Query Match      53.7%; Score 29; DB 9; Length 51;
Best Local Similarity 100.0%; Pred. No. 1.1e-06;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AAATTAATACGACTCACTATAGGAGACT 30
   |||||||||||||||||||||||||||||||
DB 1 AAATTAATACGACTCACTATAGGAGACT 29

RESULT 7
US-10-425-975-40
; Sequence 40, Application US/10425975
; Publication No. US2003022857A1
; GENERAL INFORMATION:
; APPLICANT: YANG, Yeasing Y.
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: BABOLA, Odile
; APPLICANT: TEAN, Nathalie
; APPLICANT: VERNET, Guy
; TITLE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF
; FILE REFERENCE: GP114-02.UT
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US/09/944,036
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/229,790
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 40
; LENGTH: 51
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; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Oligonucleotide primer for Reverse Transcriptase
; OTHER INFORMATION: target sequence
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (1)..(29)
US-10-425-975-40

Query Match      53.7%; Score 29; DB 16; Length 51;
Best Local Similarity 100.0%; Pred. No. 1.1e-06;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AAATTAATACGACTCACTATAGGAGACT 30
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DB 1 AAATTAATACGACTCACTATAGGAGACT 29

RESULT 8
US-10-273-707-36
; Sequence 36, Application US/10273707
; Publication No. US20030104448A1
; GENERAL INFORMATION:
; APPLICANT: HARVEY, Richard, C.
; APPLICANT: CLARK, JR., Thomas, J.
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FOR DETECTING GENETIC MARKERS
; FILE REFERENCE: GP097-03.DV1
; CURRENT APPLICATION NUMBER: US/10/273,707
; CURRENT FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: 09/493,491
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/117,640 US
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 36
; LENGTH: 52
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: construct
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (1)..(28)
US-10-273-707-36

Query Match      53.7%; Score 29; DB 15; Length 52;
Best Local Similarity 100.0%; Pred. No. 1.1e-06;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TAAATTAATACGACTCACTATAGGAGACT 29
   |||||||||||||||||||||||||||||||
DB 1 TAAATTAATACGACTCACTATAGGAGACT 29

RESULT 9
US-10-273-707-42
; Sequence 42, Application US/10273707
; Publication No. US20030104448A1
; GENERAL INFORMATION:
; APPLICANT: HARVEY, Richard, C.
; APPLICANT: CLARK, JR., Thomas, J.
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FOR DETECTING GENETIC MARKERS
; FILE REFERENCE: GP097-03.DV1
; CURRENT APPLICATION NUMBER: US/10/273,707
; CURRENT FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: 09/493,491
; PRIOR FILING DATE: 2000-01-28
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; FILE REFERENCE: GP097-03.DV1  
; CURRENT APPLICATION NUMBER: 60/117,640 US  
; PRIOR FILING DATE: 1999-01-28  
; NUMBER OF SEQ ID NOS: 50  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 42  
; LENGTH: 52  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: construct  
; NAME/KEY: promoter  
; LOCATION: (1)..(28)  
US-10-273-707-42

Query Match 53.7%; Score 29; DB 15; Length 52;  
Best Local Similarity 100.0%; Pred. No. 1.1e-06;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TAAATTAAATACGACTCACTATAGGGAGAC 29  
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Db 1 TAAATTAAATACGACTCACTATAGGGAGAC 29

RESULT 10  
US-10-273-707-30  
; Sequence 30, Application US/10273707  
; Publication No. US20030104448A1  
; GENERAL INFORMATION:  
; APPLICANT: HARVEY, Richard, C.  
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FOR DETECTING GENETIC MARKERS  
; TITLE OF INVENTION: FOR CANCER IN A BIOLOGICAL SAMPLE  
; FILE REFERENCE: GP097-03.DV1  
; CURRENT APPLICATION NUMBER: US/10/273,707  
; PRIOR FILING DATE: 2002-10-17  
; PRIOR APPLICATION NUMBER: 09/493,491  
; PRIOR FILING DATE: 2000-01-28  
; PRIOR APPLICATION NUMBER: 60/117,640 US  
; PRIOR FILING DATE: 1999-01-28  
; NUMBER OF SEQ ID NOS: 50  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 30  
; LENGTH: 54  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: construct  
; NAME/KEY: promoter  
; LOCATION: (1)..(28)  
US-10-273-707-30

Query Match 53.7%; Score 29; DB 15; Length 54;  
Best Local Similarity 100.0%; Pred. No. 1.1e-06;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TAAATTAAATACGACTCACTATAGGGAGAC 29  
|||||  
Db 1 TAAATTAAATACGACTCACTATAGGGAGAC 29

RESULT 11  
US-10-273-707-49  
; Sequence 49, Application US/10273707  
; Publication No. US20030104448A1  
; GENERAL INFORMATION:  
; APPLICANT: HARVEY, Richard, C.  
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FOR DETECTING GENETIC MARKERS  
; TITLE OF INVENTION: FOR CANCER IN A BIOLOGICAL SAMPLE

; FILE REFERENCE: GP097-03.DV1  
; CURRENT APPLICATION NUMBER: US/10/273,707  
; PRIOR FILING DATE: 2002-10-17  
; PRIOR APPLICATION NUMBER: 09/493,491  
; PRIOR FILING DATE: 2000-01-28  
; PRIOR APPLICATION NUMBER: 60/117,640 US  
; PRIOR FILING DATE: 1999-01-28  
; NUMBER OF SEQ ID NOS: 50  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 49  
; LENGTH: 54  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: construct  
; NAME/KEY: promoter  
; LOCATION: (1)..(28)  
US-10-273-707-49

Query Match 53.7%; Score 29; DB 15; Length 54;  
Best Local Similarity 100.0%; Pred. No. 1.1e-06;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TAAATTAAATACGACTCACTATAGGGAGAC 29  
|||||  
Db 1 TAAATTAAATACGACTCACTATAGGGAGAC 29

RESULT 12  
US-10-273-707-47  
; Sequence 47, Application US/10273707  
; Publication No. US20030104448A1  
; GENERAL INFORMATION:  
; APPLICANT: HARVEY, Richard, C.  
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FOR DETECTING GENETIC MARKERS  
; TITLE OF INVENTION: FOR CANCER IN A BIOLOGICAL SAMPLE  
; FILE REFERENCE: GP097-03.DV1  
; CURRENT APPLICATION NUMBER: US/10/273,707  
; PRIOR FILING DATE: 2002-10-17  
; PRIOR APPLICATION NUMBER: 09/493,491  
; PRIOR FILING DATE: 2000-01-28  
; PRIOR APPLICATION NUMBER: 60/117,640 US  
; PRIOR FILING DATE: 1999-01-28  
; NUMBER OF SEQ ID NOS: 50  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 47  
; LENGTH: 55  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: construct  
; NAME/KEY: promoter  
; LOCATION: (1)..(28)  
US-10-273-707-47

Query Match 53.7%; Score 29; DB 15; Length 55;  
Best Local Similarity 100.0%; Pred. No. 1.1e-06;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TAAATTAAATACGACTCACTATAGGGAGAC 29  
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Db 1 TAAATTAAATACGACTCACTATAGGGAGAC 29

RESULT 13  
US-09-833-782-3  
; Sequence 3, Application US/09833782  
; Publication No. US20020040131A1

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; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Wilganowski, Nathaniel L.
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: Novel Human Metalloprotease and Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0161-USA
; CURRENT APPLICATION NUMBER: US/09/833,782
; CURRENT FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: US 60/196,319
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 6306
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-833-782-3

Query Match      53.7%; Score 29; DB 13; Length 6306;
Best Local Similarity 100.0%; Pred. No. 1.2e-06;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AAATTAATACGACTCACTATAGGGAGACT 30
DB 86 AAATTAATACGACTCACTATAGGGAGACT 114

RESULT 14
US-10-273-707-44
; Sequence 44, Application US/10273707
; Publication No. US2003010448A1
; GENERAL INFORMATION:
; APPLICANT: HARVEY, Richard, C.
; APPLICANT: CLARK, JR., Thomas, J.
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FOR DETECTING GENETIC MARKERS
; FILE REFERENCE: GP097-03.DVI
; CURRENT APPLICATION NUMBER: US/10/273,707
; CURRENT FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: 09/493,491
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/117,640 US
; PRIOR FILING DATE: 1999-01-28
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 44
; LENGTH: 28
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: construct
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (1)..(28)
US-10-273-707-44

Query Match      51.9%; Score 28; DB 15; Length 28;
Best Local Similarity 100.0%; Pred. No. 3.9e-06;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TAAATTAATACGACTCACTATAGGGAGA 28
DB 1 TAAATTAATACGACTCACTATAGGGAGA 28

RESULT 15
US-09-876-527-29
; Sequence 29, Application US/09876527
; Patent No. US20020102616A1
; GENERAL INFORMATION:
; APPLICANT: Kindsvogel, Wayne
; APPLICANT: Jelinek, Laura J.

```

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; Sheppard, Paul O.
; Hagopian, William A.
; LaGasse, James M.
; TITLE OF INVENTION: ISLET CELL ANTIGEN 1851
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Zymogenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/876,527
; FILING DATE: 07-Jun-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/811,481
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Lingenfelter, Susan
; REGISTRATION NUMBER: P-41,156
; REFERENCE/DOCKET NUMBER: 95-36
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6675
; TELEFAX: 206-442-6678
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; IMMEDIATE SOURCE:
; CLONE: ZC11197
; SEQUENCE DESCRIPTION: SEQ ID NO: 29:
US-09-876-527-29

Query Match      51.9%; Score 28; DB 9; Length 30;
Best Local Similarity 100.0%; Pred. No. 3.9e-06;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AAATTAATACGACTCACTATAGGGAGAC 29
DB 1 AAATTAATACGACTCACTATAGGGAGAC 28

Search completed: May 27, 2004, 14:58:24
Job time : 284.177 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 26, 2004, 15:22:41 ; Search time 1906.62 Seconds  
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Title: US-09-121-239-1  
Perfect score: 54  
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Searched: 27513289 seqs, 14931090276 residues

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Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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7: em\_estro:\*

8: em\_htc:\*

9: gb\_est1:\*

10: gb\_est2:\*

11: gb\_hic:\*

12: gb\_est3:\*

13: gb\_est4:\*

14: gb\_est5:\*

15: em\_estfun:\*

16: em\_estom:\*

17: em\_gss\_hum:\*

18: em\_gss\_inv:\*

19: em\_gss\_pin:\*

20: em\_gss\_vrt:\*

21: em\_gss\_fun:\*

22: em\_gss\_nam:\*

23: em\_gss\_mus:\*

24: em\_gss\_pro:\*

25: em\_gss\_rod:\*

26: em\_gss\_phg:\*

27: em\_gss\_vrl:\*

28: gb\_gsa1:\*

29: gb\_gsa2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	29	53.7	560	29	CC966861 BOIFL85TR
C 2	29	53.7	571	29	CC964269 BOIEN76TR
C 3	29	53.7	585	29	CC947693 BOISQ41TR
C 4	29	53.7	592	29	CC961654 BOIDB28TR

## RESULT 1

CC966861/c

LOCUS

DEFINITION

ACCSSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

CC966861 560 bp DNA linear GSS 18-AUG-2003  
BOIFL85TR BO\_1.4\_1.6\_KB\_nuc Brassica oleracea genomic clone  
BOIFL85, genomic survey sequence.

CC966861

GSS

Brassica oleracea

Brassica oleracea

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

1 (bases 1 to 560)

Town,C.D., Van Aken,S., Utterback,T., Koo,H. and Fraser,C.M.

Whole genome shotgun sequencing of Brassica oleracea

Unpublished (2001)

Contact: Chris Town

TIGR

9712 Medical Center Drive, Rockville, MD 20850, USA.

Tel: 301-838-3523

Fax: 301-838-0208

Email: cdtown@tigr.org

DNA is from a doubled haploid provided by Tom Osborn.

Seq primer: TR

Class: sheared ends.

Location/Qualifiers

## FEATURES

## ALIGNMENTS

C	5	29	53.7	604	29	CC952121	CC952121 BOIB185TR
C	6	29	53.7	610	29	CC948768	CC948768 BOIDG32TR
C	7	29	53.7	612	29	CC947463	CC947463 BOIGK06TR
C	8	29	53.7	617	29	CC967304	CC967304 BOIFK41TR
C	9	29	53.7	621	29	CC968451	CC968451 BOIFB27TR
C	10	29	53.7	642	29	CC944751	CC944751 BOIBU81TR
C	11	29	53.7	642	29	CC946396	CC946396 BOICQ54TR
C	12	29	53.7	644	29	CC949404	CC949404 BOIGZ19TR
C	13	29	53.7	644	29	CC951454	CC951454 BOIBAG62TR
C	14	29	53.7	649	29	CC962886	CC962886 BOIGN54TR
C	15	29	53.7	651	29	CC961061	CC961061 BOICK68TR
C	16	29	53.7	684	29	CC945503	CC945503 BOIDK74TR
C	17	29	53.7	687	29	CC948738	CC948738 BOIFI28TR
C	18	29	53.7	688	29	CC944195	CC944195 BOIBL59TR
C	19	29	53.7	693	29	CC944485	CC944485 BOIHL39TR
C	20	29	53.7	705	29	CC951566	CC951566 BOIEJ65TR
C	21	29	53.7	705	29	CC958824	CC958824 BOIBM11TR
C	22	29	53.7	718	29	CC954347	CC954347 BOIBW60TR
C	23	29	53.7	719	29	CC968802	CC968802 BOICJ62TR
C	24	29	53.7	727	29	CC969001	CC969001 BOICR93TR
C	25	29	53.7	735	29	CC958105	CC958105 BOIGX30TR
C	26	29	53.7	735	29	CC961701	CC961701 BOIQD39TR
C	27	29	53.7	830	29	CC953502	CC953502 BOICE19TR
C	28	29	53.7	830	29	CC968053	CC968053 BOIGT40TR
C	29	29	53.7	859	29	CC958532	CC958532 BOIFG34TR
C	30	28	51.9	143	13	BQ102727	BQ102727 UUGC0111
C	31	28	51.9	181	10	BE391582	BE391582 601282148
C	32	28	51.9	182	10	BE262878	BE262878 601148014
C	33	28	51.9	183	10	BF976190	BF976190 602245057
C	34	28	51.9	185	10	BE314661	BE314661 601146777
C	35	28	51.9	188	12	BG475075	BG475075 602491094
C	36	28	51.9	195	10	BE397962	BE397962 601290494
C	37	28	51.9	203	10	BF974085	BF974085 602240343
C	38	28	51.9	204	10	BE410828	BE410828 601301490
C	39	28	51.9	206	10	BE398063	BE398063 601290252
C	40	28	51.9	227	10	BF027436	BF027436 601672556
C	41	28	51.9	267	13	BQ102748	BQ102748 UUGC0132
C	42	28	51.9	272	10	BE391744	BE391744 601282029
C	43	28	51.9	310	13	BQ102753	BQ102753 UUGC0137
C	44	28	51.9	329	13	BQ102710	BQ102710 UUGC0094
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/clone_lib="BO 1.4 1.6 KB nuc"
/notes="Vector: PHOS2; Site 1: BstXI; 1.4-1.6 kb sheared
nuclear DNA inserted into PHOS2 using BstXI linkers"

ORIGIN
Query Match 53.7%; Score 29; DB 29; Length 560;
Best Local Similarity 100.0%; Pred. No. 8.1e-06;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AATTAATACGACTCACTATAGGAGACTC 31
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Db 177 AATTAATACGACTCACTATAGGAGACTC 149

RESULT 2
CC964269/c
LOCUS
DEFINITION BOIEN76TR BO 1.4 1.6 KB nuc Brassica oleracea genomic clone
ACCESSION CC964269
VERSION BOIEN76, genomic survey sequence.
KEYWORDS
SOURCE
ORGANISM Brassica oleracea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE 1 (bases 1 to 571)
AUTHORS Town,C.D., Van Aken,S., Utterback,T., Koo,H. and Fraser,C.M.
TITLE Whole genome shotgun sequencing of Brassica oleracea
JOURNAL Unpublished (2001)
COMMENT Contact: Chris Town
TIGR 9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TR
Class: sheared ends.
Location/Qualifiers
1. .571
/organism="Brassica oleracea"
/mol_type="genomic DNA"
/strain="TO1000DH3"
/db_xref="taxon:3712"
/clone_lib="BO 1.4 1.6 KB nuc"
/notes="Vector: PHOS2; Site 1: BstXI; 1.4-1.6 kb sheared
nuclear DNA inserted into PHOS2 using BstXI linkers"

ORIGIN
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Best Local Similarity 100.0%; Pred. No. 8.2e-06;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AATTAATACGACTCACTATAGGAGACTC 31
|||||
Db 177 AATTAATACGACTCACTATAGGAGACTC 149

RESULT 4
CC961654/c
LOCUS
DEFINITION BOIDB28TR BO 1.4 1.6 KB nuc Brassica oleracea genomic clone
ACCESSION CC961654
VERSION BOIDB28, genomic survey sequence.
KEYWORDS
SOURCE
ORGANISM Brassica oleracea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE 1 (bases 1 to 592)
AUTHORS Town,C.D., Van Aken,S., Utterback,T., Koo,H. and Fraser,C.M.
TITLE Whole genome shotgun sequencing of Brassica oleracea
JOURNAL Unpublished (2001)
COMMENT Contact: Chris Town
TIGR 9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TR
Class: sheared ends.
Location/Qualifiers
1. .592
/organism="Brassica oleracea"
/mol_type="genomic DNA"
/strain="TO1000DH3"
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FEATURES
source
1. .592
/organism="Brassica oleracea"
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/strain="TO1000DH3"
/db_xref="taxon:3712"

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/clone="BOIDB28"
/clone_lib="BO_1.4_1.6_KB_nuc"
/notes="Vector: pHOS2; Site 1: BstXI; 1.4-1.6 kb sheared
nuclear DNA inserted into pHOS2 using BstXI linkers"

ORIGIN
Query Match      53.7%; Score 29; DB 29; Length 592;
Best Local Similarity 100.0%; Pred. No. 8.2e-06;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AATTAATACGACTCACTATAGGAGACTC 31
|||||
Db 184 AATTAATACGACTCACTATAGGAGACTC 156

RESULT 5
CC952121/c
LOCUS CC952121 BO_1.4_1.6_KB_nuc DNA linear GSS 18-AUG-2003
DEFINITION BOIB185, genomic survey sequence.
ACCESSION CC952121
VERSION CC952121.1 GI:33790560
KEYWORDS GSS.
SOURCE Brassica oleracea
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE 1 (bases 1 to 604)
AUTHORS Town,C.D., Van Aken,S., Utterback,T., Koo,H. and Fraser,C.M.
TITLE Whole genome shotgun sequencing of Brassica oleracea
JOURNAL Unpublished (2001)
COMMENT Other GSSs: BOIB185TF
Contact: Chris Town
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Other GSSs: BOIB185TF
Contact: Chris Town
TIGR
Class: sheared ends.
Location/Qualifiers
1..604
/organism="Brassica oleracea"
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/clone="BOIB185"

FEATURES
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1..604
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/clone="BOIB185"

ORIGIN
Query Match      53.7%; Score 29; DB 29; Length 604;
Best Local Similarity 100.0%; Pred. No. 8.2e-06;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AATTAATACGACTCACTATAGGAGACTC 31
|||||
Db 185 AATTAATACGACTCACTATAGGAGACTC 157

RESULT 6
CC948768/c
LOCUS CC948768 BO_1.4_1.6_KB_nuc Brassica oleracea genomic clone
DEFINITION BOIDG32, genomic survey sequence.
ACCESSION CC948768
VERSION CC948768.1 GI:33783814
KEYWORDS GSS.
SOURCE Brassica oleracea
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE 1 (bases 1 to 610)
AUTHORS Town,C.D., Van Aken,S., Utterback,T., Koo,H. and Fraser,C.M.
TITLE Whole genome shotgun sequencing of Brassica oleracea
JOURNAL Unpublished (2001)
COMMENT Other GSSs: BOIGK06TF
Contact: Chris Town
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Other GSSs: BOIGK06TF
Contact: Chris Town
TIGR
Class: sheared ends.
Location/Qualifiers
1..610
/organism="Brassica oleracea"
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/clone="BOIGK06"

FEATURES
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ORIGIN
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Best Local Similarity 100.0%; Pred. No. 8.2e-06;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AATTAATACGACTCACTATAGGAGACTC 31
|||||
Db 270 AATTAATACGACTCACTATAGGAGACTC 242

RESULT 7
CC947463/c
LOCUS CC947463 BO_1.4_1.6_KB_nuc Brassica oleracea genomic clone
DEFINITION BOIGK06, genomic survey sequence.
ACCESSION CC947463
VERSION CC947463.1 GI:33781217
KEYWORDS GSS.
SOURCE Brassica oleracea
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE 1 (bases 1 to 612)
AUTHORS Town,C.D., Van Aken,S., Utterback,T., Koo,H. and Fraser,C.M.
TITLE Whole genome shotgun sequencing of Brassica oleracea
JOURNAL Unpublished (2001)
COMMENT Other GSSs: BOIGK06TF
Contact: Chris Town
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Other GSSs: BOIGK06TF
Contact: Chris Town
TIGR
Class: sheared ends.
Location/Qualifiers
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ORIGIN
Query Match      53.7%; Score 29; DB 29; Length 612;
Best Local Similarity 100.0%; Pred. No. 8.2e-06;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AATTAATACGACTCACTATAGGAGACTC 31
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Db 270 AATTAATACGACTCACTATAGGAGACTC 242

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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE 1 (bases 1 to 610)
AUTHORS Town,C.D., Van Aken,S., Utterback,T., Koo,H. and Fraser,C.M.
TITLE Whole genome shotgun sequencing of Brassica oleracea
JOURNAL Unpublished (2001)
COMMENT Other GSSs: BOIDG32TF
Contact: Chris Town
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TR
Class: sheared ends.
Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 8.2e-06;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AATTAATACGACTCACTATAGGAGACTC 31
|||||
Db 270 AATTAATACGACTCACTATAGGAGACTC 242

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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE 1 (bases 1 to 610)
AUTHORS Town,C.D., Van Aken,S., Utterback,T., Koo,H. and Fraser,C.M.
TITLE Whole genome shotgun sequencing of Brassica oleracea
JOURNAL Unpublished (2001)
COMMENT Other GSSs: BOIDG32TF
Contact: Chris Town
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TR
Class: sheared ends.
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Best Local Similarity 100.0%; Pred. No. 8.2e-06;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AATTAATACGACTCACTATAGGAGACTC 31
|||||
Db 270 AATTAATACGACTCACTATAGGAGACTC 242

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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE 1 (bases 1 to 612)
AUTHORS Town,C.D., Van Aken,S., Utterback,T., Koo,H. and Fraser,C.M.
TITLE Whole genome shotgun sequencing of Brassica oleracea
JOURNAL Unpublished (2001)
COMMENT Other GSSs: BOIGK06TF
Contact: Chris Town
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Other GSSs: BOIGK06TF
Contact: Chris Town
TIGR
Class: sheared ends.
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Best Local Similarity 100.0%; Pred. No. 8.2e-06;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AATTAATACGACTCACTATAGGAGACTC 31
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Db 270 AATTAATACGACTCACTATAGGAGACTC 242

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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE 1 (bases 1 to 612)
AUTHORS Town,C.D., Van Aken,S., Utterback,T., Koo,H. and Fraser,C.M.
TITLE Whole genome shotgun sequencing of Brassica oleracea
JOURNAL Unpublished (2001)
COMMENT Other GSSs: BOIGK06TF
Contact: Chris Town
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Other GSSs: BOIGK06TF
Contact: Chris Town
TIGR
Class: sheared ends.
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Best Local Similarity 100.0%; Pred. No. 8.2e-06;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AATTAATACGACTCACTATAGGAGACTC 31
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Db 270 AATTAATACGACTCACTATAGGAGACTC 242

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/notes="Vector: pPOS2; Site 1: BstXI; 1.4-1.6 kb sheared
nuclear DNA inserted into pPOS2 using BstXI linkers"

ORIGIN
Query Match      53.7%; Score 29; DB 29; Length 612;
Best Local Similarity 100.0%; Pred. No. 8.2e-06;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AATTATACGACTCACTATAGGAGACTC 31
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Db 317 AATTATACGACTCACTATAGGAGACTC 289

RESULT 8
CC967304/c
LOCUS BO1FK41TR BO_1.4_1.6_KB_nuc Brassica oleracea genomic clone
DEFINITION BO1FK41, genomic survey sequence.
ACCESSION CC967304
VERSION CC967304.1 GI:33820392
KEYWORDS GSS.
SOURCE Brassica oleracea
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE 1 (bases 1 to 617)
AUTHORS Town,C.D., Van Aken,S., Utterback,T., Koo,H. and Fraser,C.M.
TITLE Whole genome shotgun sequencing of Brassica oleracea
JOURNAL Unpublished (2001)
COMMENT Contact: Chris Town
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TR
Class: sheared ends.

FEATURES
Location/Qualifiers
source 1..617
/mol_type="genomic DNA"
/strain="TO1000DH3"
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nuclear DNA inserted into pPOS2 using BstXI linkers"

ORIGIN
Query Match      53.7%; Score 29; DB 29; Length 612;
Best Local Similarity 100.0%; Pred. No. 8.3e-06;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AATTATACGACTCACTATAGGAGACTC 31
    |||
Db 187 AATTATACGACTCACTATAGGAGACTC 159

RESULT 10
CC944751/c
LOCUS BO1BU81R BO_1.4_1.6_KB_nuc Brassica oleracea genomic clone
DEFINITION BO1BU81, genomic survey sequence.
ACCESSION CC944751
VERSION CC944751.1 GI:33777617
KEYWORDS GSS.
SOURCE Brassica oleracea
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE 1 (bases 1 to 642)
AUTHORS Town,C.D., Van Aken,S., Utterback,T., Koo,H. and Fraser,C.M.
TITLE Whole genome shotgun sequencing of Brassica oleracea
JOURNAL Unpublished (2001)
COMMENT Contact: Chris Town
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TR
Class: sheared ends.

FEATURES
Location/Qualifiers
source 1..642
/mol_type="genomic DNA"
/strain="TO1000DH3"
/db_xref="taxon:3712"
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nuclear DNA inserted into pPOS2 using BstXI linkers"

ORIGIN
Query Match      53.7%; Score 29; DB 29; Length 642;
Best Local Similarity 100.0%; Pred. No. 8.3e-06;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AATTATACGACTCACTATAGGAGACTC 31
    |||
Db 324 AATTATACGACTCACTATAGGAGACTC 296

RESULT 9
CC968451/c
LOCUS BO1FB27TR BO_1.4_1.6_KB_nuc Brassica oleracea genomic clone
DEFINITION BO1FB27, genomic survey sequence.
ACCESSION CC968451
VERSION CC968451.1 GI:33822676
KEYWORDS GSS.
SOURCE Brassica oleracea
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

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REFERENCE 1 (bases 1 to 621)
AUTHORS Town,C.D., Van Aken,S., Utterback,T., Koo,H. and Fraser,C.M.
TITLE Whole genome shotgun sequencing of Brassica oleracea
JOURNAL Unpublished (2001)
COMMENT Contact: Chris Town
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TR
Class: sheared ends.

FEATURES
Location/Qualifiers
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/mol_type="genomic DNA"
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nuclear DNA inserted into pPOS2 using BstXI linkers"

ORIGIN
Query Match      53.7%; Score 29; DB 29; Length 621;
Best Local Similarity 100.0%; Pred. No. 8.3e-06;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AATTATACGACTCACTATAGGAGACTC 31
    |||
Db 187 AATTATACGACTCACTATAGGAGACTC 159

RESULT 10
CC944751/c
LOCUS BO1BU81R BO_1.4_1.6_KB_nuc Brassica oleracea genomic clone
DEFINITION BO1BU81, genomic survey sequence.
ACCESSION CC944751
VERSION CC944751.1 GI:33777617
KEYWORDS GSS.
SOURCE Brassica oleracea
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE 1 (bases 1 to 642)
AUTHORS Town,C.D., Van Aken,S., Utterback,T., Koo,H. and Fraser,C.M.
TITLE Whole genome shotgun sequencing of Brassica oleracea
JOURNAL Unpublished (2001)
COMMENT Contact: Chris Town
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TR
Class: sheared ends.

FEATURES
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nuclear DNA inserted into pPOS2 using BstXI linkers"

ORIGIN
Query Match      53.7%; Score 29; DB 29; Length 642;

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Best Local Similarity 100.0%; Pred. No. 8.3e-06;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AATTAATACGACTCACTATAGGAGACTC 31
Db 323 AATTAATACGACTCACTATAGGAGACTC 295

RESULT 11
CC946396 642 bp DNA linear GSS 18-AUG-2003
LOCUS BOICQ54TR BO_1.4_1.6_KB_nuc Brassica oleracea genomic clone
DEFINITION BOICQ54, genomic survey sequence.
ACCESSION CC946396
VERSION CC946396.1 GI:33779262
KEYWORDS GSS.
SOURCE Brassica oleracea
ORGANISM Brassica oleracea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE 1 (bases 1 to 642)
AUTHORS Town,C.D., Van Aken,S., Utterback,T., Koo,H. and Fraser,C.M.
TITLE Whole genome shotgun sequencing of Brassica oleracea
JOURNAL Unpublished (2001)
COMMENT Other_GSSs: BOICQ54TF
Contact: Chris Town
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TR
Class: sheared ends.

FEATURES
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nuclear DNA inserted into pHOS2 using BstXI linkers"

ORIGIN
Query Match 53.7%; Score 29; DB 29; Length 642;
Best Local Similarity 100.0%; Pred. No. 8.3e-06;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Best Local Similarity 100.0%; Pred. No. 8.3e-06;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AATTAATACGACTCACTATAGGAGACTC 31
Db 184 AATTAATACGACTCACTATAGGAGACTC 156

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CC949404/c
LOCUS BOIGZ19TR BO_1.4_1.6_KB_nuc Brassica oleracea genomic clone
DEFINITION BOIGZ19, genomic survey sequence.
ACCESSION CC949404
VERSION CC949404.1 GI:33785090
KEYWORDS GSS.
SOURCE Brassica oleracea
ORGANISM Brassica oleracea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE 1 (bases 1 to 644)
AUTHORS Town,C.D., Van Aken,S., Utterback,T., Koo,H. and Fraser,C.M.
TITLE Whole genome shotgun sequencing of Brassica oleracea
JOURNAL Unpublished (2001)

```

```

COMMENT
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TR
Class: sheared ends.

FEATURES
Location/Qualifiers
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/note="Vector: pHOS2; Site 1: BstXI; 1.4-1.6 kb sheared
nuclear DNA inserted into pHOS2 using BstXI linkers"

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Query Match 53.7%; Score 29; DB 29; Length 644;
Best Local Similarity 100.0%; Pred. No. 8.3e-06;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AATTAATACGACTCACTATAGGAGACTC 31
Db 177 AATTAATACGACTCACTATAGGAGACTC 149

RESULT 13
CC951454/c
LOCUS BOIEA62TR BO_1.4_1.6_KB_nuc Brassica oleracea genomic clone
DEFINITION BOIEA62, genomic survey sequence.
ACCESSION CC951454
VERSION CC951454.1 GI:33789233
KEYWORDS GSS.
SOURCE Brassica oleracea
ORGANISM Brassica oleracea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE 1 (bases 1 to 644)
AUTHORS Town,C.D., Van Aken,S., Utterback,T., Koo,H. and Fraser,C.M.
TITLE Whole genome shotgun sequencing of Brassica oleracea
JOURNAL Unpublished (2001)
COMMENT Contact: Chris Town
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TR
Class: sheared ends.

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/note="Vector: pHOS2; Site 1: BstXI; 1.4-1.6 kb sheared
nuclear DNA inserted into pHOS2 using BstXI linkers"

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Best Local Similarity 100.0%; Pred. No. 8.3e-06;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      307 AATTAATACGACTCACTATAGGAGACTC 279

RESULT 14
CC962886/c
LOCUS      649 bp      DNA      linear      GSS 18-AUG-2003
DEFINITION BOIGN54TR BO 1.4 1.6 KB nuc Brassica oleracea genomic clone
ACCESSION  CC962886
VERSION     CC962886.1 GI:33811706
KEYWORDS   GSS.
SOURCE     Brassica oleracea
ORGANISM   Brassica oleracea
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE  1 (bases 1 to 649)
AUTHORS   Town,C.D., Van Aken,S., Utterback,T., Koo,H. and Fraser,C.M.
TITLE     Whole genome shotgun sequencing of Brassica oleracea
JOURNAL   Unpublished (2001)
COMMENT   Contact: Chris Town
            TIGR
            9712 Medical Center Drive, Rockville, MD 20850, USA.
            Tel: 301-838-3523
            Fax: 301-838-0208
            Email: cdtown@tigr.org
            DNA is from a doubled haploid provided by Tom Osborn.
            Seq primer: TR
            Class: sheared ends.
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Best Local Similarity 100.0%; Pred. No. 8.4e-06;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 AATTAATACGACTCACTATAGGAGACTC 31
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Db      184 AATTAATACGACTCACTATAGGAGACTC 156

Search completed: May 26, 2004, 22:44:18
Job time : 1909.62 secs

Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TR
Class: sheared ends.
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Best Local Similarity 100.0%; Pred. No. 8.4e-06;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 AATTAATACGACTCACTATAGGAGACTC 31
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Search completed: May 26, 2004, 22:44:18
Job time : 1909.62 secs

Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TR
Class: sheared ends.
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Best Local Similarity 100.0%; Pred. No. 8.4e-06;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 AATTAATACGACTCACTATAGGAGACTC 31
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Db      184 AATTAATACGACTCACTATAGGAGACTC 156

RESULT 15
CC961061/c
LOCUS      651 bp      DNA      linear      GSS 18-AUG-2003
DEFINITION BOICX68TR BO 1.4 1.6 KB nuc Brassica oleracea genomic clone
ACCESSION  CC961061
VERSION     CC961061.1 GI:33808062
KEYWORDS   GSS.
SOURCE     Brassica oleracea
ORGANISM   Brassica oleracea
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE  1 (bases 1 to 651)
AUTHORS   Town,C.D., Van Aken,S., Utterback,T., Koo,H. and Fraser,C.M.
TITLE     Whole genome shotgun sequencing of Brassica oleracea
JOURNAL   Unpublished (2001)
COMMENT   Contact: Chris Town
            TIGR
            9712 Medical Center Drive, Rockville, MD 20850, USA.
            Tel: 301-838-3523
            Fax: 301-838-0208
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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: May 26, 2004, 16:00:31 ; Search time 1149.26 Seconds  
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Title: US-09-121-239-3

Perfect score: 54

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Scoring table: OLIGO NUC

Gapop\_60.0 , Gapext 60.0

Searched: 3470272 seqs, 21671516995 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

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13: gb\_un:

14: gb\_vi:

15: em\_ba:

16: em\_fun:

17: em\_hum:

18: em\_in:

19: em\_mu:

20: em\_om:

21: em\_or:

22: em\_ov:

23: em\_pat:

24: em\_ph:

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29: em\_vi:

30: em\_htg\_hum:

31: em\_htg\_inv:

32: em\_htg\_other:

33: em\_htg\_mus:

34: em\_htg\_pln:

35: em\_htg\_rod:

36: em\_htg\_mam:

37: em\_htg\_vrt:

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39: em\_htgo\_hum:

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41: em\_htgo\_other:

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

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C 2	54	100.0	54	6	BD222524	Methods f
C 3	54	100.0	54	6	BD222525	Methods f
C 4	54	100.0	54	6	BD222526	Methods f
C 5	49	90.7	50	6	AR352057	Sequence
C 6	32	59.3	54	6	BD236957	AR32057 Nucleic a
C 7	32	59.3	54	6	AR307443	Sequence
C 8	30	55.6	49	6	BD236963	BD236963 Nucleic a
C 9	30	55.6	49	6	AR307449	Sequence
C 10	30	55.6	50	6	BD236956	Nucleic a
C 11	30	55.6	50	6	AR307442	Sequence
C 12	30	55.6	52	6	BD236968	Nucleic a
C 13	30	55.6	52	6	AR307454	Sequence
C 14	29	53.7	37	6	I25071	Sequence 5
C 15	29	53.7	45	6	AX575411	Sequence
C 16	29	53.7	50	6	AR102985	Sequence
C 17	29	53.7	51	6	AR344851	Sequence
C 18	29	53.7	51	6	AX397806	Sequence
C 19	29	53.7	52	6	BD236961	Nucleic a
C 20	29	53.7	52	6	BD236967	Nucleic a
C 21	29	53.7	52	6	AR307447	Sequence
C 22	29	53.7	52	6	AR307453	Sequence
C 23	29	53.7	54	6	BD236955	Nucleic a
C 24	29	53.7	54	6	BD236974	Nucleic a
C 25	29	53.7	54	6	AR307441	Sequence
C 26	29	53.7	54	6	AR307460	Sequence
C 27	29	53.7	55	6	BD236972	Nucleic a
C 28	29	53.7	55	6	AR307458	Sequence
C 29	29	53.7	60	6	I25073	Sequence 7
C 30	29	53.7	79	6	I25069	Sequence 3
C 31	29	53.7	180	6	I25067	Sequence 1
C 32	29	53.7	586	6	AX701716	Sequence
C 33	29	53.7	1440	6	AX701737	Sequence
C 34	29	53.7	3073	12	CVU02284	Cloning vec
C 35	29	53.7	6306	6	AX286493	Sequence
C 36	29	53.7	7201	6	AX800664	Sequence
C 37	29	53.7	7231	6	AX806466	Sequence
C 38	29	53.7	7297	6	AX806467	Sequence
C 39	29	53.7	7429	6	AX839727	Sequence
C 40	29	53.7	7456	6	AX806465	Sequence
C 41	28	51.9	28	6	BD236969	Nucleic a
C 42	28	51.9	28	6	AR307455	Sequence
C 43	28	51.9	30	6	AR369578	Sequence
C 44	28	51.9	30	6	AR404157	Sequence
C 45	28	51.9	33	6	AR344815	Sequence

ALIGNMENTS

RESULT 1  
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LOCUS BD222523 54 bp DNA linear PAT 17-JUL-2003  
DEFINITION Methods for detecting and measuring spliced nucleic acids.  
ACCESSION BD222523  
VERSION BD222523.1 GI:33032293  
KEYWORDS JP 2002521037-A/1.  
SOURCE synthetic construct  
ORGANISM artificial sequences.  
REFERENCE 1 (bases 1 to 54)  
AUTHORS Harvey, R.C. and Eastman, P.S.  
TITLE Methods for detecting and measuring spliced nucleic acids  
JOURNAL Patent: JP 2002521037-A 1 16-JUL-2002;  
GEN PROBE INC

```
COMMENT OS Artificial Sequence
PN JP 2002521037-A/1
PD 16-JUL-2002
PF 23-JUL-1999 JP 2000561364
PI RICHARD C HARVEY, PAUL S EASTMAN
PC C1201/68, C12N15/09, C12N15/00
CC Description of Artificial Sequence: Synthetic promoter primer
CC promoter sequence at residues 1-27
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FT /organism="Artificial Sequence".

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Best Local Similarity 100.0%; Pred. No. 1.1e-20;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 54 TCTGACTTTGAGCCTCAGGCTCTGAGTCTCCCTATAGTGCCTATTAATTAA 1

RESULT 2
LOCUS BD222524/c 54 bp RNA linear PAT 17-JUL-2003
DEFINITION Methods for detecting and measuring spliced nucleic acids.
ACCESSION BD222524
VERSION BD222524.1 GI:33032294
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 54)
AUTHORS Harvey, R.C. and Eastman, P.S.
TITLE Methods for detecting and measuring spliced nucleic acids
JOURNAL Patent: JP 2002521037-A 2 16-JUL-2002;
GEN PROBE INC
COMMENT OS Artificial Sequence
PN JP 2002521037-A/2
PD 16-JUL-2002
PF 23-JUL-1999 JP 2000561364
PI RICHARD C HARVEY, PAUL S EASTMAN
PC C1201/68, C12N15/09, C12N15/00
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Db 54 TCTGACTTTGAGCCTCAGGCTCTGAGTCTCCCTATAGTGCCTATTAATTAA 1

RESULT 3
LOCUS BD222525 54 bp DNA linear PAT 17-JUL-2003
DEFINITION Methods for detecting and measuring spliced nucleic acids.
ACCESSION BD222525
VERSION BD222525.1 GI:33032295
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 54)
AUTHORS Harvey, R.C. and Eastman, P.S.
TITLE Methods for detecting and measuring spliced nucleic acids
JOURNAL Patent: JP 2002521037-A 3 16-JUL-2002;
GEN PROBE INC
COMMENT OS Artificial Sequence
PN JP 2002521037-A/3
PD 16-JUL-2002
PF 23-JUL-1999 JP 2000561364
PI RICHARD C HARVEY, PAUL S EASTMAN
PC C1201/68, C12N15/09, C12N15/00
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FT /organism="Artificial Sequence".

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Best Local Similarity 100.0%; Pred. No. 1.1e-20;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCTGACTTTGAGCCTCAGGCTCTGAGTCTCCCTATAGTGCCTATTAATTAA 54
Db 1 TCTGACTTTGAGCCTCAGGCTCTGAGTCTCCCTATAGTGCCTATTAATTAA 54

RESULT 4
LOCUS BD222526 54 bp RNA linear PAT 17-JUL-2003
DEFINITION Methods for detecting and measuring spliced nucleic acids.
ACCESSION BD222526
VERSION BD222526.1 GI:33032296
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 54)
AUTHORS Harvey, R.C. and Eastman, P.S.
TITLE Methods for detecting and measuring spliced nucleic acids
JOURNAL Patent: JP 2002521037-A 4 16-JUL-2002;
GEN PROBE INC
COMMENT OS Artificial Sequence
PN JP 2002521037-A/4
PD 16-JUL-2002
PF 23-JUL-1999 JP 2000561364
PI RICHARD C HARVEY, PAUL S EASTMAN
PC C1201/68, C12N15/09, C12N15/00
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FT /organism="Artificial Sequence".

FEATURES
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Best Local Similarity 100.0%; Pred. No. 1.1e-20;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 54 TCTGACTTTGAGCCTCAGGCTCTGAGTCTCCCTATAGTGCCTATTAATTAA 1
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Query Match 100.0%; Score 54; DB 6; Length 54;  
Best Local Similarity 100.0%; Pred. No. 1.1e-20;  
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RESULT 5  
AR352057/c  
LOCUS AR352057 50 bp DNA linear PAT 17-AUG-2003  
DEFINITION Sequence 45 from patent US 6589734.  
ACCESSION AR352057  
VERSION AR352057.1 GI:33757020  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 50)  
AUTHORS Kacian,D.L., Fultz,T.J. and McDonough,S.H.  
TITLE Detection of HIV  
JOURNAL Patent: US 6589734-A 45 08-JUL-2003;  
FEATURES Location/Qualifiers  
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Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 50 GACTTTGAGCCTCAGGCTCTGAGTCTCCCTATAGTCGATTAATT 2

RESULT 6  
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LOCUS BD236957 54 bp DNA linear PAT 17-JUL-2003  
DEFINITION Nucleic acid sequence for detecting genetic marker for cancer in biological samples.  
ACCESSION BD236957  
VERSION BD236957.1 GI:33046727  
KEYWORDS JP 2002535014-A/32.  
SOURCE synthetic construct  
ORGANISM synthetic construct  
artificial sequences.

REFERENCE 1 (bases 1 to 54)  
AUTHORS Harvey,R.C. and Jr,T.J.C.  
TITLE Nucleic acid sequence for detecting genetic marker for cancer in biological samples  
JOURNAL Patent: JP 2002535014-A 32 22-OCT-2002;  
COMMENT OS Artificial Sequence  
PN JP 2002535014-A/32  
PD 22-OCT-2002  
PR 28-JAN-2000 JP 2000596180  
PI RICHARD C HARVEY,THOMAS J CLARK JR  
PC C12N15/09,C12Q1/68,C12N15/00  
CC Description of Artificial Sequence: synthetic construct FH  
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Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 32 TGAGTCTCCCTATAGTCGATTAATTAA 1

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LOCUS AR307443 54 bp DNA linear PAT 12-JUN-2003  
DEFINITION Sequence 32 from patent US 6551778.  
ACCESSION AR307443  
VERSION AR307443.1 GI:31697982  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 54)  
AUTHORS Harvey,R.C. and Clark,T.J. Jr.  
TITLE Nucleic acid sequences for detecting genetic markers for cancer in a biological sample  
JOURNAL Patent: US 6551778-A 32 22-APR-2003;  
FEATURES Location/Qualifiers  
source  
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## ORIGIN

Query Match 59.3%; Score 32; DB 6; Length 54;  
Best Local Similarity 100.0%; Pred. No. 1e-07;  
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 32 TGAGTCTCCCTATAGTCGATTAATTAA 1

RESULT 8  
BD236963/c  
LOCUS BD236963 49 bp DNA linear PAT 17-JUL-2003  
DEFINITION Nucleic acid sequence for detecting genetic marker for cancer in biological samples.  
ACCESSION BD236963  
VERSION BD236963.1 GI:33046733  
KEYWORDS JP 2002535014-A/38.  
SOURCE synthetic construct  
ORGANISM synthetic construct  
artificial sequences.

REFERENCE 1 (bases 1 to 49)  
AUTHORS Harvey,R.C. and Jr,T.J.C.  
TITLE Nucleic acid sequence for detecting genetic marker for cancer in biological samples  
JOURNAL Patent: JP 2002535014-A 38 22-OCT-2002;  
COMMENT OS Artificial Sequence  
PN JP 2002535014-A/38  
PD 22-OCT-2002  
PR 28-JAN-2000 JP 2000596180  
PI RICHARD C HARVEY,THOMAS J CLARK JR  
PC C12N15/09,C12Q1/68,C12N15/00  
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Location/Qualifiers  
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1..49

## ORIGIN

Query Match 55.6%; Score 30; DB 6; Length 49;  
Best Local Similarity 100.0%; Pred. No. 1.5e-06;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 25 AGTCTCCCTATAGTGAGTCGTATTAATTTA 54  
|||||  
Db 30 AGTCTCCCTATAGTGAGTCGTATTAATTTA 1

## RESULT 9

AR307449/c  
LOCUS AR307449 49 bp DNA linear PAT 12-JUN-2003

DEFINITION Sequence 38 from patent US 6551778.

ACCESSION AR307449

VERSION AR307449.1 GI:31697988

KEYWORDS

SOURCE Unknown.

ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 49)

AUTHORS Harvey, R.C. and Clark, T.J., Jr.

TITLE Nucleic acid sequences for detecting genetic markers for cancer in

a biological sample

JOURNAL Patent: US 6551778-A 38 22-APR-2003;

FEATURES Location/Qualifiers

source 1..49

/organism="unknown"

/mol\_type="genomic DNA"

ORIGIN

Query Match 55.6%; Score 30; DB 6; Length 49;  
Best Local Similarity 100.0%; Pred. No. 1.5e-06;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 25 AGTCTCCCTATAGTGAGTCGTATTAATTTA 54  
|||||  
Db 30 AGTCTCCCTATAGTGAGTCGTATTAATTTA 1

## RESULT 10

BD236956/c  
LOCUS BD236956 50 bp DNA linear PAT 17-JUL-2003

DEFINITION Nucleic acid sequence for detecting genetic marker for cancer in

biological samples.

ACCESSION BD236956

VERSION BD236956.1 GI:33046726

KEYWORDS JP 2002535014-A/31.

SOURCE synthetic construct

ORGANISM artificial sequences.

REFERENCE 1 (bases 1 to 50)

AUTHORS Harvey, R.C. and Jr, T.J.C.

TITLE Nucleic acid sequence for detecting genetic marker for cancer in

biological samples

JOURNAL Patent: JP 2002535014-A 31 22-OCT-2002;

COMMENT GEN PROBE INC

OS Artificial Sequence

PN JP 2002535014-A/31

PD 22-OCT-2002

PF 28-JAN-2000 JP 2000596180

PR 28-JAN-1999 US 60/117640

PI RICHARD C HARVEY, THOMAS J CLARK JR

PC C12N15/09, C12Q1/68, C12N15/00

CC Description of Artificial Sequence: synthetic construct PH

Key Location/Qualifiers

FT promoter (1)..(28).

Location/Qualifiers

source 1..50

/organism="synthetic construct"

/mol\_type="genomic DNA"

/db\_xref="taxon:32630"

ORIGIN

Query Match 55.6%; Score 30; DB 6; Length 50;  
Best Local Similarity 100.0%; Pred. No. 1.5e-06;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 25 AGTCTCCCTATAGTGAGTCGTATTAATTTA 54  
|||||  
Db 30 AGTCTCCCTATAGTGAGTCGTATTAATTTA 1

## RESULT 11

AR307442/c  
LOCUS AR307442 50 bp DNA linear PAT 12-JUN-2003

DEFINITION Sequence 31 from patent US 6551778.

ACCESSION AR307442

VERSION AR307442.1 GI:31697981

KEYWORDS

SOURCE Unknown.

ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 50)

AUTHORS Harvey, R.C. and Clark, T.J., Jr.

TITLE Nucleic acid sequences for detecting genetic markers for cancer in

a biological sample

JOURNAL Patent: US 6551778-A 31 22-APR-2003;

FEATURES Location/Qualifiers

source 1..50

/organism="unknown"

/mol\_type="genomic DNA"

ORIGIN

Query Match 55.6%; Score 30; DB 6; Length 50;  
Best Local Similarity 100.0%; Pred. No. 1.5e-06;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 25 AGTCTCCCTATAGTGAGTCGTATTAATTTA 54  
|||||  
Db 30 AGTCTCCCTATAGTGAGTCGTATTAATTTA 1

## RESULT 12

BD236968/c  
LOCUS BD236968 52 bp DNA linear PAT 17-JUL-2003

DEFINITION Nucleic acid sequence for detecting genetic marker for cancer in

biological samples.

ACCESSION BD236968

VERSION BD236968.1 GI:33046738

KEYWORDS JP 2002535014-A/43.

SOURCE synthetic construct

ORGANISM artificial sequences.

REFERENCE 1 (bases 1 to 52)

AUTHORS Harvey, R.C. and Jr, T.J.C.

TITLE Nucleic acid sequence for detecting genetic marker for cancer in

biological samples

JOURNAL Patent: JP 2002535014-A 43 22-OCT-2002;

COMMENT GEN PROBE INC

OS Artificial Sequence

PN JP 2002535014-A/43

PD 22-OCT-2002

PF 28-JAN-2000 JP 2000596180

PR 28-JAN-1999 US 60/117640

PI RICHARD C HARVEY, THOMAS J CLARK JR

PC C12N15/09, C12Q1/68, C12N15/00

CC Description of Artificial Sequence: synthetic construct PH

Key Location/Qualifiers

FT promoter (1)..(28).

Location/Qualifiers

source 1..52

/organism="synthetic construct"

/mol\_type="genomic DNA"

/db\_xref="taxon:32630"

ORIGIN

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Query Match      55.6%; Score 30; DB 6; Length 52;
Best Local Similarity 100.0%; Pred. No. 1.5e-06;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 25 AGTCCTCCCTATAGTAGTCGTATTATTTA 54
    |||
Db 30 AGTCCTCCCTATAGTAGTCGTATTATTTA 1

RESULT 13
LOCUS AR307454/c
DEFINITION Sequence 43 from patent US 6551778.
ACCESSION AR307454
VERSION AR307454.1 GI:31697993
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 52)
AUTHORS Harvey,R.C. and Clark,T.J. Jr.
TITLE Nucleic acid sequences for detecting genetic markers for cancer in
a biological sample
JOURNAL Patent: US 6551778-A 43 22-APR-2003;
FEATURES Location/Qualifiers
    source
        1..52
            /organism="unknown"
            /mol_type="genomic DNA"
ORIGIN

Query Match      55.6%; Score 30; DB 6; Length 52;
Best Local Similarity 100.0%; Pred. No. 1.5e-06;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 25 AGTCCTCCCTATAGTAGTCGTATTATTTA 54
    |||
Db 30 AGTCCTCCCTATAGTAGTCGTATTATTTA 1

RESULT 14
LOCUS I25071/c
DEFINITION Sequence 5 from patent US 5547862.
ACCESSION I25071
VERSION I25071.1 GI:1604941
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 37)
AUTHORS Meador,J., McElroy,H.E., Herrmann,M.L. and Winkler,M.
TITLE Vectors containing multiple promoters in the same orientation
JOURNAL Patent: US 5547862-A 5 20-AUG-1996;
FEATURES Location/Qualifiers
    source
        1..37
            /organism="unknown"
            /mol_type="unassigned DNA"
ORIGIN

Query Match      53.7%; Score 29; DB 6; Length 37;
Best Local Similarity 100.0%; Pred. No. 6.3e-06;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 GAGTCTCCCTATAGTAGTCGTATTAAATT 52
    |||
Db 29 GAGTCTCCCTATAGTAGTCGTATTAAATT 1

RESULT 15
LOCUS AX575411/c
DEFINITION Sequence 4 from Patent WO02068635.
ACCESSION AX575411
```

---

```
VERSION AX575411.1 GI:27552050
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Billy,E., Filipowicz,W. and Mueller,U.
TITLE Methods of inhibiting expression of a target gene in mammalian
cells
JOURNAL Novartis Forschungsstiftung Zweigniederlassung (CH)
FEATURES Location/Qualifiers
    source
        1..45
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="oligonucleotide"
ORIGIN

Query Match      53.7%; Score 29; DB 6; Length 45;
Best Local Similarity 100.0%; Pred. No. 6.1e-06;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 CTGAGTCTCCCTATAGTAGTCGTATTAA 50
    |||
Db 29 CTGAGTCTCCCTATAGTAGTCGTATTAA 1

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Job time : 1149.26 secs
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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: May 26, 2004, 14:55:11 ; Search time 240.833 Seconds  
(without alignments)  
952.539 Million cell updates/sec

Title: US-09-121-239-3  
Perfect score: 54  
Sequence: 1 TCTGACTTGACCTCAGGG.....TAGTGAGTCGTATTAAATTA 54

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 3373863 seqs, 2124099041 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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1: Geneseqn1980s:\*  
2: Geneseqn1990s:\*  
3: Geneseqn2000s:\*  
4: Geneseqn2001as:\*  
5: Geneseqn2001bs:\*  
6: Geneseqn2002s:\*  
7: Geneseqn2003as:\*  
8: Geneseqn2003bs:\*  
9: Geneseqn2003cs:\*  
10: Geneseqn2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	54	100.0	54	AAZ60843	Aaz60843 Oligonucleotide
2	54	100.0	54	AAZ60841	Aaz60841 Oligonucleotide
3	54	100.0	54	AAZ60840	Aaz60840 Oligonucleotide
4	54	100.0	54	AAZ60842	Aaz60842 Oligonucleotide
5	49	90.7	50	AAQ86626	Aaq86626 CML chrom
6	49	90.7	50	AAT15571	Aat15571 CML-2 chr
7	49	90.7	50	AAT42417	Aat42417 CML chrom
8	49	90.7	50	AAV66349	Aav66349 CML-2 chr
9	49	90.7	50	AAZ623191	Aaz623191 CML chrom
10	49	90.7	50	AAZ62600	Aaz62600 CML chrom
11	32	59.3	54	AAZ60843	Aaz60843 Human pro
12	30	55.6	49	AAZ6206	Aaz6206 Human pro
13	30	55.6	49	AAZ60843	Aaz60843 Human pro
14	30	55.6	49	AAZ6206	Aaz6206 Human pro
15	29	53.7	45	ABZ59191	Abz59191 LacZ RNA
16	29	53.7	50	AAZ623191	Aaz623191 T7 gene 1
17	29	53.7	51	ABK531140	Abk531140 HIV-1 rev
18	29	53.7	51	AAZ6206	Aaz6206 HIV-1 pol
19	29	53.7	52	AAZ6210	Aaz6210 Human pro
20	29	53.7	52	AAZ6204	Aaz6204 Human pro
21	29	53.7	54	AAZ6220	Aaz6220 Human pro
22	29	53.7	54	AAZ60843	Aaz60843 Human pro
23	29	53.7	55	AAZ6218	Aaz6218 Human pro

C 24	29	53.7	180	2	AAT41733	Aat41733 Promoter
C 25	29	53.7	1442	7	ABZ70392	Abz70392 Autofluor
C 26	29	53.7	6306	6	ABA03923	Aba03923 Human NHP
C 27	29	53.7	7201	8	ACF05731	Acf05731 Plasmid p
C 28	29	53.7	7231	8	ACF06299	Acf06299 Plasmid p
C 29	29	53.7	7297	8	ACF06300	Acf06300 SigptdIPA
C 30	29	53.7	7429	8	ACF05558	Acf05558 Plasmid p
C 31	29	53.7	7456	8	ACF06298	Acf06298 Plasmid p
C 32	28	51.9	28	3	AAA76212	Aaa76212 Human pro
C 33	28	51.9	30	2	AAT95233	Aat95233 Macaque s
C 34	28	51.9	33	4	AAD11020	Aad11020 Bacteriop
C 35	28	51.9	33	4	AAD11286	Aad11286 Bacteriop
C 36	28	51.9	33	6	ABK53104	Abk53104 T7 promot
C 37	28	51.9	33	6	ABK93905	Abk93905 Human imm
C 38	28	51.9	33	6	AAZ60843	Aaz60843 Bacteriop
C 39	28	51.9	35	2	AAV05796	Aav05796 Primer fo
C 40	28	51.9	35	2	AAV05794	Aav05794 Primer fo
C 41	28	51.9	35	6	AAZ50495	Aal50495 3-frame H
C 42	28	51.9	35	8	ADA24416	Ada24416 His-tag v
C 43	28	51.9	36	4	AAC64735	Aac64735 Human pro
C 44	28	51.9	36	6	ABQ81381	Abq81381 Human pro
C 45	28	51.9	36	9	ADB71188	Adb71188 Human pro

## ALIGNMENTS

RESULT 1  
AAZ60843  
ID AAZ60843 standard; RNA; 54 BP.  
XX  
AC AAZ60843;  
XX  
DT 16-MAY-2000 (first entry)  
XX  
DE Oligonucleotide used to detect bcr b3-abl fusion transcripts.  
XX  
KW Fusion transcript; translocation; bcr b3 region; abl gene;  
KW amplification assay; detection assay; medical diagnosis;  
KW clinical monitoring; chimeric RNA; fusion RNA; condition marker;  
KW disease marker; cancer; leukemia; ss.  
XX  
OS Synthetic.  
XX  
PN WO200005418-A1.  
XX  
PD 03-FEB-2000.  
XX  
PF 23-JUL-1999; 99WO-US016832.  
XX  
PR 23-JUL-1998; 98US-00121239.  
XX  
PA (GENP-) GEN-PROBE INC.  
XX  
PI Harvey RC, Eastman PS;  
XX  
DR WPI; 2000-182730/16.  
XX  
PT Novel methods for preparing RNA from biological samples, used for the  
XX detection and measurement of nucleic acids and fusion nucleic acids.  
XX  
PS Claim 19; Page 40; 49pp; English.  
XX  
CC Oligonucleotides AAZ60840-62 and AAZ60865-66 are used in the method of  
CC the invention to detect fusion transcripts produced from a translocation  
CC between the bcr b3 region and the abl gene. The specification describes a  
CC method for detecting a fusion nucleic acid [particularly chimeric mRNA  
CC species], in a biological sample. The method comprises contacting a  
CC sample of fusion nucleic acid with primers, amplifying the hybridized  
CC fusion nucleic acid, and detecting the target hybrid. The method is used  
CC for the simple and rapid preparation of RNA from a biological sample,  
CC particularly from the cytoplasm of eukaryotic cells, which is suitable  
CC for use in an amplification and detection assay. The methods are used for



Query Match 100.0%; Score 54; DB 3; Length 54;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-19;  
 Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TCTGACTTTGAGCCTCAGGCTCTGAGTCTCCCTATAGTGCATTAATTATTA 54  
 |||||  
 DB 54 TCTGACTTTGAGCCTCAGGCTCTGAGTCTCCCTATAGTGCATTAATTATTA 1

RESULT 4  
 AAZ60842  
 ID AAZ60842 standard; DNA; 54 BP.  
 XX  
 AC AAZ60842;  
 XX  
 DT 16-MAY-2000 (first entry)  
 XX  
 DE Oligonucleotide used to detect bcr b3-abl fusion transcripts.  
 XX  
 KW Fusion transcript; translocation; bcr b3 region; abl gene;  
 KW amplification assay; detection assay; medical diagnosis;  
 KW clinical monitoring; chimeric RNA; fusion RNA; condition marker;  
 KW disease marker; cancer; leukemia; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200005418-A1.  
 XX  
 PD 03-FEB-2000.  
 XX  
 PF 23-JUL-1999; 99WO-US016832.  
 XX  
 PR 23-JUL-1998; 98US-00121239.  
 XX  
 PA (GENP-) GEN-PROBE INC.  
 XX  
 PI Harvey RC, Eastman PS;  
 XX  
 DR WPI; 2000-182730/16.  
 XX  
 PT Novel methods for preparing RNA from biological samples, used for the  
 PT detection and measurement of nucleic acids and fusion nucleic acids.  
 XX  
 PS Claim 19; Page 40; 49pp; English.  
 XX  
 CC Oligonucleotides AAZ60840-62 and AAZ60865-66 are used in the method of  
 CC the invention to detect fusion transcripts produced from a translocation  
 CC between the bcr b3 region and the abl gene. The specification describes a  
 CC method for detecting a fusion nucleic acid (particularly chimeric mRNA  
 CC sample), in a biological sample. The method comprises contacting a  
 CC sample of fusion nucleic acid with primers, amplifying the hybridized  
 CC fusion nucleic acid, and detecting the target hybrid. The method is used  
 CC for the simple and rapid preparation of RNA from a biological sample,  
 CC particularly from the cytoplasm of eukaryotic cells, which is suitable  
 CC for use in an amplification and detection assay. The methods are used for  
 CC the analysis and detection of nucleic acids in biological samples. The  
 CC methods are useful in the human medical and veterinary fields, for  
 CC medical diagnoses and clinical monitoring of a patient's response to  
 CC therapy where a disease or medical condition is associated with a  
 CC particular type and/or level of mRNA present in the sample. The methods  
 CC are also useful for detecting or quantifying fusion or chimeric RNA  
 CC species, and for detecting a translocation as a marker for a given  
 CC condition or disease, e.g. translocations associate with cancers,  
 CC particularly forms of leukemia  
 XX  
 SQ Sequence 54 BP; 11 A; 11 C; 12 G; 20 T; 0 U; 0 Other;

Query Match 100.0%; Score 54; DB 3; Length 54;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-19;  
 Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TCTGACTTTGAGCCTCAGGCTCTGAGTCTCCCTATAGTGCATTAATTATTA 54  
 |||||  
 DB 1 TCTGACTTTGAGCCTCAGGCTCTGAGTCTCCCTATAGTGCATTAATTATTA 54

Db 1 TCTGACTTTGAGCCTCAGGCTCTGAGTCTCCCTATAGTGCATTAATTATTA 54

RESULT 5  
 AAQ86626/c  
 ID AAQ86626 standard; DNA; 50 BP.  
 XX  
 AC AAQ86626;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 15-NOV-1995 (first entry)  
 XX  
 DE CML chromosomal translocation minus strand primer.  
 XX  
 KW Primer; autocatalytic; target; CML; translocation; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN US5399491-A.  
 XX  
 PD 21-MAR-1995.  
 XX  
 PF 19-MAR-1992; 92US-00855732.  
 XX  
 PR 11-JUL-1989; 89US-00379501.  
 PR 10-JUL-1990; 90US-00550837.  
 XX  
 PA (GENP-) GEN-PROBE INC.  
 XX  
 PI Fultz TJ, Kacian DL;  
 XX  
 DR WPI; 1995-130686/17.  
 XX  
 PT Amplification of nucleic acid targets - using a reverse transcriptase  
 PT with RNase H activity and a RNA polymerase at constant temp.  
 XX  
 PS Disclosure; Col 9; 58pp; English.  
 XX  
 CC AAQ86626-28 are primers and a probe for the CML chromosomal  
 CC translocation. They are used to produce autocatalytic oligonucleotides  
 CC which require no change in the experimental conditions i.e. constant  
 CC temperature, pH and ionic strength. These sequences are useful in  
 CC generating multiple copies of specific nucleic acid target sequences.  
 CC (Updated on 25-MAR-2003 to correct PF field.)  
 XX  
 SQ Sequence 50 BP; 17 A; 12 C; 11 G; 10 T; 0 U; 0 Other;

Query Match 90.7%; Score 49; DB 2; Length 50;  
 Best Local Similarity 100.0%; Pred. No. 8.8e-17;  
 Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 GACTTTGAGCCTCAGGCTCTGAGTCTCCCTATAGTGCATTAATTATTA 52  
 |||||  
 DB 50 GACTTTGAGCCTCAGGCTCTGAGTCTCCCTATAGTGCATTAATTATTA 2

RESULT 6  
 AAT15571/c  
 ID AAT15571 standard; DNA; 50 BP.  
 XX  
 AC AAT15571;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 17-JUL-1996 (first entry)  
 XX  
 DE CML-2 chromosomal translocation major breakpoint t(9;22) (-) primer.  
 XX  
 KW CML-2 chromosomal translocation major breakpoint; t(9; 22); primer;  
 KW auto-catalytic; synthesis; RNA target sequence; assay; detection;  
 KW quantification; ss.  
 XX  
 OS Synthetic.

PN US5480784-A.  
 XX  
 PD 02-JAN-1996.  
 XX  
 PF 10-JUL-1990; 90US-00550837.  
 XX  
 PR 11-JUL-1989; 89US-00379501.  
 XX  
 XX (GENP-) GEN-PROBE INC.  
 XX  
 PI Fultz TJ, Kacian DL;  
 XX  
 DR WPI; 1996-068248/07.  
 XX  
 XX Auto-catalytic synthesis of multiple copies of an RNA target sequence -  
 PT uses cooperative action of a DNA and RNA polymerase in presence of Rnase  
 PT H, useful for detection of target sequence e.g. in clinical or  
 PT environmental sample.  
 XX  
 PS Example; Col 9-10; 51pp; English.  
 XX  
 CC The present sequence is a primer for the CML-2 chromosomal translocation  
 CC major breakpoint t(9;22), which was used to demonstrate an improved  
 CC method for synthesising multiple copies of a RNA target sequence. The  
 CC method comprises combining the target with a primer which hybridises to  
 CC the 3'-terminal portion of the target, a promoter primer which hybridises  
 CC with a portion of the DNA primer extension prod., reverse transcriptase,  
 CC Rnase H and transcriptase. It can be used as a component of an assay to  
 CC detect and/or quantitate specific target sequences in clinical,  
 CC environmental or forensic samples. It also has the advantages of being  
 CC autocatalytic, using the cooperative action of a DNA polymerase, e.g. a  
 CC reverse transcriptase and avoids repetitive manipulations of reaction  
 CC conditions, e.g. temp., ionic strength and pH. (Updated on 25-MAR-2003 to  
 CC correct PF field.)  
 XX  
 SQ Sequence 50 BP; 17 A; 12 C; 11 G; 10 T; 0 U; 0 Other;  
 Query Match 90.7%; Score 49; DB 2; Length 50;  
 Best Local Similarity 100.0%; Pred. No. 8.8e-17;  
 Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 GACTTTGAGCCTCAGGCTCTGAGTCTCCCTATAGTCGATCGTATTAAATT 52  
 Db 50 GACTTTGAGCCTCAGGCTCTGAGTCTCCCTATAGTCGATCGTATTAAATT 2  
 RESULT 7  
 AAT42417/c  
 ID AAT42417 standard; DNA; 50 BP.  
 XX  
 AC AAT42417;  
 XX  
 XX 25-MAR-2003 (revised)  
 DT 28-APR-1997 (first entry)  
 XX  
 DE CML chromosomal translocation primer #1.  
 XX  
 XX HIV; probe; primer; amplify; polymerase chain reaction; microorganism;  
 KW BCL-2; PCR; hepatitis B virus; HBV; CML; ss.  
 XX  
 OS Synthetic.  
 XX  
 XX EP731175-A2.  
 PN  
 XX  
 PD 11-SEP-1996.  
 XX  
 PF 10-JUL-1990; 96EP-00101621.  
 XX  
 PR 11-JUL-1989; 89US-00379501.  
 PR 10-JUL-1990; 90EP-00307503.  
 XX  
 XX (GENP-) GEN-PROBE INC.  
 PA  
 XX

PI Mcdonough S;  
 XX  
 DR WPI; 1996-403995/41.  
 XX  
 PT Detection of HIV nucleic acids in samples - using new specific oligo-  
 PT nucleotide(s) for the amplification and detection of target sequences.  
 XX  
 PS Disclosure; Page 8; 66pp; English.  
 XX  
 CC AAT42417-T42419 represent primers and a probe for the CML chromosomal  
 CC translocation t(9;22). These sequences can be used in modified versions  
 CC of the kits of the invention. The kits of the invention, are for  
 CC detecting the presence of HIV nucleic acid sequences in a sample. The  
 CC kits comprise two amplification primers (such as AAT40182 and AAT40183),  
 CC and a probe (such as AAT42404) for detection of the amplified sequence.  
 CC By using these sequences, the amplification of HIV nucleic acid sequences  
 CC is improved. The kits can also be used for the detection of other  
 CC microorganisms, by using different probe sequences. Other sequences that  
 CC can be detected using this method include those from HBV (using the  
 CC sequences shown in AAT42410-T42412), and BCL-2 (using AAT42413-T42416).  
 CC The samples can be clinical, environmental or forensic samples, and the  
 CC method produces large amounts of the target sequence for a variety of  
 CC uses. The method can also be used to produce multiple copies of a target  
 CC sequence for use in cloning, and sequencing, and to produce probes for  
 CC the target sequence. (Updated on 25-MAR-2003 to correct PF field.)  
 CC (Updated on 25-MAR-2003 to correct PR field.)  
 XX  
 SQ Sequence 50 BP; 17 A; 12 C; 11 G; 10 T; 0 U; 0 Other;  
 Query Match 90.7%; Score 49; DB 2; Length 50;  
 Best Local Similarity 100.0%; Pred. No. 8.8e-17;  
 Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 GACTTTGAGCCTCAGGCTCTGAGTCTCCCTATAGTCGATCGTATTAAATT 52  
 Db 50 GACTTTGAGCCTCAGGCTCTGAGTCTCCCTATAGTCGATCGTATTAAATT 2  
 RESULT 8  
 AAV66349/c  
 ID AAV66349 standard; DNA; 50 BP.  
 XX  
 AC AAV66349;  
 XX  
 DT 06-JAN-1999 (first entry)  
 XX  
 DE CML-2 chromosomal translocation t(9;22) primer.  
 XX  
 KW CML-2 chromosomal translocation t(9;22); block splice template;  
 KW autocatalytic RNA amplification; primer; ss.  
 OS Synthetic.  
 XX  
 XX US5824518-A.  
 PN  
 XX 20-OCT-1998.  
 PD  
 XX 06-JUN-1995; 95US-00469067.  
 PF  
 XX 11-JUL-1989; 89US-00379501.  
 PR  
 PR 10-JUL-1990; 90US-00550837.  
 XX  
 XX (GENP-) GEN-PROBE INC.  
 PA  
 XX Fultz TJ, Kacian DL;  
 PI  
 XX WPI; 1998-582557/49.  
 DR  
 XX Block splice template useful for amplification of nucleic acids -  
 PT comprises two nucleic acid regions, the first region located 3' of the  
 PT second region and blocked at its 3' terminus to inhibit primer extension  
 PT by a DNA polymerase.  
 XX

PS Example 15; Col 9; Sipp; English.

XX AAV6349-50 represent CML-2 chromosomal translocation t(9;22) primers, for the (+) and (-) strands respectively. The primers are used to amplify the invention, together with probe AAV6351. The specification describes methods of synthesising multiple copies of a target nucleic acid sequence autocatalytically under conditions of substantially constant temperature, ionic strength and pH are provided in which multiple RNA copies of the target sequence autocatalytically generate additional copies. The target sequence is a block splice template which comprises two nucleic acid regions. The first region is located 3' of the second region and is blocked at its 3' terminus to inhibit primer extension by a DNA polymerase, and the second region comprises a promoter sequence recognised by an RNA polymerase. The methods are used to amplify nucleic acids, especially RNA, for analysis, cloning or probe production

XX Sequence 50 BP; 17 A; 12 C; 11 G; 10 T; 0 U; 0 Other;

Query Match 90.7%; Score 49; DB 2; Length 50;  
Best Local Similarity 100.0%; Pred. No. 8.8e-17; Mismatches 0; Gaps 0;  
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GACTTTGAGCCTCAGGCTCTGAGTCTCCCTATAGTGCATTAATT 52  
|||||  
Db 50 GACTTTGAGCCTCAGGCTCTGAGTCTCCCTATAGTGCATTAATT 2

RESULT 9  
AA23191/c  
ID AAX23191 standard; DNA; 50 BP.  
XX AAX23191;  
AC AAX23191;  
XX 11-JUN-1999 (first entry)  
XX CML chromosomal translocation t(9;22) primer #1.  
XX Autocatalytic amplification; transcription-based amplification; CML; thermalcycling; diagnostic; environmental testing; probe; detection; genetic disease; infectious disease; microorganism; food; forensic; paternity; primer; ss.  
XX Synthetic.  
XX US5888779-A.  
XX 30-MAR-1999.  
XX 05-JUN-1995; 95US-00461654.  
XX 11-JUL-1989; 89US-00379501.  
XX 10-JUL-1990; 90US-00550837.  
XX (GENP-) GEN-PROBE INC.  
XX Fultz TJ, Kacian DL;  
XX WPI; 1999-253231/21.  
XX Kit for autocatalytic amplification of RNA targets.  
XX Disclosure; Col 9; Sipp; English.

XX This invention describes a novel method for the autocatalytic amplification of an RNA target in a transcription-based amplification system without thermalcycling. The method generates oligonucleotides for diagnostic or environmental testing, for use e.g. as probes and in cloning. Typical applications are the detection of genetic or infectious diseases, the monitoring of responses to therapy, the quantitation or detection of microorganisms in foods, forensic studies and the establishment of paternity. Kits containing the products of the invention provide many copies of selected RNA targets under conditions of constant temperature, ionic strength and pH. Specific amplification of RNA targets

CC increases sensitivity, convenience, accuracy and the reliability of assays

XX Sequence 50 BP; 17 A; 12 C; 11 G; 10 T; 0 U; 0 Other;

Query Match 90.7%; Score 49; DB 2; Length 50;  
Best Local Similarity 100.0%; Pred. No. 8.8e-17; Mismatches 0; Gaps 0;  
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GACTTTGAGCCTCAGGCTCTGAGTCTCCCTATAGTGCATTAATT 52  
|||||  
Db 50 GACTTTGAGCCTCAGGCTCTGAGTCTCCCTATAGTGCATTAATT 2

RESULT 10  
AAD62600/c  
ID AAD62600 standard; DNA; 50 BP.  
XX AAD62600;  
AC AAD62600;  
XX 15-JAN-2004 (first entry)  
XX CML chromosomal translocation t(9;22) PCR primer #2.  
XX Amplification; human immunodeficiency virus; environmental testing; HIV; detection; diagnostic testing; PCR; primer; ss.  
XX Unidentified.  
XX US6589734-B1.  
XX 08-JUL-2003.  
XX 08-OCT-1998; 98US-00168947.  
XX 11-JUL-1989; 89US-00379501.  
XX 10-JUL-1990; 90US-00550837.  
XX 06-JUN-1995; 95US-00469067.  
XX (GENP-) GEN-PROBE INC.  
XX Kacian DL, Fultz TJ, McDonough SH;  
XX WPI; 2003-810379/76.  
XX New oligonucleotide probe, useful in detecting HIV nucleic acid in a sample and for environmental and diagnostic testing.  
XX Disclosure; Col 9; 62pp; English.

XX The invention relates to oligonucleotides useful in amplifying and detecting human immunodeficiency virus (HIV) nucleic acid in a sample. The invention is used for environmental testing, diagnostic testing, research studies and for the preparation of reagents or materials for cloning or other purposes. The present sequence is CML chromosomal translocation t(9;22) PCR primer. This sequence is used in the invention

XX Sequence 50 BP; 17 A; 12 C; 11 G; 10 T; 0 U; 0 Other;

Query Match 90.7%; Score 49; DB 9; Length 50;  
Best Local Similarity 100.0%; Pred. No. 8.8e-17; Mismatches 0; Gaps 0;  
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GACTTTGAGCCTCAGGCTCTGAGTCTCCCTATAGTGCATTAATT 52  
|||||  
Db 50 GACTTTGAGCCTCAGGCTCTGAGTCTCCCTATAGTGCATTAATT 2

RESULT 11  
AAA76067/c  
ID AAA76067 standard; DNA; 54 BP.  
XX AAA76067;  
AC AAA76067;

```
XX 25-JAN-2001 (first entry)
XX Human prostate specific antigen PCR primer SEQ ID NO: 29.
XX Prostate specific antigen; PSA; prostate-specific membrane antigen; PSMA;
XX glandular kallikrein-2; hK2; prostate cancer; breast cancer; probe;
XX PCR primer; ss.
XX Homo sapiens.
XX WO200044940-A2.
XX 03-AUG-2000.
XX 28-JAN-2000; 2000WO-US002270.
XX 28-JAN-1999; 99US-0117640P.
XX (GENP-) GEN-PROBE INC.
XX Harvey RC, Clark TJ;
XX WPI; 2000-505986/45.
XX Detecting prostate-specific antigen (PSA), prostate specific membrane
XX antigen (PSMA) or human kallikrein 2 (hK2) nucleic acids in samples using
XX probe molecules, useful for the diagnosis of prostate and breast cancers.
XX Claim 1; Page 12; 77pp; English.
XX The present invention is concerned with the detection of nucleic acid
XX markers for prostate and breast cancer, and PCR primers and probes which
XX are able to detect and quantify these markers. Prostate specific antigen
XX (PSA), prostate-specific membrane antigen (PSMA) and glandular kallikrein
XX -2 (hK2) have all been linked to prostate and breast cancers, and the
XX primers and probes of the invention are able to detect the abnormal
XX presence of mRNA expressed by their coding sequences in tissues other
XX than the prostate. This enables the presence of cancer to be perceived
XX and aids in the detection of metastases
XX Sequence 54 BP; 16 A; 13 C; 11 G; 14 T; 0 U; 0 Other;
Query Match 59.3%; Score 32; DB 3; Length 54;
Best Local Similarity 100.0%; Pred. No. 1.3e-07;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 23 TGAGTCTCCCTATAGTGCAGTCGTATTAAATTTA 54
DB 32 TGAGTCTCCCTATAGTGCAGTCGTATTAAATTTA 1
RESULT 12
AAA76206/c
ID AAA76206 standard; DNA; 49 BP.
XX
XX AAA76206;
XX
XX 25-JAN-2001 (first entry)
XX Human prostate specific antigen PCR primer SEQ ID NO: 35.
XX Prostate specific antigen; PSA; prostate-specific membrane antigen; PSMA;
XX glandular kallikrein-2; hK2; prostate cancer; breast cancer; probe;
XX PCR primer; ss.
XX Homo sapiens.
XX WO200044940-A2.
XX 03-AUG-2000.
XX 28-JAN-2000; 2000WO-US002270.
XX 28-JAN-1999; 99US-0117640P.
XX (GENP-) GEN-PROBE INC.
XX Harvey RC, Clark TJ;
XX WPI; 2000-505986/45.
XX Detecting prostate-specific antigen (PSA), prostate specific membrane
XX antigen (PSMA) or human kallikrein 2 (hK2) nucleic acids in samples using
XX probe molecules, useful for the diagnosis of prostate and breast cancers.
XX Claim 1; Page 12; 77pp; English.
XX The present invention is concerned with the detection of nucleic acid
XX markers for prostate and breast cancer, and PCR primers and probes which
XX are able to detect and quantify these markers. Prostate specific antigen
XX (PSA), prostate-specific membrane antigen (PSMA) and glandular kallikrein
XX -2 (hK2) have all been linked to prostate and breast cancers, and the
XX primers and probes of the invention are able to detect the abnormal
XX presence of mRNA expressed by their coding sequences in tissues other
XX than the prostate. This enables the presence of cancer to be perceived
XX and aids in the detection of metastases
XX Sequence 54 BP; 16 A; 13 C; 11 G; 14 T; 0 U; 0 Other;
Query Match 59.3%; Score 32; DB 3; Length 54;
Best Local Similarity 100.0%; Pred. No. 1.3e-07;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 23 TGAGTCTCCCTATAGTGCAGTCGTATTAAATTTA 54
DB 32 TGAGTCTCCCTATAGTGCAGTCGTATTAAATTTA 1
RESULT 13
AAA76066/c
ID AAA76066 standard; DNA; 50 BP.
XX
XX AAA76066;
XX
XX 25-JAN-2001 (first entry)
XX Human prostate specific antigen PCR primer SEQ ID NO: 28.
XX Prostate specific antigen; PSA; prostate-specific membrane antigen; PSMA;
XX glandular kallikrein-2; hK2; prostate cancer; breast cancer; probe;
XX PCR primer; ss.
XX Homo sapiens.
XX WO200044940-A2.
XX 03-AUG-2000.
XX 28-JAN-2000; 2000WO-US002270.
XX 28-JAN-1999; 99US-0117640P.
XX (GENP-) GEN-PROBE INC.
XX Harvey RC, Clark TJ;
XX WPI; 2000-505986/45.
XX Detecting prostate-specific antigen (PSA), prostate specific membrane
XX antigen (PSMA) or human kallikrein 2 (hK2) nucleic acids in samples using
XX probe molecules, useful for the diagnosis of prostate and breast cancers.
XX Claim 1; Page 12; 77pp; English.
XX The present invention is concerned with the detection of nucleic acid
```

CC markers for prostate and breast cancer, and PCR primers and probes which  
CC are able to detect and quantify these markers. Prostate specific antigen  
CC (PSA), prostate-specific membrane antigen (PSMA) and glandular kallikrein  
CC -2 (hk2) have all been linked to prostate and breast cancers, and the  
CC primers and probes of the invention are able to detect the abnormal  
CC presence of mRNA expressed by their coding sequences in tissues other  
CC than the prostate. This enables the presence of cancer to be perceived  
CC and aids in the detection of metastases

XX  
SQ Sequence 50 BP; 16 A; 11 C; 11 G; 12 T; 0 U; 0 Other;  
Query Match 55.6%; Score 30; DB 3; Length 50;  
Best Local Similarity 100.0%; Pred. No. 1.5e-06;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 25 AGTCTCCCTATAGTGAGTCGTATTATTTA 54  
DB 30 AGTCTCCCTATAGTGAGTCGTATTATTTA 1

RESULT 14  
AAA76211/C  
ID AAA76211 standard; DNA; 52 BP.  
XX  
AC AAA76211;  
XX  
DT 25-JAN-2001 (first entry)  
XX  
DE Human prostate specific antigen PCR primer SEQ ID NO: 40.  
XX  
KW Prostate specific antigen; PSA; prostate-specific membrane antigen; PSMA;  
KW glandular kallikrein-2; hk2; prostate cancer; breast cancer; probe;  
KW PCR primer; ss.  
OS Homo sapiens.  
XX  
PN WO200044940-A2.  
XX  
PD 03-AUG-2000.  
XX  
PF 28-JAN-2000; 2000WO-US002270.  
XX  
PR 28-JAN-1999; 99US-0117640P.  
XX  
PA (GENP-) GEN-PROBE INC.  
PI Harvey RC, Clark TJ;  
XX  
DR WPI; 2000-505986/45.  
XX  
PT Detecting prostate-specific antigen (PSA), prostate specific membrane  
PT antigen (PSMA) or human kallikrein 2 (hk2) nucleic acids in samples using  
PT probe molecules, useful for the diagnosis of prostate and breast cancers.  
XX  
PS Claim 1; Page 13; 77pp; English.

CC The present invention is concerned with the detection of nucleic acid  
CC markers for prostate and breast cancer, and PCR primers and probes which  
CC are able to detect and quantify these markers. Prostate specific antigen  
CC (PSA), prostate-specific membrane antigen (PSMA) and glandular kallikrein  
CC -2 (hk2) have all been linked to prostate and breast cancers, and the  
CC primers and probes of the invention are able to detect the abnormal  
CC presence of mRNA expressed by their coding sequences in tissues other  
CC than the prostate. This enables the presence of cancer to be perceived  
CC and aids in the detection of metastases

XX  
SQ Sequence 52 BP; 17 A; 11 C; 11 G; 13 T; 0 U; 0 Other;  
Query Match 55.6%; Score 30; DB 3; Length 52;  
Best Local Similarity 100.0%; Pred. No. 1.5e-06;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 25 AGTCTCCCTATAGTGAGTCGTATTATTTA 54

DB 30 AGTCTCCCTATAGTGAGTCGTATTATTTA 1

RESULT 15  
ABZ59191/C  
ID ABZ59191 standard; DNA; 45 BP.  
XX  
AC ABZ59191;  
XX  
DT 15-MAY-2003 (first entry)  
XX  
DE LacZ RNA generating primer.  
XX  
KW LacZ; gene expression; gene function; pharmaceutical; PCR; primer; ss.  
OS Synthetic.  
XX  
PN WO200268635-A2.  
XX  
PD 06-SEP-2002.  
XX  
PF 27-FEB-2002; 2002WO-EP002098.  
XX  
PR 28-FEB-2001; 2001GB-00004948.  
XX  
PA (NOVS ) NOVARTIS FORSCHUNGSSTIFTUNG ZWEIGNIEDERL.  
PI Billy E, Filipowicz W, Mueller U;  
XX  
DR WPI; 2002-706992/76.  
XX  
PT Inhibiting expression of a target gene, useful for identifying gene  
PT function in an organism, comprises exposing a mammalian cell to a  
PT partially double-stranded ribonucleic acid with at least 60% sequence  
PT identity to a target gene.  
XX  
PS Example 1; Page 16; 31pp; English.

CC The invention relates to inhibiting expression of a target gene. The  
CC method involves exposing a renewable, mammalian cell to a partially  
CC double-stranded ribonucleic acid and with at least 60% sequence identity  
CC to a target gene. The method is useful for identifying gene function in  
CC an organism, in determining potential targets for pharmaceuticals,  
CC and determining signal pathways responsible for post-natal development,  
CC aging. The method may also be used to allow the inhibition of essential  
CC genes which may be required for cell or organism viability at particular  
CC stages of development or cellular compartments, and to allow addition or  
CC expression of RNA at specific times of development and locations in the  
CC organism without introducing permanent mutations into the target genome.  
CC The present sequence represents a PCR primer for generating a lacZ RNA,  
CC used in the preparation of dsRNA

XX  
SQ Sequence 45 BP; 15 A; 10 C; 10 G; 10 T; 0 U; 0 Other;  
Query Match 53.7%; Score 29; DB 6; Length 45;  
Best Local Similarity 100.0%; Pred. No. 5.3e-06;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 CTGAGTCTCCCTATAGTGAGTCGTATTAA 50  
DB 29 CTGAGTCTCCCTATAGTGAGTCGTATTAA 1

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Job time : 240.833 secs

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OM nucleic - nucleic search, using sw model

Run on: May 26, 2004, 16:02:51 ; Search time 45.5117 Seconds  
(without alignments)  
658.454 Million cell updates/sec

Title: US-09-121-239-3

Perfect score: 54

Sequence: 1 TCTGACTTGGACCTCAGGG.....TAGTGAGTCGTATTAAATTTA 54

Scoring table: OLIGO NUC

Gapop\_60.0 , Gapext 60.0

Searched: 682709 seqs, 277475446 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : Issued Patents NA.\*

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- 4: /cgn2\_6/prodata/2/ina/6B COMB.seq.\*
- 5: /cgn2\_6/prodata/2/ina/PCTUS COMB.seq.\*
- 6: /cgn2\_6/prodata/2/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	49	90.7	50	4 US-09-168-947-45	Sequence 45, Appl
C 2	32	59.3	54	4 US-09-493-491-29	Sequence 29, Appl
C 3	32	59.3	54	4 US-09-493-491A-32	Sequence 32, Appl
C 4	30	55.6	49	4 US-09-493-491-35	Sequence 35, Appl
C 5	30	55.6	49	4 US-09-493-491A-38	Sequence 38, Appl
C 6	30	55.6	50	4 US-09-493-491-28	Sequence 28, Appl
C 7	30	55.6	50	4 US-09-493-491A-31	Sequence 31, Appl
C 8	30	55.6	52	4 US-09-493-491-40	Sequence 40, Appl
C 9	30	55.6	52	4 US-09-493-491A-43	Sequence 43, Appl
C 10	29	53.7	37	1 US-08-099-867-5	Sequence 5, Appl
C 11	29	53.7	50	3 US-08-972-799A-25	Sequence 25, Appl
C 12	29	53.7	50	3 US-09-506-282-25	Sequence 25, Appl
C 13	29	53.7	50	5 PCT-US95-0339-25	Sequence 25, Appl
C 14	29	53.7	51	4 US-09-944-036-40	Sequence 40, Appl
C 15	29	53.7	52	4 US-09-493-491-33	Sequence 33, Appl
C 16	29	53.7	52	4 US-09-493-491-39	Sequence 39, Appl
C 17	29	53.7	52	4 US-09-493-491A-36	Sequence 36, Appl
C 18	29	53.7	52	4 US-09-493-491A-42	Sequence 42, Appl
C 19	29	53.7	54	4 US-09-493-491-27	Sequence 27, Appl
C 20	29	53.7	54	4 US-09-493-491-49	Sequence 49, Appl
C 21	29	53.7	54	4 US-09-493-491A-30	Sequence 30, Appl
C 22	29	53.7	54	4 US-09-493-491A-39	Sequence 49, Appl
C 23	29	53.7	55	4 US-09-493-491-47	Sequence 47, Appl
C 24	29	53.7	55	4 US-09-493-491A-47	Sequence 47, Appl
C 25	29	53.7	60	1 US-08-099-867-7	Sequence 7, Appl
C 26	29	53.7	79	1 US-08-099-867-3	Sequence 3, Appl
C 27	29	53.7	180	1 US-08-099-867-1	Sequence 1, Appl

C 28	28	51.9	28	4 US-09-493-491-41	Sequence 41, Appl
C 29	28	51.9	28	4 US-09-493-491A-44	Sequence 44, Appl
C 30	28	51.9	30	4 US-08-811-481-29	Sequence 29, Appl
C 31	28	51.9	30	4 US-09-876-527-29	Sequence 29, Appl
C 32	28	51.9	33	4 US-09-944-036-4	Sequence 4, Appl
C 33	28	51.9	33	4 US-09-738-274-36	Sequence 36, Appl
C 34	28	51.9	35	2 US-08-360-051A-22	Sequence 22, Appl
C 35	28	51.9	35	2 US-08-360-051A-27	Sequence 24, Appl
C 36	28	51.9	35	2 US-09-732-990-15	Sequence 15, Appl
C 37	28	51.9	35	4 US-09-202-972-17	Sequence 15, Appl
C 38	28	51.9	35	4 US-09-202-972-15	Sequence 15, Appl
C 39	28	51.9	35	4 US-09-955-636-7	Sequence 17, Appl
C 40	28	51.9	36	3 US-09-944-036-2	Sequence 7, Appl
C 41	28	51.9	37	4 US-09-944-036-2	Sequence 2, Appl
C 42	28	51.9	41	4 US-09-425-585-15	Sequence 15, Appl
C 43	28	51.9	41	4 US-09-953-321-15	Sequence 15, Appl
C 44	28	51.9	47	3 US-08-678-735A-9	Sequence 9, Appl
C 45	28	51.9	47	4 US-08-418-992-9	Sequence 9, Appl

#### ALIGNMENTS

##### RESULT 1

US-09-168-947-45/c  
; Sequence 45, Application US/09168947  
; Patent No. 6589734  
; GENERAL INFORMATION:  
; APPLICANT: KACIAN, DANIEL L.  
; APPLICANT: FULTZ, TIMOTHY J.  
; APPLICANT: MCDONOUGH, SHERROL H.  
; TITLE OF INVENTION: DETECTION OF HIV  
; FILE REFERENCE: 218/130  
; CURRENT APPLICATION NUMBER: US/09/168,947  
; EARLIER FILING DATE: 1998-10-08  
; EARLIER APPLICATION NUMBER: 08/469,067  
; EARLIER FILING DATE: 1995-06-06  
; EARLIER APPLICATION NUMBER: 07/550,837  
; EARLIER FILING DATE: 1990-07-10  
; NUMBER OF SEQ ID NOS: 46  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 45  
; LENGTH: 50  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthesized nucleic acid molecule  
US-09-168-947-45

Query Match 90.7%; Score 49; DB 4; Length 50;  
Best Local Similarity 100.0%; Pred. No. 4.1e-18;  
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GACTTGGACCTCAGGTCGTAGTCTCCCTAGTATAGTCGATTAATT 52  
DB 50 GACTTGGACCTCAGGTCGTAGTCTCCCTAGTATAGTCGATTAATT 2

##### RESULT 2

US-09-493-491-29/c  
; Sequence 29, Application US/09493491  
; Patent No. 6391556  
; GENERAL INFORMATION:  
; APPLICANT: HARVEY, Richard, C.  
; APPLICANT: CLARK, JR., Thomas, J.  
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FOR DETECTING GENETIC MARKERS  
; FILE REFERENCE: GP097-02.UT  
; FILE REFERENCE: FOR CAN IN A BIOLOGICAL SAMPLE  
; CURRENT APPLICATION NUMBER: US/09/493,491  
; CURRENT FILING DATE: 2000-01-28  
; EARLIER APPLICATION NUMBER: 60/117,640 US  
; EARLIER FILING DATE: 1999-01-28  
; NUMBER OF SEQ ID NOS: 50

; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 29  
; LENGTH: 54  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: construct  
US-09-493-491-29

Query Match 59.3%; Score 32; DB 4; Length 54;  
Best Local Similarity 100.0%; Pred. No. 9.1e-09;  
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 TGAGTCTCCCTATAGTGAGTCGATTAAATTTA 54  
|||||

Db 32 TGAGTCTCCCTATAGTGAGTCGATTAAATTTA 1  
|||||

RESULT 3  
US-09-493-491A-32/c  
; Sequence 32, Application US/09493491A  
; Patent No. 6551778  
; GENERAL INFORMATION:  
; APPLICANT: HARVEY, Richard, C.  
; APPLICANT: CLARK, JR., Thomas, J.  
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FOR DETECTING GENETIC MARKERS  
; TITLE OF INVENTION: FOR CANCER IN A BIOLOGICAL SAMPLE  
; FILE REFERENCE: GP097-02.UT  
; CURRENT APPLICATION NUMBER: US/09/493,491A  
; PRIOR FILING DATE: 2000-01-28  
; PRIOR APPLICATION NUMBER: 60/117,640 US  
; PRIOR FILING DATE: 1999-01-28  
; NUMBER OF SEQ ID NOS: 50  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 32  
; LENGTH: 54  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: construct  
; FEATURE:  
; NAME/KEY: promoter  
; LOCATION: (1)..(28)  
US-09-493-491A-32

Query Match 59.3%; Score 32; DB 4; Length 54;  
Best Local Similarity 100.0%; Pred. No. 9.1e-09;  
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 TGAGTCTCCCTATAGTGAGTCGATTAAATTTA 54  
|||||

Db 32 TGAGTCTCCCTATAGTGAGTCGATTAAATTTA 1  
|||||

RESULT 4  
US-09-493-491-35/c  
; Sequence 35, Application US/09493491  
; Patent No. 6391556  
; GENERAL INFORMATION:  
; APPLICANT: HARVEY, Richard, C.  
; APPLICANT: CLARK, JR., Thomas, J.  
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FOR DETECTING GENETIC MARKERS  
; TITLE OF INVENTION: FOR CANCER IN A BIOLOGICAL SAMPLE  
; FILE REFERENCE: GP097-02.UT  
; CURRENT APPLICATION NUMBER: US/09/493,491  
; CURRENT FILING DATE: 2000-01-28  
; PRIOR APPLICATION NUMBER: 60/117,640 US  
; PRIOR FILING DATE: 1999-01-28  
; NUMBER OF SEQ ID NOS: 50  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 35

; LENGTH: 49  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: construct  
US-09-493-491-35

Query Match 55.6%; Score 30; DB 4; Length 49;  
Best Local Similarity 100.0%; Pred. No. 1.2e-07;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 25 AGTCTCCCTATAGTGAGTCGATTAAATTTA 54  
|||||

Db 30 AGTCTCCCTATAGTGAGTCGATTAAATTTA 1  
|||||

RESULT 5  
US-09-493-491A-38/c  
; Sequence 38, Application US/09493491A  
; Patent No. 6551778  
; GENERAL INFORMATION:  
; APPLICANT: HARVEY, Richard, C.  
; APPLICANT: CLARK, JR., Thomas, J.  
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FOR DETECTING GENETIC MARKERS  
; TITLE OF INVENTION: FOR CANCER IN A BIOLOGICAL SAMPLE  
; FILE REFERENCE: GP097-02.UT  
; CURRENT APPLICATION NUMBER: US/09/493,491A  
; CURRENT FILING DATE: 2000-01-28  
; PRIOR APPLICATION NUMBER: 60/117,640 US  
; PRIOR FILING DATE: 1999-01-28  
; NUMBER OF SEQ ID NOS: 50  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 38  
; LENGTH: 49  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: construct  
; FEATURE:  
; NAME/KEY: promoter  
; LOCATION: (1)..(28)  
US-09-493-491A-38

Query Match 55.6%; Score 30; DB 4; Length 49;  
Best Local Similarity 100.0%; Pred. No. 1.2e-07;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 25 AGTCTCCCTATAGTGAGTCGATTAAATTTA 54  
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Db 30 AGTCTCCCTATAGTGAGTCGATTAAATTTA 1  
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RESULT 6  
US-09-493-491-28/c  
; Sequence 28, Application US/09493491  
; Patent No. 6391556  
; GENERAL INFORMATION:  
; APPLICANT: HARVEY, Richard, C.  
; APPLICANT: CLARK, JR., Thomas, J.  
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FOR DETECTING GENETIC MARKERS  
; TITLE OF INVENTION: FOR CANCER IN A BIOLOGICAL SAMPLE  
; FILE REFERENCE: GP097-02.UT  
; CURRENT APPLICATION NUMBER: US/09/493,491  
; CURRENT FILING DATE: 2000-01-28  
; PRIOR APPLICATION NUMBER: 60/117,640 US  
; PRIOR FILING DATE: 1999-01-28  
; NUMBER OF SEQ ID NOS: 50  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 28  
; LENGTH: 50  
; TYPE: DNA

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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: construct
US-09-493-491-28
Query Match          55.6%; Score 30; DB 4; Length 50;
Best Local Similarity 100.0%; Pred. No. 1.2e-07;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 25 AGTCTCCCTATAGTAGTCGATGCGTATTATTTA 54
    |||||
Db 30 AGTCTCCCTATAGTAGTCGATGCGTATTATTTA 1

RESULT 7
US-09-493-491A-31/c
; Sequence 31, Application US/09493491A
; Patent No. 6551778
; GENERAL INFORMATION:
; APPLICANT: HARVEY, Richard, C.
; APPLICANT: CLARK, JR., Thomas, J.
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FOR DETECTING GENETIC MARKERS
; FILE REFERENCE: GP097-02.UT
; CURRENT APPLICATION NUMBER: US/09/493,491A
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/117,640 US
; PRIOR FILING DATE: 1999-01-28
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 31
; TYPE: DNA
; LENGTH: 50
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: construct
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (1)..(28)
US-09-493-491A-31
Query Match          55.6%; Score 30; DB 4; Length 50;
Best Local Similarity 100.0%; Pred. No. 1.2e-07;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 25 AGTCTCCCTATAGTAGTCGATGCGTATTATTTA 54
    |||||
Db 30 AGTCTCCCTATAGTAGTCGATGCGTATTATTTA 1

RESULT 8
US-09-493-491-40/c
; Sequence 40, Application US/09493491
; Patent No. 6391556
; GENERAL INFORMATION:
; APPLICANT: HARVEY, Richard, C.
; APPLICANT: CLARK, JR., Thomas, J.
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FOR DETECTING GENETIC MARKERS
; FILE REFERENCE: GP097-02.UT
; CURRENT APPLICATION NUMBER: US/09/493,491
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/117,640 US
; EARLIER FILING DATE: 1999-01-28
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 40
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: construct
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (1)..(28)
US-09-493-491A-43/c
; Sequence 43, Application US/09493491A
; Patent No. 6551778
; GENERAL INFORMATION:
; APPLICANT: HARVEY, Richard, C.
; APPLICANT: CLARK, JR., Thomas, J.
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FOR DETECTING GENETIC MARKERS
; FILE REFERENCE: GP097-02.UT
; CURRENT APPLICATION NUMBER: US/09/493,491A
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/117,640 US
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 43
; TYPE: DNA
; LENGTH: 52
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: construct
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (1)..(28)
US-09-493-491A-43
Query Match          55.6%; Score 30; DB 4; Length 52;
Best Local Similarity 100.0%; Pred. No. 1.2e-07;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 25 AGTCTCCCTATAGTAGTCGATGCGTATTATTTA 54
    |||||
Db 30 AGTCTCCCTATAGTAGTCGATGCGTATTATTTA 1

RESULT 9
US-09-493-491A-43/c
; Sequence 43, Application US/09493491A
; Patent No. 6551778
; GENERAL INFORMATION:
; APPLICANT: HARVEY, Richard, C.
; APPLICANT: CLARK, JR., Thomas, J.
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FOR DETECTING GENETIC MARKERS
; FILE REFERENCE: GP097-02.UT
; CURRENT APPLICATION NUMBER: US/09/493,491A
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/117,640 US
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 43
; TYPE: DNA
; LENGTH: 52
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: construct
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (1)..(28)
US-09-493-491A-43
Query Match          55.6%; Score 30; DB 4; Length 52;
Best Local Similarity 100.0%; Pred. No. 1.2e-07;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 25 AGTCTCCCTATAGTAGTCGATGCGTATTATTTA 54
    |||||
Db 30 AGTCTCCCTATAGTAGTCGATGCGTATTATTTA 1

RESULT 10
US-08-099-867-5/c
; Sequence 5, Application US/08099867
; Patent No. 5547862
; GENERAL INFORMATION:
; APPLICANT: James Meador
; APPLICANT: Hoyt E. McElroy
; APPLICANT: Michelle L. Herrmann
; APPLICANT: Matthew Winkler
; TITLE OF INVENTION: Vectors Containing Multiple Promoters
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
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PCT-US95-03339-25/c  
; Sequence 25, Application PC/TUS9503339  
; GENERAL INFORMATION:  
; APPLICANT:  
; TITLE OF INVENTION: ISOTHERMAL STRAND DISPLACEMENT NUCLEIC ACID  
; TITLE OF INVENTION: AMPLIFICATION  
; NUMBER OF SEQUENCES: 27  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US95/03339  
; FILING DATE:  
; CLASSIFICATION:  
; INFORMATION FOR SEQ ID NO: 25:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 50 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
PCT-US95-03339-25

Query Match 53.7%; Score 29; DB 5; Length 50;  
Best Local Similarity 100.0%; Pred. No. 4.1e-07;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 25 AGTCTCCCTATAGTGCATTAATTT 53  
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DB 30 AGTCTCCCTATAGTGCATTAATTT 2

## RESULT 14

US-09-944-036-40/c  
; Sequence 40, Application US/09944036  
; Patent No. 6582920  
; GENERAL INFORMATION:  
; APPLICANT: YANG, Yeasing Y.  
; APPLICANT: BRENTANO, Steven T.  
; APPLICANT: BABOLA, Odile  
; APPLICANT: TRAN, Nathalie  
; APPLICANT: VERNET, Guy  
; TITLE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF  
; TITLE OF INVENTION: SEQUENCES ASSOCIATED WITH DRUG-RESISTANCE MUTATIONS  
; FILE REFERENCE: GP114-02 UT  
; CURRENT APPLICATION NUMBER: US/09/944,036  
; CURRENT FILING DATE: 2001-08-31  
; PRIOR APPLICATION NUMBER: US 60/229,790  
; PRIOR FILING DATE: 2000-09-01  
; NUMBER OF SEQ ID NOS: 70  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 40  
; LENGTH: 51  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:  
; OTHER INFORMATION: Oligonucleotide primer for Reverse Transcriptase  
; OTHER INFORMATION: target sequence  
; NAME/KEY: promoter  
; LOCATION: (1)..(29)  
US-09-944-036-40

Query Match 53.7%; Score 29; DB 4; Length 51;  
Best Local Similarity 100.0%; Pred. No. 4.1e-07;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 25 AGTCTCCCTATAGTGCATTAATTT 53  
|||  
DB 29 AGTCTCCCTATAGTGCATTAATTT 1

## RESULT 15

US-09-493-491-33/c  
; Sequence 33, Application US/09493491  
; Patent No. 6391556  
; GENERAL INFORMATION:  
; APPLICANT: HARVEY, Richard, C.  
; APPLICANT: CLARK, JR., Thomas, J.  
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FOR DETECTING GENETIC MARKERS  
; TITLE OF INVENTION: FOR CANCER IN A BIOLOGICAL SAMPLE  
; FILE REFERENCE: GP097-02 UT  
; CURRENT APPLICATION NUMBER: US/09/493,491  
; CURRENT FILING DATE: 2000-01-28  
; EARLIER APPLICATION NUMBER: 60/117,640 US  
; EARLIER FILING DATE: 1999-01-28  
; NUMBER OF SEQ ID NOS: 50  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 33  
; LENGTH: 52  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: construct  
US-09-493-491-33

Query Match 53.7%; Score 29; DB 4; Length 52;  
Best Local Similarity 100.0%; Pred. No. 4.1e-07;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 GTCTCCCTATAGTGCATTAATTTA 54  
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DB 29 GTCTCCCTATAGTGCATTAATTTA 1

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Job time : 45.5117 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 27, 2004, 11:30:47 ; Search time 284.177 Seconds  
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864.392 Million cell updates/sec

Title: US-09-121-239-3  
Perfect score: 54  
Sequence: 1 TCTGACTTGAGCCTCAGGG.....TAGTGAGTCGTATTAAATTA 54

Scoring table: OLIGO NUC  
Gapop 60.0 , Gapext 60.0

Searched: 2960401 seqs, 2274450654 residues

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Minimum DB seq length: 0

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Post-processing: Listing first 45 summaries

Database : Published Applications NA.\*

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- 18: /cgn2\_6/ptodata/2/pubpna/US10\_PUBCOMB.seq.\*
- 19: /cgn2\_6/ptodata/2/pubpna/US10\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	49	90.7	50	15	US-10-244-490-45
C 2	32	59.3	54	15	US-10-273-707-32
C 3	30	55.6	49	15	US-10-273-707-38
C 4	30	55.6	50	15	US-10-273-707-31
C 5	30	55.6	52	15	US-10-273-707-43
C 6	29	53.7	51	9	US-09-944-036-40
C 7	29	53.7	51	16	US-10-425-975-40
C 8	29	53.7	52	15	US-10-273-707-36
C 9	29	53.7	52	15	US-10-273-707-42
C 10	29	53.7	54	15	US-10-273-707-30
C 11	29	53.7	54	15	US-10-273-707-49
C 12	29	53.7	55	15	US-10-273-707-47
C 13	29	53.7	6306	13	US-09-833-782-3
C 14	28	51.9	28	15	US-10-273-707-44

C 15	51.9	28	30	9	US-09-876-527-29	Sequence 29, Appl
C 16	51.9	28	30	15	US-10-124-089-29	Sequence 29, Appl
C 17	51.9	28	33	9	US-09-738-972-10	Sequence 10, Appl
C 18	51.9	28	33	9	US-09-944-036-4	Sequence 4, Appl
C 19	51.9	28	33	10	US-09-738-274-36	Sequence 36, Appl
C 20	51.9	28	33	14	US-10-001-407-29	Sequence 29, Appl
C 21	51.9	28	33	16	US-10-425-975-4	Sequence 4, Appl
C 22	51.9	28	35	9	US-09-202-972-15	Sequence 15, Appl
C 23	51.9	28	35	9	US-09-202-972-17	Sequence 17, Appl
C 24	51.9	28	35	10	US-09-897-776A-14	Sequence 14, Appl
C 25	51.9	28	35	10	US-09-897-776A-19	Sequence 19, Appl
C 26	51.9	28	36	13	US-09-803-810-7	Sequence 7, Appl
C 27	51.9	28	36	15	US-10-298-330-7	Sequence 7, Appl
C 28	51.9	28	37	9	US-09-944-036-2	Sequence 2, Appl
C 29	51.9	28	37	16	US-10-425-975-2	Sequence 2, Appl
C 30	51.9	28	39	12	US-10-651-563-9	Sequence 9, Appl
C 31	51.9	28	41	9	US-09-953-321-15	Sequence 15, Appl
C 32	51.9	28	49	15	US-10-273-707-37	Sequence 37, Appl
C 33	51.9	28	49	15	US-10-273-707-39	Sequence 39, Appl
C 34	51.9	28	50	15	US-10-273-707-40	Sequence 40, Appl
C 35	51.9	28	51	9	US-09-944-036-41	Sequence 41, Appl
C 36	51.9	28	51	15	US-10-273-707-41	Sequence 41, Appl
C 37	51.9	28	51	16	US-10-425-975-41	Sequence 41, Appl
C 38	51.9	28	52	9	US-09-944-036-39	Sequence 39, Appl
C 39	51.9	28	52	9	US-09-944-036-43	Sequence 43, Appl
C 40	51.9	28	52	10	US-09-738-274-12	Sequence 12, Appl
C 41	51.9	28	52	16	US-10-425-975-39	Sequence 39, Appl
C 42	51.9	28	52	16	US-10-425-975-43	Sequence 43, Appl
C 43	51.9	28	53	9	US-09-944-036-34	Sequence 34, Appl
C 44	51.9	28	53	9	US-09-944-036-35	Sequence 35, Appl
C 45	51.9	28	53	9	US-09-944-036-36	Sequence 36, Appl

ALIGNMENTS

RESULT 1

US-10-244-490-45/c  
; Sequence 45, Application US/10244490  
; Publication No. US20030152916A1  
; GENERAL INFORMATION:  
; APPLICANT: KACIAN, DANIEL L.  
; APPLICANT: MCDONOUGH, SHERROL H.  
; TITLE OF INVENTION: DETECTION OF HIV  
; FILE REFERENCE: 218/130  
; CURRENT APPLICATION NUMBER: US/10/244,490  
; PRIOR FILING DATE: 2002-09-16  
; PRIOR APPLICATION NUMBER: US/09/168,947  
; PRIOR FILING DATE: 1998-10-08  
; PRIOR APPLICATION NUMBER: 08/469,067  
; PRIOR FILING DATE: 1995-06-06  
; PRIOR APPLICATION NUMBER: 07/550,837  
; PRIOR FILING DATE: 1990-07-10  
; NUMBER OF SEQ ID NOS: 46  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 45  
; LENGTH: 50  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthesized nucleic acid molecule  
US-10-244-490-45

Query Match 90.7%; Score 49; DB 15; Length 50;  
Best Local Similarity 100.0%; Pred. No. 3.4e-18; Indels 0; Gaps 0;  
Matches 49; Conservative 0; Mismatches 0;

QY 4 GACTTTGAGCCTCAGGGTCTGAGTCTCCCTATGATGTCGTATTAAATT 52  
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DB 50 GACTTTGAGCCTCAGGGTCTGAGTCTCCCTATGATGTCGTATTAAATT 2  
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RESULT 2
US-10-273-707-32/c
; Sequence 32, Application US/10273707
; Publication No. US20030104448A1
; GENERAL INFORMATION:
; APPLICANT: HARVEY, Richard, C.
; APPLICANT: CLARK, JR., Thomas, J.
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FOR DETECTING GENETIC MARKERS
; TITLE OF INVENTION: FOR CANCER IN A BIOLOGICAL SAMPLE
; FILE REFERENCE: GP097-03.DVI
; CURRENT APPLICATION NUMBER: US/10/273,707
; CURRENT FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: 09/493,491
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/117,640 US
; PRIOR FILING DATE: 1999-01-28
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 32
; LENGTH: 54
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: construct
; NAME/KEY: promoter
; LOCATION: (1)..(28)
US-10-273-707-32

Query Match          59.3%; Score 32; DB 15; Length 54;
Best Local Similarity 100.0%; Pred. No. 2e-08;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 TGAGTCTCCCTATAGTAGTGCATTAATTTA 54
Db 32 TGAGTCTCCCTATAGTAGTGCATTAATTTA 1

RESULT 3
US-10-273-707-38/c
; Sequence 38, Application US/10273707
; Publication No. US20030104448A1
; GENERAL INFORMATION:
; APPLICANT: HARVEY, Richard, C.
; APPLICANT: CLARK, JR., Thomas, J.
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FOR DETECTING GENETIC MARKERS
; TITLE OF INVENTION: FOR CANCER IN A BIOLOGICAL SAMPLE
; FILE REFERENCE: GP097-03.DVI
; CURRENT APPLICATION NUMBER: US/10/273,707
; CURRENT FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: 09/493,491
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/117,640 US
; PRIOR FILING DATE: 1999-01-28
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 38
; LENGTH: 49
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: construct
; NAME/KEY: promoter
; LOCATION: (1)..(28)
US-10-273-707-38

Query Match          55.6%; Score 30; DB 15; Length 49;
Best Local Similarity 100.0%; Pred. No. 2.8e-07;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 25 AGTCTCCCTATAGTAGTGCATTAATTTA 54
Db 30 AGTCTCCCTATAGTAGTGCATTAATTTA 1

RESULT 4
US-10-273-707-31/c
; Sequence 31, Application US/10273707
; Publication No. US20030104448A1
; GENERAL INFORMATION:
; APPLICANT: HARVEY, Richard, C.
; APPLICANT: CLARK, JR., Thomas, J.
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FOR DETECTING GENETIC MARKERS
; TITLE OF INVENTION: FOR CANCER IN A BIOLOGICAL SAMPLE
; FILE REFERENCE: GP097-03.DVI
; CURRENT APPLICATION NUMBER: US/10/273,707
; CURRENT FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: 09/493,491
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/117,640 US
; PRIOR FILING DATE: 1999-01-28
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 31
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: construct
; NAME/KEY: promoter
; LOCATION: (1)..(28)
US-10-273-707-31

Query Match          55.6%; Score 30; DB 15; Length 50;
Best Local Similarity 100.0%; Pred. No. 2.8e-07;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 25 AGTCTCCCTATAGTAGTGCATTAATTTA 54
Db 30 AGTCTCCCTATAGTAGTGCATTAATTTA 1

RESULT 5
US-10-273-707-43/c
; Sequence 43, Application US/10273707
; Publication No. US20030104448A1
; GENERAL INFORMATION:
; APPLICANT: HARVEY, Richard, C.
; APPLICANT: CLARK, JR., Thomas, J.
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FOR DETECTING GENETIC MARKERS
; TITLE OF INVENTION: FOR CANCER IN A BIOLOGICAL SAMPLE
; FILE REFERENCE: GP097-03.DVI
; CURRENT APPLICATION NUMBER: US/10/273,707
; CURRENT FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: 09/493,491
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/117,640 US
; PRIOR FILING DATE: 1999-01-28
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 43
; LENGTH: 52
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: construct
; NAME/KEY: promoter
; LOCATION: (1)..(28)
US-10-273-707-43
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Query Match 55.6%; Score 30; DB 15; Length 52;  
Best Local Similarity 100.0%; Pred. No. 2.8e-07;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 25 AGTCTCCCTATAGTGAGTCGTATTAAATTTA 54  
|||||  
DB 30 AGTCTCCCTATAGTGAGTCGTATTAAATTTA 1

RESULT 6  
US-09-944-036-40/c  
; Sequence 40, Application US/09944036  
; Patent No. US20020055095A1  
; GENERAL INFORMATION:  
; APPLICANT: YANG, Yeasing Y.  
; APPLICANT: BRENTANO, Steven T.  
; APPLICANT: BABOLA, Odile  
; APPLICANT: TRAN, Nathalie  
; APPLICANT: VERNET, Guy  
; TITLE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF  
; FILE REFERENCE: GP114-02.UT  
; CURRENT APPLICATION NUMBER: US/09/944,036  
; PRIOR FILING DATE: 2001-08-31  
; PRIOR APPLICATION NUMBER: US 60/229,790  
; PRIOR FILING DATE: 2000-09-01  
; NUMBER OF SEQ ID NOS: 70  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 40  
; LENGTH: 51  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:  
; OTHER INFORMATION: Oligonucleotide primer for Reverse Transcriptase  
; NAME/KEY: promoter  
; LOCATION: (1)..(29)  
US-09-944-036-40

Query Match 53.7%; Score 29; DB 9; Length 51;  
Best Local Similarity 100.0%; Pred. No. 1.1e-06;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 25 AGTCTCCCTATAGTGAGTCGTATTAAATTT 53  
|||||  
DB 29 AGTCTCCCTATAGTGAGTCGTATTAAATTT 1

RESULT 7  
US-10-425-975-40/c  
; Sequence 40, Application US/10425975  
; Publication No. US20030228574A1  
; GENERAL INFORMATION:  
; APPLICANT: YANG, Yeasing Y.  
; APPLICANT: BRENTANO, Steven T.  
; APPLICANT: BABOLA, Odile  
; APPLICANT: TRAN, Nathalie  
; APPLICANT: VERNET, Guy  
; TITLE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF  
; FILE REFERENCE: GP114-02.UT  
; CURRENT APPLICATION NUMBER: US/10/425,975  
; PRIOR FILING DATE: 2003-04-28  
; PRIOR APPLICATION NUMBER: US/09/944,036  
; PRIOR FILING DATE: 2001-08-31  
; PRIOR APPLICATION NUMBER: US 60/229,790  
; PRIOR FILING DATE: 2000-09-01  
; NUMBER OF SEQ ID NOS: 70  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 40  
; LENGTH: 51

; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:  
; OTHER INFORMATION: Oligonucleotide primer for Reverse Transcriptase  
; OTHER INFORMATION: target sequence  
; FEATURE:  
; NAME/KEY: promoter  
; LOCATION: (1)..(29)  
US-10-425-975-40

Query Match 53.7%; Score 29; DB 16; Length 51;  
Best Local Similarity 100.0%; Pred. No. 1.1e-06;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 25 AGTCTCCCTATAGTGAGTCGTATTAAATTT 53  
|||||  
DB 29 AGTCTCCCTATAGTGAGTCGTATTAAATTT 1

RESULT 8  
US-10-273-707-36/c  
; Sequence 36, Application US/10273707  
; Publication No. US20030104448A1  
; GENERAL INFORMATION:  
; APPLICANT: HARVEY, Richard, C.  
; APPLICANT: CLARK, JR., Thomas, J.  
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FOR DETECTING GENETIC MARKERS  
; FILE REFERENCE: GP097-03.DV1  
; CURRENT APPLICATION NUMBER: US/10/273,707  
; CURRENT FILING DATE: 2002-10-17  
; PRIOR APPLICATION NUMBER: 09/493,491  
; PRIOR FILING DATE: 2000-01-28  
; PRIOR APPLICATION NUMBER: 60/117,640 US  
; PRIOR FILING DATE: 1999-01-28  
; NUMBER OF SEQ ID NOS: 50  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 36  
; LENGTH: 52  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: construct  
; FEATURE:  
; NAME/KEY: promoter  
; LOCATION: (1)..(28)  
US-10-273-707-36

Query Match 53.7%; Score 29; DB 15; Length 52;  
Best Local Similarity 100.0%; Pred. No. 1.1e-06;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 GTCTCCCTATAGTGAGTCGTATTAAATTTA 54  
|||||  
DB 29 GTCTCCCTATAGTGAGTCGTATTAAATTTA 1

RESULT 9  
US-10-273-707-42/c  
; Sequence 42, Application US/10273707  
; Publication No. US20030104448A1  
; GENERAL INFORMATION:  
; APPLICANT: HARVEY, Richard, C.  
; APPLICANT: CLARK, JR., Thomas, J.  
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FOR DETECTING GENETIC MARKERS  
; FILE REFERENCE: GP097-03.DV1  
; CURRENT APPLICATION NUMBER: US/10/273,707  
; CURRENT FILING DATE: 2002-10-17  
; PRIOR APPLICATION NUMBER: 09/493,491  
; PRIOR FILING DATE: 2000-01-28

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; FILE REFERENCE: GP097-03.DV1
; CURRENT APPLICATION NUMBER: US/10/273,707
; CURRENT FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: 09/493,491
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/117,640 US
; PRIOR FILING DATE: 1999-01-28
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 42
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; NAME/KEY: promoter
; LOCATION: (1)..(28)
US-10-273-707-42

Query Match          53.7%; Score 29; DB 15; Length 52;
Best Local Similarity 100.0%; Pred. No. 1.1e-06;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      26  GTCCTCCCTATAGTGAGTCGTATTAAATTTA 54
Db      29  GTCCTCCCTATAGTGAGTCGTATTAAATTTA 1

RESULT 10
US-10-273-707-30/c
; Sequence 30, Application US/10273707
; Publication No. US20030104448A1
; GENERAL INFORMATION:
; APPLICANT: HARVEY, Richard, C.
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FOR DETECTING GENETIC MARKERS
; FILE REFERENCE: GP097-03.DV1
; CURRENT APPLICATION NUMBER: US/10/273,707
; CURRENT FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: 09/493,491
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/117,640 US
; PRIOR FILING DATE: 1999-01-28
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; NAME/KEY: promoter
; LOCATION: (1)..(28)
US-10-273-707-30

Query Match          53.7%; Score 29; DB 15; Length 54;
Best Local Similarity 100.0%; Pred. No. 1.1e-06;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      26  GTCCTCCCTATAGTGAGTCGTATTAAATTTA 54
Db      29  GTCCTCCCTATAGTGAGTCGTATTAAATTTA 1

RESULT 11
US-10-273-707-49/c
; Sequence 49, Application US/10273707
; Publication No. US20030104448A1
; GENERAL INFORMATION:
; APPLICANT: HARVEY, Richard, C.
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FOR DETECTING GENETIC MARKERS
; FILE REFERENCE: GP097-03.DV1
; CURRENT APPLICATION NUMBER: US/10/273,707
; CURRENT FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: 09/493,491
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/117,640 US
; PRIOR FILING DATE: 1999-01-28
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 49
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; NAME/KEY: promoter
; LOCATION: (1)..(28)
US-10-273-707-49

Query Match          53.7%; Score 29; DB 15; Length 54;
Best Local Similarity 100.0%; Pred. No. 1.1e-06;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      26  GTCCTCCCTATAGTGAGTCGTATTAAATTTA 54
Db      29  GTCCTCCCTATAGTGAGTCGTATTAAATTTA 1

RESULT 12
US-10-273-707-47/c
; Sequence 47, Application US/10273707
; Publication No. US20030104448A1
; GENERAL INFORMATION:
; APPLICANT: HARVEY, Richard, C.
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FOR DETECTING GENETIC MARKERS
; FILE REFERENCE: GP097-03.DV1
; CURRENT APPLICATION NUMBER: US/10/273,707
; CURRENT FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: 09/493,491
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/117,640 US
; PRIOR FILING DATE: 1999-01-28
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 47
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; NAME/KEY: promoter
; LOCATION: (1)..(28)
US-10-273-707-47

Query Match          53.7%; Score 29; DB 15; Length 55;
Best Local Similarity 100.0%; Pred. No. 1.1e-06;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      26  GTCCTCCCTATAGTGAGTCGTATTAAATTTA 54
Db      29  GTCCTCCCTATAGTGAGTCGTATTAAATTTA 1

RESULT 13
US-09-833-782-3/c
; Sequence 3, Application US/09833782
; Publication No. US20020040131A1
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; FILE REFERENCE: GP097-03.DV1
; CURRENT APPLICATION NUMBER: US/10/273,707
; CURRENT FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: 09/493,491
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/117,640 US
; PRIOR FILING DATE: 1999-01-28
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 49
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; NAME/KEY: promoter
; LOCATION: (1)..(28)
US-10-273-707-49

Query Match          53.7%; Score 29; DB 15; Length 54;
Best Local Similarity 100.0%; Pred. No. 1.1e-06;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      26  GTCCTCCCTATAGTGAGTCGTATTAAATTTA 54
Db      29  GTCCTCCCTATAGTGAGTCGTATTAAATTTA 1

RESULT 12
US-10-273-707-47/c
; Sequence 47, Application US/10273707
; Publication No. US20030104448A1
; GENERAL INFORMATION:
; APPLICANT: HARVEY, Richard, C.
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FOR DETECTING GENETIC MARKERS
; FILE REFERENCE: GP097-03.DV1
; CURRENT APPLICATION NUMBER: US/10/273,707
; CURRENT FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: 09/493,491
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/117,640 US
; PRIOR FILING DATE: 1999-01-28
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 47
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; NAME/KEY: promoter
; LOCATION: (1)..(28)
US-10-273-707-47

Query Match          53.7%; Score 29; DB 15; Length 55;
Best Local Similarity 100.0%; Pred. No. 1.1e-06;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      26  GTCCTCCCTATAGTGAGTCGTATTAAATTTA 54
Db      29  GTCCTCCCTATAGTGAGTCGTATTAAATTTA 1

RESULT 13
US-09-833-782-3/c
; Sequence 3, Application US/09833782
; Publication No. US20020040131A1
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```

; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Wilganowski, Nathaniel L.
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: Novel Human Metalloprotease and Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0161-USA
; CURRENT APPLICATION NUMBER: US/09/833,782
; CURRENT FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: US 60/196,319
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 6306
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-833-782-3

Query Match      53.7%; Score 29; DB 13; Length 6306;
Best Local Similarity 100.0%; Pred. No. 1.2e-06;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 25 AGTCTCCCTATAGTGCATTAATTT 53
DB 114 AGTCTCCCTATAGTGCATTAATTT 86

RESULT 14
US-10-273-707-44/c
; Sequence 44, Application US/10273707
; Publication No. US2003010448A1
; GENERAL INFORMATION:
; APPLICANT: HARVEY, Richard, C.
; APPLICANT: CLARK, JR., Thomas, J.
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FOR DETECTING GENETIC MARKERS
; FILE REFERENCE: GP097-03.DV1
; CURRENT APPLICATION NUMBER: US/10/273,707
; CURRENT FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: 09/493,491
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/117,640 US
; PRIOR FILING DATE: 1999-01-28
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 44
; LENGTH: 28
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: construct
; NAME/KEY: promoter
; LOCATION: (1)..(28)
US-10-273-707-44

Query Match      51.9%; Score 28; DB 15; Length 28;
Best Local Similarity 100.0%; Pred. No. 3.9e-06;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 TCTCCCTATAGTGCATTAATTTA 54
DB 28 TCTCCCTATAGTGCATTAATTTA 1

RESULT 15
US-09-876-527-29/c
; Sequence 29, Application US/09876527
; Patent No. US20020102616A1
; GENERAL INFORMATION:
; APPLICANT: Kindsvogel, Wayne
; APPLICANT: Jelinek, Laura J.

```

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; Sheppard, Paul O.
; Hagopian, William A.
; LaCasse, James M.
; TITLE OF INVENTION: ISLET CELL ANTIGEN 1851
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/876,527
; FILING DATE: 07-Jun-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/811,481
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Lingenfelter, Susan
; REGISTRATION NUMBER: P-41,156
; REFERENCE/DOCKET NUMBER: 95-36
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6675
; TELEFAX: 206-442-6678
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; IMMEDIATE SOURCE:
; CLONE: ZC11197
; SEQUENCE DESCRIPTION: SEQ ID NO: 29:
US-09-876-527-29

Query Match      51.9%; Score 28; DB 9; Length 30;
Best Local Similarity 100.0%; Pred. No. 3.9e-06;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 GTCTCCCTATAGTGCATTAATTT 53
DB 28 GTCTCCCTATAGTGCATTAATTT 1

Search completed: May 27, 2004, 14:58:25
Job time : 285.177 secs

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OM nucleic - nucleic search, using sw model

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(without alignments)  
845.770 Million cell updates/sec

Title: US-09-121-239-3

Perfect score: 54

Sequence: 1 TCTGACTTTCAGCCTCAGGG.....TAGTGAGTCGTATTATTTTA 54

Scoring table:

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Post-processing: Listing first 45 summaries

Database :

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1: em\_estba:\*  
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6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_hcc:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_hcc:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_estom:\*  
17: em\_gss\_hum:\*  
18: em\_gss\_inv:\*  
19: em\_gss\_pln:\*  
20: em\_gss\_vrt:\*  
21: em\_gss\_fun:\*  
22: em\_gss\_mam:\*  
23: em\_gss\_mus:\*  
24: em\_gss\_pro:\*  
25: em\_gss\_rod:\*  
26: em\_gss\_pbg:\*  
27: em\_gss\_vrl:\*  
28: gb\_gss1:\*  
29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	29	53.7	560	29	CC966861 BOIFL85TR
2	29	53.7	571	29	CC964269 BOIEN76TR
3	29	53.7	585	29	CC947693 BOISQ41TR
4	29	53.7	592	29	CC961654 BOIDB28TR

#### FEATURES

5	29	53.7	604	29	CC952121	BOIBI85TR
6	29	53.7	610	29	CC948768	BOIDG32TR
7	29	53.7	612	29	CC947463	BOIGK06TR
8	29	53.7	617	29	CC967304	BOIFK41TR
9	29	53.7	621	29	CC968451	BOIFB27TR
10	29	53.7	642	29	CC944751	BOIBU81TR
11	29	53.7	642	29	CC946396	BOICQ54TR
12	29	53.7	644	29	CC949404	BOIGZ19TR
13	29	53.7	644	29	CC951454	BOIEA62TR
14	29	53.7	649	29	CC962886	BOIGN54TR
15	29	53.7	651	29	CC961061	BOICX68TR
16	29	53.7	684	29	CC945503	BOIDK74TR
17	29	53.7	687	29	CC948738	BOIFI28TR
18	29	53.7	688	29	CC944195	CC944195 BOIBU59TR
19	29	53.7	693	29	CC944485	CC944485 BOIHL39TR
20	29	53.7	705	29	CC951566	CC951566 BOIRJ65TR
21	29	53.7	718	29	CC958824	BOIBW11TR
22	29	53.7	718	29	CC954347	CC954347 BOIBW60TR
23	29	53.7	719	29	CC968802	CC968802 BOICU62TR
24	29	53.7	727	29	CC969001	CC969001 BOICR93TR
25	29	53.7	735	29	CC961701	CC961701 BOIDQ39TR
26	29	53.7	830	29	CC953502	CC953502 BOIGT40TR
27	29	53.7	830	29	CC968053	CC968053 BOICE19TR
28	29	53.7	859	29	CC958532	CC958532 BOIFG34TR
29	28	51.9	143	13	BQ102727	BQ102727 UUGC0111
30	28	51.9	181	10	BE391582	BE391582 6011480148
31	28	51.9	182	10	BE262878	BE262878 6011480148
32	28	51.9	183	10	BF976190	BF976190 602245057
33	28	51.9	185	10	BE314661	BE314661 601146777
34	28	51.9	188	12	BG475075	BG475075 602491094
35	28	51.9	195	10	BE397962	BE397962 601290494
36	28	51.9	203	10	BF974085	BF974085 602240343
37	28	51.9	204	10	BE410828	BE410828 601301490
38	28	51.9	206	10	BE398063	BE398063 601290252
39	28	51.9	227	10	BQ27436	BQ27436 601672556
40	28	51.9	267	13	BQ102748	BQ102748 UUGC0132
41	28	51.9	272	10	BE391744	BE391744 601282029
42	28	51.9	310	13	BQ102753	BQ102753 UUGC0137
43	28	51.9	329	13	BQ102710	BQ102710 UUGC0094
44	28	51.9	334	12	BG425691	BG425691 602448292
45	28	51.9				

#### ALIGNMENTS

RESULT 1	CC966861	BOIFL85TR	BO_1.4_1.6_KB_nuc	Brassica oleracea	genomic clone	560 bp	DNA	linear	GSS 18-AUG-2003
LOCUS	CC966861	BOIFL85	genomic survey sequence.						
DEFINITION	CC966861								
ACCESSION	CC966861.1	GI:33819522							
VERSION									
KEYWORDS	GSS.								
SOURCE	Brassica oleracea								
ORGANISM	Brassica oleracea								
REFERENCE	1	(bases 1 to 560)							
AUTHORS	Town, C.D., Van Aken, S., Utterback, T., Koo, H. and Fraser, C.M.								
TITLE	Whole genome shotgun sequencing of Brassica oleracea								
JOURNAL	Unpublished (2001)								
COMMENT	Contact: Chris Town								

TIGR  
9712 Medical Center Drive, Rockville, MD 20850, USA.  
Tel: 301-838-3523  
Fax: 301-838-0208  
Email: cdtown@tigr.org  
DNA is from a doubled haploid provided by Tom Osborn.  
Seq primer: TR  
Class: sheared ends.  
Location/Qualifiers

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source
1. .560
/organism="Brassica oleracea"
/mol_type="genomic DNA"
/strain="TO1000DH3"
/db_xref="taxon:3712"
/clone="BO1FL85"
/notes="Vector: pHOS2; Site 1: BstXI; 1.4-1.6 kb sheared
nuclear DNA inserted into pHOS2 using BstXI linkers"

ORIGIN
Query Match 53.7%; Score 29; DB 29; Length 560;
Best Local Similarity 100.0%; Pred. No. 8.1e-06;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 GAGTCTCCCTATAGTCGATCGTATTAAATT 52
|||||
Db 149 GAGTCTCCCTATAGTCGATCGTATTAAATT 177

RESULT 2
LOCUS CC964269 571 bp DNA linear GSS 18-AUG-2003
DEFINITION BO1EN76R BO_1.4_1.6_KB_nuc Brassica oleracea genomic clone
ACCESSION CC964269
VERSION CC964269.1 GI:33814428
KEYWORDS GSS.
SOURCE Brassica oleracea
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE 1 (bases 1 to 571)
AUTHORS Town,C.D., Van Aken,S., Utterback,T., Koo,H. and Fraser,C.M.
TITLE Whole genome shotgun sequencing of Brassica oleracea
JOURNAL Unpublished (2001)
COMMENT Contact: Chris Town
TIGR 9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TR
Class: sheared ends.
Location/Qualifiers
1. .571
/organism="Brassica oleracea"
/mol_type="genomic DNA"
/strain="TO1000DH3"
/db_xref="taxon:3712"
/clone="BO1EN76"
/clone_lib="BO_1.4_1.6_KB_nuc"
/notes="Vector: pHOS2; Site 1: BstXI; 1.4-1.6 kb sheared
nuclear DNA inserted into pHOS2 using BstXI linkers"

ORIGIN
Query Match 53.7%; Score 29; DB 29; Length 571;
Best Local Similarity 100.0%; Pred. No. 8.1e-06;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 GAGTCTCCCTATAGTCGATCGTATTAAATT 52
|||||
Db 151 GAGTCTCCCTATAGTCGATCGTATTAAATT 179

RESULT 3
LOCUS CC947693 585 bp DNA linear GSS 18-AUG-2003
DEFINITION BO1EQ41R BO_1.4_1.6_KB_nuc Brassica oleracea genomic clone
ACCESSION CC947693
VERSION CC947693.1 GI:33781675
KEYWORDS GSS.
SOURCE Brassica oleracea
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE 1 (bases 1 to 585)
AUTHORS Town,C.D., Van Aken,S., Utterback,T., Koo,H. and Fraser,C.M.
TITLE Whole genome shotgun sequencing of Brassica oleracea
JOURNAL Unpublished (2001)
COMMENT Contact: Chris Town
TIGR 9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TR
Class: sheared ends.
Location/Qualifiers
1. .585
/organism="Brassica oleracea"
/mol_type="genomic DNA"
/strain="TO1000DH3"
/db_xref="taxon:3712"
/clone="BO1EQ41"
/clone_lib="BO_1.4_1.6_KB_nuc"
/notes="Vector: pHOS2; Site 1: BstXI; 1.4-1.6 kb sheared
nuclear DNA inserted into pHOS2 using BstXI linkers"

ORIGIN
Query Match 53.7%; Score 29; DB 29; Length 585;
Best Local Similarity 100.0%; Pred. No. 8.2e-06;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 GAGTCTCCCTATAGTCGATCGTATTAAATT 52
|||||
Db 149 GAGTCTCCCTATAGTCGATCGTATTAAATT 177

RESULT 4
LOCUS CC961654 592 bp DNA linear GSS 18-AUG-2003
DEFINITION BO1DB28R BO_1.4_1.6_KB_nuc Brassica oleracea genomic clone
ACCESSION CC961654
VERSION CC961654.1 GI:33809231
KEYWORDS GSS.
SOURCE Brassica oleracea
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE 1 (bases 1 to 592)
AUTHORS Town,C.D., Van Aken,S., Utterback,T., Koo,H. and Fraser,C.M.
TITLE Whole genome shotgun sequencing of Brassica oleracea
JOURNAL Unpublished (2001)
COMMENT Contact: Chris Town
TIGR 9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TR
Class: sheared ends.
Location/Qualifiers
1. .592
/organism="Brassica oleracea"
/mol_type="genomic DNA"
/strain="TO1000DH3"
/db_xref="taxon:3712"
/clone="BO1DB28"
/clone_lib="BO_1.4_1.6_KB_nuc"
/notes="Vector: pHOS2; Site 1: BstXI; 1.4-1.6 kb sheared
nuclear DNA inserted into pHOS2 using BstXI linkers"

ORIGIN
Query Match 53.7%; Score 29; DB 29; Length 592;
Best Local Similarity 100.0%; Pred. No. 8.2e-06;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 GAGTCTCCCTATAGTCGATCGTATTAAATT 52
|||||
Db 149 GAGTCTCCCTATAGTCGATCGTATTAAATT 177
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/clone_lib="BO_1.4_1.6_KB_nuc"
/notes="Vector: PHOS2; Site 1: BatXI; 1.4-1.6 kb sheared
nuclear DNA inserted into PHOS2 using BstXI linkers"

ORIGIN
Query Match          53.7%; Score 29; DB 29; Length 592;
Best Local Similarity 100.0%; Pred. No. 8.2e-06;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 GAGTCTCCCTATAGTCGATCGTATTAAAT 52
|||||
Db 156 GAGTCTCCCTATAGTCGATCGTATTAAAT 184

RESULT 5
CC952121
LOCUS BO_1.4_1.6_KB_nuc 604 bp DNA linear GSS 18-AUG-2003
DEFINITION BOIB185TR BO_1.4_1.6_KB_nuc Brassica oleracea genomic clone
BOIB185, genomic survey sequence.
ACCESSION CC952121
VERSION CC952121.1 GI:33790560
KEYWORDS GSS.
SOURCE Brassica oleracea
ORGANISM Brassica oleracea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
1 (bases 1 to 604)
Town, C.D., Van Aken, S., Utterback, T., Koo, H. and Fraser, C.M.
Whole genome shotgun sequencing of Brassica oleracea
Unpublished (2001)
Other GSSs: BOIB185TF
Contact: Chris Town
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TR
Class: sheared ends.

FEATURES
Location/Qualifiers
1..604
/organism="Brassica oleracea"
/mol_type="genomic DNA"
/strain="TO1000DH3"
/db_xref="taxon:3712"
/clone_lib="BO_1.4_1.6_KB_nuc"
/notes="Vector: PHOS2; Site 1: BatXI; 1.4-1.6 kb sheared
nuclear DNA inserted into PHOS2 using BstXI linkers"

REFERENCE
AUTHORS Town, C.D., Van Aken, S., Utterback, T., Koo, H. and Fraser, C.M.
TITLE Whole genome shotgun sequencing of Brassica oleracea
JOURNAL Unpublished (2001)
COMMENT Other GSSs: BOIB185TF
Contact: Chris Town
TIGR
Query Match          53.7%; Score 29; DB 29; Length 610;
Best Local Similarity 100.0%; Pred. No. 8.2e-06;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 GAGTCTCCCTATAGTCGATCGTATTAAAT 52
|||||
Db 242 GAGTCTCCCTATAGTCGATCGTATTAAAT 270

RESULT 7
CC947463
LOCUS BO_1.4_1.6_KB_nuc 612 bp DNA linear GSS 18-AUG-2003
DEFINITION BOIGK06TR BO_1.4_1.6_KB_nuc Brassica oleracea genomic clone
BOIGK06, genomic survey sequence.
ACCESSION CC947463
VERSION CC947463.1 GI:33781217
KEYWORDS GSS.
SOURCE Brassica oleracea
ORGANISM Brassica oleracea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
1 (bases 1 to 612)
Town, C.D., Van Aken, S., Utterback, T., Koo, H. and Fraser, C.M.
Whole genome shotgun sequencing of Brassica oleracea
Unpublished (2001)
Other GSSs: BOIGK06TF
Contact: Chris Town
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TR
Class: sheared ends.

FEATURES
Location/Qualifiers
1..612
/organism="Brassica oleracea"
/mol_type="genomic DNA"
/strain="TO1000DH3"
/db_xref="taxon:3712"
/clone_lib="BO_1.4_1.6_KB_nuc"

/clone_lib="BO_1.4_1.6_KB_nuc"
/notes="Vector: PHOS2; Site 1: BatXI; 1.4-1.6 kb sheared
nuclear DNA inserted into PHOS2 using BstXI linkers"

ORIGIN
Query Match          53.7%; Score 29; DB 29; Length 604;
Best Local Similarity 100.0%; Pred. No. 8.2e-06;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 GAGTCTCCCTATAGTCGATCGTATTAAAT 52
|||||
Db 157 GAGTCTCCCTATAGTCGATCGTATTAAAT 185

RESULT 6
CC948768
LOCUS BO_1.4_1.6_KB_nuc 610 bp DNA linear GSS 18-AUG-2003
DEFINITION BOIDG32TR BO_1.4_1.6_KB_nuc Brassica oleracea genomic clone
BOIDG32, genomic survey sequence.
ACCESSION CC948768
VERSION CC948768.1 GI:33783814
KEYWORDS GSS.
SOURCE Brassica oleracea
ORGANISM Brassica oleracea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
1 (bases 1 to 610)
Town, C.D., Van Aken, S., Utterback, T., Koo, H. and Fraser, C.M.
Whole genome shotgun sequencing of Brassica oleracea
Unpublished (2001)
Other GSSs: BOIDG32TF
Contact: Chris Town
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TR
Class: sheared ends.

FEATURES
Location/Qualifiers
1..610
/organism="Brassica oleracea"
/mol_type="genomic DNA"
/strain="TO1000DH3"
/db_xref="taxon:3712"
/clone_lib="BO_1.4_1.6_KB_nuc"
/notes="Vector: PHOS2; Site 1: BatXI; 1.4-1.6 kb sheared
nuclear DNA inserted into PHOS2 using BstXI linkers"

REFERENCE
AUTHORS Town, C.D., Van Aken, S., Utterback, T., Koo, H. and Fraser, C.M.
TITLE Whole genome shotgun sequencing of Brassica oleracea
JOURNAL Unpublished (2001)
COMMENT Other GSSs: BOIDG32TF
Contact: Chris Town
TIGR
Query Match          53.7%; Score 29; DB 29; Length 604;
Best Local Similarity 100.0%; Pred. No. 8.2e-06;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 GAGTCTCCCTATAGTCGATCGTATTAAAT 52
|||||
Db 157 GAGTCTCCCTATAGTCGATCGTATTAAAT 185

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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
1 (bases 1 to 610)
Town, C.D., Van Aken, S., Utterback, T., Koo, H. and Fraser, C.M.
Whole genome shotgun sequencing of Brassica oleracea
Unpublished (2001)
Other GSSs: BOIDG32TF
Contact: Chris Town
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TR
Class: sheared ends.

FEATURES
Location/Qualifiers
1..610
/organism="Brassica oleracea"
/mol_type="genomic DNA"
/strain="TO1000DH3"
/db_xref="taxon:3712"
/clone_lib="BOIDG32"
/clone_lib="BO_1.4_1.6_KB_nuc"
/notes="Vector: PHOS2; Site 1: BatXI; 1.4-1.6 kb sheared
nuclear DNA inserted into PHOS2 using BstXI linkers"

ORIGIN
Query Match          53.7%; Score 29; DB 29; Length 610;
Best Local Similarity 100.0%; Pred. No. 8.2e-06;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 GAGTCTCCCTATAGTCGATCGTATTAAAT 52
|||||
Db 242 GAGTCTCCCTATAGTCGATCGTATTAAAT 270

RESULT 7
CC947463
LOCUS BO_1.4_1.6_KB_nuc 612 bp DNA linear GSS 18-AUG-2003
DEFINITION BOIGK06TR BO_1.4_1.6_KB_nuc Brassica oleracea genomic clone
BOIGK06, genomic survey sequence.
ACCESSION CC947463
VERSION CC947463.1 GI:33781217
KEYWORDS GSS.
SOURCE Brassica oleracea
ORGANISM Brassica oleracea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
1 (bases 1 to 612)
Town, C.D., Van Aken, S., Utterback, T., Koo, H. and Fraser, C.M.
Whole genome shotgun sequencing of Brassica oleracea
Unpublished (2001)
Other GSSs: BOIGK06TF
Contact: Chris Town
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TR
Class: sheared ends.

FEATURES
Location/Qualifiers
1..612
/organism="Brassica oleracea"
/mol_type="genomic DNA"
/strain="TO1000DH3"
/db_xref="taxon:3712"
/clone_lib="BOIGK06"
/clone_lib="BO_1.4_1.6_KB_nuc"

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/notes=Vector: PHOS2; Site 1: BstXI; 1.4-1.6 kb sheared
nuclear DNA inserted into PHOS2 using BstXI linkers"

ORIGIN

Query Match      53.7%; Score 29; DB 29; Length 612;
Best Local Similarity 100.0%; Pred. No. 8.2e-06;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 GAGTCTCCCTATAGTGAGTCGTATTAAATT 52
|||||
Db 289 GAGTCTCCCTATAGTGAGTCGTATTAAATT 317

RESULT 8
CC967304 617 bp DNA linear GSS 18-AUG-2003
LOCUS BOIFK41TR BO_1.4_1.6_KB_nuc Brassica oleracea genomic clone
DEFINITION BOIFK41, genomic survey sequence.
ACCESSION CC967304
VERSION CC967304.1 GI:33820392
KEYWORDS GSS.
SOURCE Brassica oleracea
ORGANISM Brassica oleracea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE 1 (bases 1 to 617)
AUTHORS Town,C.D., Van Aken,S., Utterback,T., Koo,H. and Fraser,C.M.
TITLE Whole genome shotgun sequencing of Brassica oleracea
JOURNAL Unpublished (2001)
COMMENT Contact: Chris Town
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TR
Class: sheared ends.

FEATURES
source
1. .617
/organism="Brassica oleracea"
/mol_type="genomic DNA"
/strain="TO1000DH3"
/db_xref="taxon:3712"
/clone="BOIFK41"
/clone_lib="BO_1.4_1.6_KB_nuc"
/notes=Vector: PHOS2; Site 1: BstXI; 1.4-1.6 kb sheared
nuclear DNA inserted into PHOS2 using BstXI linkers"

ORIGIN

Query Match      53.7%; Score 29; DB 29; Length 617;
Best Local Similarity 100.0%; Pred. No. 8.3e-06;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 GAGTCTCCCTATAGTGAGTCGTATTAAATT 52
|||||
Db 296 GAGTCTCCCTATAGTGAGTCGTATTAAATT 324

RESULT 9
CC968451 621 bp DNA linear GSS 18-AUG-2003
LOCUS BOIFB27TR BO_1.4_1.6_KB_nuc Brassica oleracea genomic clone
DEFINITION BOIFB27, genomic survey sequence.
ACCESSION CC968451
VERSION CC968451.1 GI:33822676
KEYWORDS GSS.
SOURCE Brassica oleracea
ORGANISM Brassica oleracea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

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```

REFERENCE 1 (bases 1 to 621)
AUTHORS Town,C.D., Van Aken,S., Utterback,T., Koo,H. and Fraser,C.M.
TITLE Whole genome shotgun sequencing of Brassica oleracea
JOURNAL Unpublished (2001)
COMMENT Contact: Chris Town
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TR
Class: sheared ends.

FEATURES
source
1. .621
/organism="Brassica oleracea"
/mol_type="genomic DNA"
/strain="TO1000DH3"
/db_xref="taxon:3712"
/clone="BOIFB27"
/clone_lib="BO_1.4_1.6_KB_nuc"
/notes=Vector: PHOS2; Site 1: BstXI; 1.4-1.6 kb sheared
nuclear DNA inserted into PHOS2 using BstXI linkers"

ORIGIN

Query Match      53.7%; Score 29; DB 29; Length 621;
Best Local Similarity 100.0%; Pred. No. 8.3e-06;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 GAGTCTCCCTATAGTGAGTCGTATTAAATT 52
|||||
Db 159 GAGTCTCCCTATAGTGAGTCGTATTAAATT 187

RESULT 10
CC944751 642 bp DNA linear GSS 18-AUG-2003
LOCUS BOIBU81TR BO_1.4_1.6_KB_nuc Brassica oleracea genomic clone
DEFINITION BOIBU81, genomic survey sequence.
ACCESSION CC944751
VERSION CC944751.1 GI:33777617
KEYWORDS GSS.
SOURCE Brassica oleracea
ORGANISM Brassica oleracea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE 1 (bases 1 to 642)
AUTHORS Town,C.D., Van Aken,S., Utterback,T., Koo,H. and Fraser,C.M.
TITLE Whole genome shotgun sequencing of Brassica oleracea
JOURNAL Unpublished (2001)
COMMENT Contact: Chris Town
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TR
Class: sheared ends.

FEATURES
source
1. .642
/organism="Brassica oleracea"
/mol_type="genomic DNA"
/strain="TO1000DH3"
/db_xref="taxon:3712"
/clone="BOIBU81"
/clone_lib="BO_1.4_1.6_KB_nuc"
/notes=Vector: PHOS2; Site 1: BstXI; 1.4-1.6 kb sheared
nuclear DNA inserted into PHOS2 using BstXI linkers"

ORIGIN

Query Match      53.7%; Score 29; DB 29; Length 642;

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Best Local Similarity 100.0%; Pred. No. 8.3e-06;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 GAGTCTCCCTATAGTCGATCGTATTAAATT 52
|||||
Db 295 GAGTCTCCCTATAGTCGATCGTATTAAATT 323

RESULT 11
CC946396 642 bp DNA linear GSS 18-AUG-2003
LOCUS BOICQ54TR BO.1.4.1.6_KB_nuc Brassica oleracea genomic clone
DEFINITION BOICQ54, genomic survey sequence.
ACCESSION CC946396
VERSION /strain="TOL000DH3"
KEYWORDS /db_xref="taxon:3712"
SOURCE /clone="BOICG219"
ORGANISM /clone_lib="BO.1.4.1.6_KB_nuc"
Brassica oleracea
Brassica oleracea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE 1 (bases 1 to 642)
AUTHORS Town,C.D., Van Aken,S., Utterback,T., Koo,H. and Fraser,C.M.
TITLE Whole genome shotgun sequencing of Brassica oleracea
JOURNAL Unpublished (2001)
COMMENT Other_GSSs: BOICQ54TF
Contact: Chris Town
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TR
Class: sheared ends.

FEATURES
source
1..642
/organism="Brassica oleracea"
/mol_type="genomic DNA"
/strain="TOL000DH3"
/db_xref="taxon:3712"
/clone="BOICQ54"
/note="Vector: pHOS2; Site 1: BstXI; 1.4-1.6 kb sheared
nuclear DNA inserted into pHOS2 using BstXI linkers"

ORIGIN
Query Match 53.7%; Score 29; DB 29; Length 642;
Best Local Similarity 100.0%; Pred. No. 8.3e-06;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 12
CC949404 644 bp DNA linear GSS 18-AUG-2003
LOCUS BOIGZ19TR BO.1.4.1.6_KB_nuc Brassica oleracea genomic clone
DEFINITION BOIGZ19, genomic survey sequence.
ACCESSION CC949404
VERSION /strain="TOL000DH3"
KEYWORDS /db_xref="taxon:3712"
SOURCE /clone="BOIEA62"
ORGANISM /clone_lib="BO.1.4.1.6_KB_nuc"
Brassica oleracea
Brassica oleracea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE 1 (bases 1 to 644)
AUTHORS Town,C.D., Van Aken,S., Utterback,T., Koo,H. and Fraser,C.M.
TITLE Whole genome shotgun sequencing of Brassica oleracea
JOURNAL Unpublished (2001)
COMMENT Other_GSSs: BOIEA62TF
Contact: Chris Town
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TR
Class: sheared ends.

FEATURES
source
1..644
/organism="Brassica oleracea"
/mol_type="genomic DNA"
/strain="TOL000DH3"
/db_xref="taxon:3712"
/clone="BOIEA62"
/note="Vector: pHOS2; Site 1: BstXI; 1.4-1.6 kb sheared
nuclear DNA inserted into pHOS2 using BstXI linkers"

ORIGIN
Query Match 53.7%; Score 29; DB 29; Length 644;
Best Local Similarity 100.0%; Pred. No. 8.3e-06;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 GAGTCTCCCTATAGTCGATCGTATTAAATT 52
|||||
Db 156 GAGTCTCCCTATAGTCGATCGTATTAAATT 184

RESULT 12
CC949404 644 bp DNA linear GSS 18-AUG-2003
LOCUS BOIGZ19TR BO.1.4.1.6_KB_nuc Brassica oleracea genomic clone
DEFINITION BOIGZ19, genomic survey sequence.
ACCESSION CC949404
VERSION /strain="TOL000DH3"
KEYWORDS /db_xref="taxon:3712"
SOURCE /clone="BOIEA62"
ORGANISM /clone_lib="BO.1.4.1.6_KB_nuc"
Brassica oleracea
Brassica oleracea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE 1 (bases 1 to 644)
AUTHORS Town,C.D., Van Aken,S., Utterback,T., Koo,H. and Fraser,C.M.
TITLE Whole genome shotgun sequencing of Brassica oleracea
JOURNAL Unpublished (2001)
COMMENT Other_GSSs: BOIEA62TF
Contact: Chris Town
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TR
Class: sheared ends.

FEATURES
source
1..644
/organism="Brassica oleracea"
/mol_type="genomic DNA"
/strain="TOL000DH3"
/db_xref="taxon:3712"
/clone="BOIEA62"
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nuclear DNA inserted into pHOS2 using BstXI linkers"

ORIGIN
Query Match 53.7%; Score 29; DB 29; Length 642;
Best Local Similarity 100.0%; Pred. No. 8.3e-06;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 GAGTCTCCCTATAGTCGATCGTATTAAATT 52
|||||
Db 156 GAGTCTCCCTATAGTCGATCGTATTAAATT 184

```

```

COMMENT
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TR
Class: sheared ends.
Location/Qualifiers
1..644
/organism="Brassica oleracea"
/mol_type="genomic DNA"
/strain="TOL000DH3"
/db_xref="taxon:3712"
/clone="BOIGZ19"
/clone_lib="BO.1.4.1.6_KB_nuc"
/note="Vector: pHOS2; Site 1: BstXI; 1.4-1.6 kb sheared
nuclear DNA inserted into pHOS2 using BstXI linkers"

ORIGIN
Query Match 53.7%; Score 29; DB 29; Length 644;
Best Local Similarity 100.0%; Pred. No. 8.3e-06;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 GAGTCTCCCTATAGTCGATCGTATTAAATT 52
|||||
Db 149 GAGTCTCCCTATAGTCGATCGTATTAAATT 177

RESULT 13
CC951454 644 bp DNA linear GSS 18-AUG-2003
LOCUS BOIEA62TR BO.1.4.1.6_KB_nuc Brassica oleracea genomic clone
DEFINITION BOIEA62, genomic survey sequence.
ACCESSION CC951454
VERSION /strain="TOL000DH3"
KEYWORDS /db_xref="taxon:3712"
SOURCE /clone="BOIEA62"
ORGANISM /clone_lib="BO.1.4.1.6_KB_nuc"
Brassica oleracea
Brassica oleracea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE 1 (bases 1 to 644)
AUTHORS Town,C.D., Van Aken,S., Utterback,T., Koo,H. and Fraser,C.M.
TITLE Whole genome shotgun sequencing of Brassica oleracea
JOURNAL Unpublished (2001)
COMMENT Other_GSSs: BOIEA62TF
Contact: Chris Town
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TR
Class: sheared ends.
Location/Qualifiers
1..644
/organism="Brassica oleracea"
/mol_type="genomic DNA"
/strain="TOL000DH3"
/db_xref="taxon:3712"
/clone="BOIEA62"
/note="Vector: pHOS2; Site 1: BstXI; 1.4-1.6 kb sheared
nuclear DNA inserted into pHOS2 using BstXI linkers"

ORIGIN
Query Match 53.7%; Score 29; DB 29; Length 644;
Best Local Similarity 100.0%; Pred. No. 8.3e-06;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 GAGTCTCCCTATAGTCGATCGTATTAAATT 52
|||||
Db 149 GAGTCTCCCTATAGTCGATCGTATTAAATT 177

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Db 279 GAGTCTCCCTATAGTCGAGTCGTATTAAATT 307  
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RESULT 14

CC962886

LOCUS

DEFINITION

BOIGN54TR BO 1.4 1.6 KB nuc Brassica oleracea genomic clone

BOIGN54 genomic survey sequence.

ACCESSION

CC962886

VERSION

CC962886.1 GI:33811706

KEYWORDS

GSS.

SOURCE

Brassica oleracea

ORGANISM

Brassica oleracea

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

1 (bases 1 to 649)

Town,C.D., Van Aken,S., Utterback,T., Koo,H. and Fraser,C.M.

Whole genome shotgun sequencing of Brassica oleracea

Unpublished (2001)

CONTACT: Chris Town

TIGR

9712 Medical Center Drive, Rockville, MD 20850, USA.

Tel: 301-838-3523

Fax: 301-838-0208

Email: cdtown@tigr.org

DNA is from a doubled haploid provided by Tom Osborn.

Seq primer: TR

Class: sheared ends.

Location/Qualifiers

1..649

/organism="Brassica oleracea"

/mol\_type="genomic DNA"

/strain="TO1000DH3"

/db\_xref="taxon:3712"

/clone="BOIGN54"

/clone\_lib="BO 1.4 1.6 KB nuc"

/notes="Vector: PHOS2; Site 1: BstXI; 1.4-1.6 kb sheared

nuclear DNA inserted into PHOS2 using BstXI linkers"

Query Match 53.7%; Score 29; DB 29; Length 649;

Best Local Similarity 100.0%; Pred. No. 8.4e-06;

Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 GAGTCTCCCTATAGTCGAGTCGTATTAAATT 52

Db 156 GAGTCTCCCTATAGTCGAGTCGTATTAAATT 184

|||||

RESULT 15

CC961061

LOCUS

DEFINITION

BOICX68TR BO 1.4 1.6 KB nuc Brassica oleracea genomic clone

BOICX68 genomic survey sequence.

ACCESSION

CC961061

VERSION

CC961061.1 GI:33808062

KEYWORDS

GSS.

SOURCE

Brassica oleracea

ORGANISM

Brassica oleracea

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

1 (bases 1 to 651)

Town,C.D., Van Aken,S., Utterback,T., Koo,H. and Fraser,C.M.

Whole genome shotgun sequencing of Brassica oleracea

Unpublished (2001)

CONTACT: Chris Town

TIGR

9712 Medical Center Drive, Rockville, MD 20850, USA.

Tel: 301-838-3523

Fax: 301-838-0208

Email: cdtown@tigr.org  
DNA is from a doubled haploid provided by Tom Osborn.

Seq primer: TR

Class: sheared ends.

Location/Qualifiers

1..651

/organism="Brassica oleracea"

/mol\_type="genomic DNA"

/strain="TO1000DH3"

/db\_xref="taxon:3712"

/clone="BOICX68"

/clone\_lib="BO 1.4 1.6 KB nuc"

/note="Vector: PHOS2; Site 1: BstXI; 1.4-1.6 kb sheared

nuclear DNA inserted into PHOS2 using BstXI linkers"

Query Match 53.7%; Score 29; DB 29; Length 651;

Best Local Similarity 100.0%; Pred. No. 8.4e-06;

Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 GAGTCTCCCTATAGTCGAGTCGTATTAAATT 52

Db 156 GAGTCTCCCTATAGTCGAGTCGTATTAAATT 184

|||||

Search completed: May 26, 2004, 22:44:18

Job time : 1906.62 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: May 26, 2004, 16:00:31 ; Search time 1149.26 Seconds  
(without alignments)  
2036.547 Million cell updates/sec

Title: US-09-121-239-4  
Perfect score: 54  
Sequence: 1 UCUGACUUGAGCCUACGGG.....UAGUGAGUCGUUAUUAUUUA 54

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 3470272 seqs, 21671516995 residues

Word size : 0  
Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : GenEmbl.\*

- 1: gb\_ba.\*
- 2: gb\_htg.\*
- 3: gb\_in.\*
- 4: gb\_om.\*
- 5: gb\_ov.\*
- 6: gb\_pat.\*
- 7: gb\_ph.\*
- 8: gb\_pl.\*
- 9: gb\_pr.\*
- 10: gb\_ro.\*
- 11: gb\_sta.\*
- 12: gb\_sy.\*
- 13: gb\_un.\*
- 14: gb\_vi.\*
- 15: em\_ba.\*
- 16: em\_fun.\*
- 17: em\_hum.\*
- 18: em\_in.\*
- 19: em\_mu.\*
- 20: em\_om.\*
- 21: em\_or.\*
- 22: em\_ov.\*
- 23: em\_pat.\*
- 24: em\_ph.\*
- 25: em\_pl.\*
- 26: em\_ro.\*
- 27: em\_sta.\*
- 28: em\_un.\*
- 29: em\_vi.\*
- 30: em\_htg\_hum.\*
- 31: em\_htg\_inv.\*
- 32: em\_htg\_other.\*
- 33: em\_htg\_mus.\*
- 34: em\_htg\_pln.\*
- 35: em\_htg\_rod.\*
- 36: em\_htg\_man.\*
- 37: em\_htg\_vrt.\*
- 38: em\_sy.\*
- 39: em\_higo\_hum.\*
- 40: em\_higo\_mus.\*
- 41: em\_higo\_other.\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
C 1	54	100.0	54	6	BD222523	Methods f
C 2	54	100.0	54	6	BD222524	Methods f
C 3	54	100.0	54	6	BD222525	Methods f
C 4	54	100.0	54	6	BD222526	Methods f
C 5	49	90.7	50	6	AR352057	Sequence
C 6	32	59.3	54	6	BD236957	Nucleic a
C 7	32	59.3	54	6	AR307443	Sequence
C 8	30	55.6	49	6	BD236963	Nucleic a
C 9	30	55.6	49	6	AR307449	Sequence
C 10	30	55.6	50	6	BD236956	Nucleic a
C 11	30	55.6	50	6	AR307442	Sequence
C 12	30	55.6	52	6	BD236968	Nucleic a
C 13	30	55.6	52	6	AR307454	Sequence
C 14	29	53.7	37	6	I25071	Sequence 5
C 15	29	53.7	45	6	AX575411	Sequence
C 16	29	53.7	50	6	AR102985	Sequence
C 17	29	53.7	51	6	AR344851	Sequence
C 18	29	53.7	51	6	AX397806	Sequence
C 19	29	53.7	52	6	BD236961	Nucleic a
C 20	29	53.7	52	6	BD236967	Nucleic a
C 21	29	53.7	52	6	AR307447	Sequence
C 22	29	53.7	52	6	AR307453	Sequence
C 23	29	53.7	54	6	BD236955	Nucleic a
C 24	29	53.7	54	6	BD236974	Nucleic a
C 25	29	53.7	54	6	AR307441	Sequence
C 26	29	53.7	54	6	AR307460	Sequence
C 27	29	53.7	55	6	BD236972	Nucleic a
C 28	29	53.7	55	6	AR307458	Sequence
C 29	29	53.7	60	6	I25073	Sequence 7
C 30	29	53.7	79	6	I25069	Sequence 3
C 31	29	53.7	180	6	I25067	Sequence 1
C 32	29	53.7	586	6	AX701716	Sequence
C 33	29	53.7	1440	6	AX701737	Sequence
C 34	29	53.7	3073	12	CVU02284	Cloning vec
C 35	29	53.7	6306	6	AX286493	Sequence
C 36	29	53.7	7201	6	AX800664	Sequence
C 37	29	53.7	7231	6	AX806466	Sequence
C 38	29	53.7	7297	6	AX806467	Sequence
C 39	29	53.7	7429	6	AX839727	Sequence
C 40	29	53.7	7456	6	AX806465	Sequence
C 41	28	51.9	28	6	BD236969	Nucleic a
C 42	28	51.9	28	6	AR307455	Sequence
C 43	28	51.9	30	6	AR369578	Sequence
C 44	28	51.9	30	6	AR404157	Sequence
C 45	28	51.9	33	6	AR344815	Sequence

ALIGNMENTS

RESULT 1  
BD222523/c  
LOCUS BD222523 Methods for detecting and measuring spliced nucleic acids.  
DEFINITION  
ACCESSION BD222523  
VERSION BD222523.1 GI:33032293  
KEYWORDS JP 2002521037-A/1.  
SOURCE synthetic construct  
ORGANISM artificial sequences.  
REFERENCE 1 (bases 1 to 54)  
AUTHORS Harvey,R.C. and Eastman,P.S.  
TITLE Methods for detecting and measuring spliced nucleic acids  
JOURNAL Patent: JP 2002521037-A 1 16-JUL-2002;  
GEN PROBE INC

54 bp DNA linear PAT 17-JUL-2003



Query Match 100.0%; Score 54; DB 6; Length 54;  
Best Local Similarity 63.0%; Pred. No. 1.le-20;  
Matches 34; Conservative 20; Mismatches 0; Indels 0; Gaps 0;

QY 1 UCUGACUUGGCGCCUAGGCGUCGAGUCUCCUUAUAGUGAGUCGUAAUUA 54  
DB 1 TCCTGACCTTTGAGCCTCAGGCTCTGAGTCTCCCTATAGTCGATGCTATTATTTA 54

RESULT 5  
AR352057/c  
LOCUS AR352057 50 bp DNA linear PAT 17-AUG-2003  
DEFINITION Sequence 45 from patent US 6589734.  
ACCESSION AR352057  
VERSION AR352057.1 GI:33757020  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 50)  
AUTHORS Kacian,D.L., Fultz,T.J. and McDonough,S.H.  
TITLE Detection of HIV  
JOURNAL Patent: US 6589734-A 45 08-JUL-2003;  
FEATURES Location/Qualifiers  
source 1..50  
/organism="unknown"  
/mol\_type="genomic DNA"

## ORIGIN

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Best Local Similarity 65.3%; Pred. No. 1.le-17;  
Matches 32; Conservative 17; Mismatches 0; Indels 0; Gaps 0;

QY 4 GACUUGAGCCUAGGCGUCGAGUCUCCUUAUAGUGAGUCGUAAUUA 52  
DB 50 GACTTTGAGCCTCAGGCTCTGAGTCTCCCTATAGTCGATGCTATTATTT 2

RESULT 6  
BD236957/c  
LOCUS BD236957 54 bp DNA linear PAT 17-JUL-2003  
DEFINITION Nucleic acid sequence for detecting genetic marker for cancer in biological samples.

ACCESSION BD236957  
VERSION BD236957.1 GI:33046727  
KEYWORDS JP 2002535014-A/32.  
SOURCE synthetic construct  
ORGANISM artificial sequences.  
REFERENCE 1 (bases 1 to 54)  
AUTHORS Harvey,R.C. and Jr,T.J.C.  
TITLE Nucleic acid sequence for detecting genetic marker for cancer in biological samples  
JOURNAL Patent: JP 2002535014-A 32 22-OCT-2002;  
GEN PROBE INC

COMMENT OS Artificial Sequence  
PN JP 2002535014-A/32  
PD 22-OCT-2002  
PP 28-JAN-2000 JP 2000596180  
PR 28-JAN-1999 US 60/117640  
PI RICHARD C HARVEY,THOMAS J CLARK JR  
PC C12N15/09,C12Q1/68,C12N15/00  
CC Description of Artificial Sequence: synthetic construct FH  
KEY Location/Qualifiers  
FT promoter (1)..(28).  
Location/Qualifiers  
1..54  
/organism="synthetic construct"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"

FEATURES  
source

## ORIGIN

Query Match 59.3%; Score 32; DB 6; Length 54;  
Best Local Similarity 59.4%; Pred. No. 1.le-07;  
Matches 19; Conservative 13; Mismatches 0; Indels 0; Gaps 0;

QY 23 UGAGUCCUUAUAGUGAGUCGUAAUUA 54  
DB 32 TGAGTCTCCCTATAGTCGATGCTATTATTTA 1

RESULT 7  
AR307443/c  
LOCUS AR307443 54 bp DNA linear PAT 12-JUN-2003  
DEFINITION Sequence 32 from patent US 6551778.  
ACCESSION AR307443  
VERSION AR307443.1 GI:31697982  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 54)  
AUTHORS Harvey,R.C. and Clark,T.J. Jr.  
TITLE Nucleic acid sequences for detecting genetic markers for cancer in a biological sample  
JOURNAL Patent: US 6551778-A 32 22-APR-2003;  
FEATURES Location/Qualifiers  
source 1..54  
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## ORIGIN

Query Match 59.3%; Score 32; DB 6; Length 54;  
Best Local Similarity 59.4%; Pred. No. 1.le-07;  
Matches 19; Conservative 13; Mismatches 0; Indels 0; Gaps 0;

QY 23 UGAGUCCUUAUAGUGAGUCGUAAUUA 54  
DB 32 TGAGTCTCCCTATAGTCGATGCTATTATTTA 1

RESULT 8  
BD236963/c  
LOCUS BD236963 49 bp DNA linear PAT 17-JUL-2003  
DEFINITION Nucleic acid sequence for detecting genetic marker for cancer in biological samples.

ACCESSION BD236963  
VERSION BD236963.1 GI:33046733  
KEYWORDS JP 2002535014-A/38.  
SOURCE synthetic construct  
ORGANISM artificial sequences.  
REFERENCE 1 (bases 1 to 49)  
AUTHORS Harvey,R.C. and Jr,T.J.C.  
TITLE Nucleic acid sequence for detecting genetic marker for cancer in biological samples  
JOURNAL Patent: JP 2002535014-A 38 22-OCT-2002;  
GEN PROBE INC

COMMENT OS Artificial Sequence  
PN JP 2002535014-A/38  
PD 22-OCT-2002  
PP 28-JAN-2000 JP 2000596180  
PR 28-JAN-1999 US 60/117640  
PI RICHARD C HARVEY,THOMAS J CLARK JR  
PC C12N15/09,C12Q1/68,C12N15/00  
CC Description of Artificial Sequence: synthetic construct FH  
KEY Location/Qualifiers  
FT promoter (1)..(28).  
Location/Qualifiers  
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/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"

FEATURES  
source

## ORIGIN

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Best Local Similarity 60.0%; Pred. No. 1.5e-06;
Matches 18; Conservative 12; Mismatches 0; Indels 0; Gaps 0;

QY 25 AGUCUCCCUAUGAGUCGUAUUAUUUA 54
Db 30 AGTCTCCCTATAGTAGTCGTATTAATTTA 1

RESULT 9
AR307449/c
LOCUS      AR307449
DEFINITION Sequence 38 from patent US 6551778.
ACCESSION  AR307449
VERSION     AR307449.1 GI:31697988
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 49)
AUTHORS    Harvey,R.C. and Clark,T.J. Jr.
TITLE      Nucleic acid sequences for detecting genetic markers for cancer in
            a biological sample
JOURNAL    Patent: US 6551778-A 38 22-APR-2003;
FEATURES   Location/Qualifiers
            source
            1..49
            /organism="unknown"
            /mol_type="genomic DNA"
ORIGIN

Query Match      55.6%; Score 30; DB 6; Length 49;
Best Local Similarity 60.0%; Pred. No. 1.5e-06;
Matches 18; Conservative 12; Mismatches 0; Indels 0; Gaps 0;

QY 25 AGUCUCCCUAUGAGUCGUAUUAUUUA 54
Db 30 AGTCTCCCTATAGTAGTCGTATTAATTTA 1

RESULT 10
BD236956/c
LOCUS      BD236956
DEFINITION Nucleic acid sequence for detecting genetic marker for cancer in
            biological samples.
ACCESSION  BD236956
VERSION     BD236956.1 GI:33046726
KEYWORDS    JP 2002535014-A/31.
SOURCE      synthetic construct
ORGANISM    artificial sequences.
REFERENCE   1 (bases 1 to 50)
AUTHORS     Harvey,R.C. and Jr,T.J.C.
TITLE       Nucleic acid sequence for detecting genetic marker for cancer in
            biological samples
JOURNAL     Patent: JP 2002535014-A 31 22-OCT-2002;
COMMENT     GEN PROBE INC
            OS Artificial Sequence
            PN JP 2002535014-A/31
            PD 22-OCT-2002
            PF 28-JAN-2000 JP 2000596180
            PR 28-JAN-1999 US 60/117640
            PI RICHARD C HARVEY,THOMAS J CLARK JR
            PC C12N15/09.C12Q1/68.C12N15/00
            CC Description of Artificial Sequence: synthetic construct FH
            Key promoter Location/Qualifiers
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            source
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ORIGIN

Query Match      55.6%; Score 30; DB 6; Length 49;
Best Local Similarity 60.0%; Pred. No. 1.5e-06;
Matches 18; Conservative 12; Mismatches 0; Indels 0; Gaps 0;

QY 25 AGUCUCCCUAUGAGUCGUAUUAUUUA 54
Db 30 AGTCTCCCTATAGTAGTCGTATTAATTTA 1

RESULT 11
AR307442/c
LOCUS      AR307442
DEFINITION Sequence 31 from patent US 6551778.
ACCESSION  AR307442
VERSION     AR307442.1 GI:31697981
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 50)
AUTHORS    Harvey,R.C. and Clark,T.J. Jr.
TITLE      Nucleic acid sequences for detecting genetic markers for cancer in
            a biological sample
JOURNAL    Patent: US 6551778-A 31 22-APR-2003;
FEATURES   Location/Qualifiers
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ORIGIN

Query Match      55.6%; Score 30; DB 6; Length 50;
Best Local Similarity 60.0%; Pred. No. 1.5e-06;
Matches 18; Conservative 12; Mismatches 0; Indels 0; Gaps 0;

QY 25 AGUCUCCCUAUGAGUCGUAUUAUUUA 54
Db 30 AGTCTCCCTATAGTAGTCGTATTAATTTA 1

RESULT 12
BD236968/c
LOCUS      BD236968
DEFINITION Nucleic acid sequence for detecting genetic marker for cancer in
            biological samples.
ACCESSION  BD236968
VERSION     BD236968.1 GI:33046738
KEYWORDS    JP 2002535014-A/43.
SOURCE      synthetic construct
ORGANISM    artificial sequences.
REFERENCE   1 (bases 1 to 52)
AUTHORS     Harvey,R.C. and Jr,T.J.C.
TITLE       Nucleic acid sequence for detecting genetic marker for cancer in
            biological samples
JOURNAL     Patent: JP 2002535014-A 43 22-OCT-2002;
COMMENT     GEN PROBE INC
            OS Artificial Sequence
            PN JP 2002535014-A/43
            PD 22-OCT-2002
            PF 28-JAN-2000 JP 2000596180
            PR 28-JAN-1999 US 60/117640
            PI RICHARD C HARVEY,THOMAS J CLARK JR
            PC C12N15/09.C12Q1/68.C12N15/00
            CC Description of Artificial Sequence: synthetic construct PH
            Key promoter Location/Qualifiers
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            /mol_type="genomic DNA"
            /db_xref="taxon:32630"
ORIGIN
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VERSION      AX575411.1  GI:27552050
KEYWORDS
SOURCE
ORGANISM     synthetic construct
              synthetic construct
              artificial sequences.
REFERENCE    1
AUTHORS      Billy, E., Filipowicz, W. and Mueller, U.
TITLE        Methods of inhibiting expression of a target gene in mammalian
              cells
JOURNAL      Patent: WO 02068635-A 4 06-SEP-2002;
              Novartis Forschungsstiftung Zweigniederlassung (CH)
              Location/Qualifiers
              1..45
              /organism="synthetic construct"
              /mol_type="unassigned DNA"
              /db_xref="taxon:32630"
              /note="oligonucleotide"
FEATURES
source
ORIGIN
Query Match      53.7%; Score 29; DB 6; Length 45;
Best Local Similarity 65.5%; Pred. No. 6.1e-06;
Matches 19; Conservative 10; Mismatches 0; Indels 0; Gaps
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DB      29  CTGATCTCCCTATAGTCGATTTAA 1
Search completed: May 27, 2004, 02:16:34
Job time : 1149.26 secs

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: May 26, 2004, 14:55:11 ; Search time 240.833 Seconds  
(without alignments)  
952.539 Million cell updates/sec

Title: US-09-121-239-4  
Perfect score: 54  
Sequence: 1 UCUGACUUGAGCCUAGGG.....UAGUGAGUGCUUAUUAUUUA 54

Scoring table: OLIGO\_NUC  
Gapop\_60.0 , Gapext 60.0

Searched: 3373863 seqs, 2124099041 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Listing first 45 summaries

Database : N\_Geneseq\_29Jan04: \*  
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2: Geneseqn1990s: \*  
3: Geneseqn2000s: \*  
4: Geneseqn2001as: \*  
5: Geneseqn2001bs: \*  
6: Geneseqn2002s: \*  
7: Geneseqn2003as: \*  
8: Geneseqn2003bs: \*  
9: Geneseqn2003cs: \*  
10: Geneseqn2004s: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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1	54	100.0	54	3	Aaz60843 Oligonucl
2	54	100.0	54	3	Aaz60841 Oligonucl
3	54	100.0	54	3	Aaz60840 Oligonucl
4	54	100.0	54	3	Aaz60842 Oligonucl
5	49	90.7	50	2	Aaq86626 CML chrom
6	49	90.7	50	2	Aat15571 CML-2 chr
7	49	90.7	50	2	Aat42417 CML chrom
8	49	90.7	50	2	Aav66349 CML-2 chr
9	49	90.7	50	2	Aax23191 CML chrom
10	49	90.7	50	9	Aad52600 CML chrom
11	32	59.3	54	3	Aaa76067 Human pro
12	30	55.6	49	3	Aaa76206 Human pro
13	30	55.6	49	3	Aaa76066 Human pro
14	30	55.6	52	3	Aaa76211 Human pro
15	29	53.7	45	6	Abz59191 LacZ RNA
16	29	53.7	50	2	Aat07445 T7 gene 1
17	29	53.7	51	6	Abk53140 HIV-1 rev
18	29	53.7	51	6	Aal45502 HIV-1 pol
19	29	53.7	52	3	Aaa76210 Human pro
20	29	53.7	52	3	Aaa76204 Human pro
21	29	53.7	54	3	Aaa76220 Human pro
22	29	53.7	54	3	Aaa76085 Human pro
23	29	53.7	55	3	Aaa76218 Human gra

C 24	29	53.7	180	2	AAT41733	Aat41733 Promoter
C 25	29	53.7	1442	7	ABZ70392	Abz70392 AutoFluor
C 26	29	53.7	6306	6	ABA03923	Aba03923 Human NHP
C 27	29	53.7	7201	8	ACF05731	Acf05731 Plasmid p
C 28	29	53.7	7231	8	ACF06299	Acf06299 Plasmid p
C 29	29	53.7	7297	8	ACF06300	Acf06300 SigmuidIPA
C 30	29	53.7	7429	8	ACF05558	Acf05558 Plasmid p
C 31	29	53.7	7456	8	ACF06298	Acf06298 Plasmid p
C 32	28	51.9	28	3	AAA76212	Aaa76212 Human pro
C 33	28	51.9	30	2	AAT95233	Aat95233 Macaque s
C 34	28	51.9	33	4	AAD11020	Aad11020 Bacteriop
C 35	28	51.9	33	4	AAD11286	Aad11286 Bacteriop
C 36	28	51.9	33	6	ABK53104	Abk53104 T7 promot
C 37	28	51.9	33	6	ABK93905	Abk93905 Human imm
C 38	28	51.9	33	6	AAL45466	Aal45466 Bacteriop
C 39	28	51.9	35	2	AAV05796	Aav05796 Primer fo
C 40	28	51.9	35	2	AAV05794	Aav05794 Primer fo
C 41	28	51.9	35	6	AAL50495	Aal50495 3-frame H
C 42	28	51.9	35	8	ADA24416	Ada24416 His-tag v
C 43	28	51.9	36	4	AAC64735	Aac64735 Human pro
C 44	28	51.9	36	6	ABQ81381	Abq81381 Human pro
C 45	28	51.9	36	9	ADB71188	Adb71188 Human pro

## ALIGNMENTS

RESULT 1  
AAZ60843  
ID AAZ60843 standard; RNA; 54 BP.  
XX  
AC AAZ60843;  
XX  
DT 16-MAY-2000 (first entry)  
XX  
DE Oligonucleotide used to detect bcr b3-abl fusion transcripts.  
XX  
KW Fusion transcript; translocation; bcr b3 region; abl gene;  
KW amplification assay; detection assay; medical diagnosis;  
KW clinical monitoring; chimeric RNA; fusion RNA; condition marker;  
KW disease marker; cancer; leukemia; ss.  
XX  
OS Synthetic.  
XX  
PN WO200005418-A1.  
XX  
PD 03-FEB-2000.  
XX  
PF 23-JUL-1999; 99WO-US016832.  
XX  
PR 23-JUL-1998; 98US-00121239.  
XX  
PA (GENP-) GEN-PROBE INC.  
XX  
PI Harvey RC, Eastman PS;  
XX  
DR WPI; 2000-182730/16.  
XX  
PT Novel methods for preparing RNA from biological samples, used for the  
XX detection and measurement of nucleic acids and fusion nucleic acids.  
XX  
PS Claim 19; Page 40; 49pp; English.  
XX  
CC Oligonucleotides AAZ60840-62 and AAZ60865-66 are used in the method of  
CC the invention to detect fusion transcripts produced from a translocation  
CC between the bcr b3 region and the abl gene. The specification describes a  
CC method for detecting a fusion nucleic acid (particularly chimeric mRNA  
CC species), in a biological sample. The method comprises contacting a  
CC sample of fusion nucleic acid with primers, amplifying the hybridized  
CC fusion nucleic acid, and detecting the target hybrid. The method is used  
CC for the simple and rapid preparation of RNA from a biological sample,  
CC particularly from the cytoplasm of eukaryotic cells, which is suitable  
CC for use in an amplification and detection assay. The methods are used for



```

Query Match          100.0%; Score 54; DB 3; Length 54;
Best Local Similarity 63.0%; Pred. No. 1.8e-19;
Matches 34; Conservative 20; Mismatches 0; Indels 0; Gaps 0;

QY      1 UCUGACUUUGAGCCUCAGGGGUCUGAGUCCCUAAGAGUCGUUAUUUA 54
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Db      54 TCTGACTTGGCGCTCAGGGGTGAGTCTCCCTATGATGAGTCGTATTATTTA 1

RESULT 4
AAZ60842
ID AAZ60842 standard; DNA; 54 BP.
XX
AC AAZ60842;
XX
DT 16-MAY-2000 (first entry)
XX
DE Oligonucleotide used to detect bcr b3-abl fusion transcripts.
XX
KW Fusion transcript; translocation; bcr b3 region; abl gene;
KW amplification assay; detection assay; medical diagnosis;
KW clinical monitoring; chimeric RNA; fusion RNA; condition marker;
KW disease marker; cancer; leukemia; ss.
XX
OS Synthetic.
XX
WQ 2000005418-A1.
XX
PD 03-FEB-2000.
XX
PF 23-JUL-1999; 99WO-US016832.
XX
PR 23-JUL-1998; 98US-00121239.
XX
PA (GENP-) GEN-PROBE INC.
XX
PI Harvey RC, Eastman PS;
XX
DR WPI; 2000-182730/16.
XX
PT Novel methods for preparing RNA from biological samples, used for the
PT detection and measurement of nucleic acids and fusion nucleic acids.
XX
PS Claim 19; Page 40; 49pp; English.
XX
CC Oligonucleotides AAZ60840-62 and AAZ60865-66 are used in the method of
CC the invention to detect fusion transcripts produced from a translocation
CC between the bcr b3 region and the abl gene. The specification describes a
CC method for detecting a fusion nucleic acid (particularly chimeric mRNA
CC species), in a biological sample. The method comprises contacting a
CC sample of fusion nucleic acid with primers, amplifying the hybridized
CC fusion nucleic acid, and detecting the target hybrid. The method is used
CC for the simple and rapid preparation of RNA from a biological sample,
CC particularly from the cytoplasm of eukaryotic cells, which is suitable
CC for use in an amplification and detection assay. The methods are used for
CC the analysis and detection of nucleic acids in biological samples. The
CC methods are useful in the human medical and veterinary fields, for
CC medical diagnoses and clinical monitoring of a patient's response to
CC therapy where a disease or medical condition is associated with a
CC particular type and/or level of mRNA present in the sample. The methods
CC are also useful for detecting or quantifying fusion or chimeric RNA
CC species, and for detecting a translocation as a marker for a given
CC condition or disease, e.g., translocations associate with cancers,
CC particularly forms of leukemia
XX
SQ Sequence 54 BP; 11 A; 11 C; 12 G; 20 T; 0 U; 0 Other;

Query Match          100.0%; Score 54; DB 3; Length 54;
Best Local Similarity 63.0%; Pred. No. 1.8e-19;
Matches 34; Conservative 20; Mismatches 0; Indels 0; Gaps 0;

QY      1 UCUGACUUUGAGCCUCAGGGGUCUGAGUCCCUAAGAGUCGUUAUUUA 54
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PN US5480784-A.  
 XX  
 PD 02-JAN-1996.  
 XX  
 PF 10-JUL-1990; 90US-00550837.  
 XX  
 PR 11-JUL-1989; 89US-00379501.  
 XX  
 XX (GENP-) GEN-PROBE INC.  
 XX  
 PI Fultz TJ, Kacian DL;  
 XX  
 DR WPI; 1996-068248/07.  
 XX  
 PT Auto-catalytic synthesis of multiple copies of an RNA target sequence -  
 PT uses cooperative action of a DNA and RNA polymerase in presence of RNase  
 PT H, useful for detection of target sequence e.g. in clinical or  
 PT environmental sample.  
 XX  
 PS Example; Col 9-10; 5lpp; English.  
 XX  
 CC The present sequence is a primer for the CML-2 chromosomal translocation  
 CC major breakpoint t(9;22), which was used to demonstrate an improved  
 CC method for synthesising multiple copies of a RNA target sequence. The  
 CC method comprises combining the target with a primer which hybridises to  
 CC the 3'-terminal portion of the target, a promoter primer which hybridises  
 CC with a portion of the DNA primer extension prod., reverse transcriptase,  
 CC RNase H and transcriptase. It can be used as a component of an assay to  
 CC detect and/or quantitate specific target sequences in clinical,  
 CC environmental or forensic samples. It also has the advantages of being  
 CC autocatalytic, using the cooperative action of a DNA polymerase, e.g. a  
 CC reverse transcriptase and avoids repetitive manipulations of reaction  
 CC conditions, e.g. temp., ionic strength and pH. (Updated on 25-MAR-2003 to  
 CC correct PF field.)  
 XX  
 SQ Sequence 50 BP; 17 A; 12 C; 11 G; 10 T; 0 U; 0 Other;  
 Query Match 90.7%; Score 49; DB 2; Length 50;  
 Best Local Similarity 65.3%; Pred. No. 8.8e-17;  
 Matches 32; Conservative 17; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 GACUUGAGCCUAGGUCUGAGUCUCCUAGUAGUCGUCGUAAUAAU 52  
 Db 50 GACTTTGAGCCTCAGGCTCGAGTCTCCCTATAGTGCATTAATT 2  
 RESULT 7  
 AAT42417/c  
 ID AAT42417 standard; DNA; 50 BP.  
 XX  
 AC AAT42417;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 28-APR-1997 (first entry)  
 XX  
 DE CML chromosomal translocation primer #1.  
 XX  
 KW HIV; probe; primer; amplify; polymerase chain reaction; microorganism;  
 KW BCL-2; PCR; hepatitis B virus; HBV; CML; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN EP731175-A2.  
 XX  
 PD 11-SEP-1996.  
 XX  
 PF 10-JUL-1990; 96EP-00101621.  
 XX  
 PR 11-JUL-1989; 89US-00379501.  
 PR 10-JUL-1990; 90EP-00307503.  
 XX  
 XX (GENP-) GEN-PROBE INC.  
 XX  
 XX

PI McDonough S;  
 XX  
 DR WPI; 1996-403995/41.  
 XX  
 PT Detection of HIV nucleic acids in samples - using new specific oligo-  
 PT nucleotide(s) for the amplification and detection of target sequences.  
 XX  
 PS Disclosure; Page 8; 66pp; English.  
 XX  
 CC AAT42417-T42419 represent primers and a probe for the CML chromosomal  
 CC translocation t(9;22). These sequences can be used in modified versions  
 CC of the kits of the invention. The kits of the invention, are for  
 CC detecting the presence of HIV nucleic acid sequences in a sample. The  
 CC kits comprise two amplification primers (such as AAT40182 and AAT40183),  
 CC and a probe (such as AAT42404) for detection of the amplified sequence.  
 CC By using these sequences, the amplification of HIV nucleic acid sequences  
 CC is improved. The kits can also be used for the detection of other  
 CC microorganisms, by using different probe sequences. Other sequences that  
 CC can be detected using this method include those from HBV (using the  
 CC sequences shown in AAT42410-T42412), and BCL-2 (using AAT42413-T42416).  
 CC The samples can be clinical, environmental or forensic samples, and the  
 CC method produces large amounts of the target sequence for a variety of  
 CC uses. The method can also be used to produce multiple copies of a target  
 CC sequence for use in cloning, and sequencing, and to produce probes for  
 CC the target sequence. (Updated on 25-MAR-2003 to correct PF field.)  
 CC (Updated on 25-MAR-2003 to correct PR field.)  
 XX  
 SQ Sequence 50 BP; 17 A; 12 C; 11 G; 10 T; 0 U; 0 Other;  
 Query Match 90.7%; Score 49; DB 2; Length 50;  
 Best Local Similarity 65.3%; Pred. No. 8.8e-17;  
 Matches 32; Conservative 17; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 GACUUGAGCCUAGGUCUGAGUCUCCUAGUAGUCGUCGUAAUAAU 52  
 Db 50 GACTTTGAGCCTCAGGCTCGAGTCTCCCTATAGTGCATTAATT 2  
 RESULT 8  
 AAV66349/c  
 ID AAV66349 standard; DNA; 50 BP.  
 XX  
 AC AAV66349;  
 XX  
 DT 06-JAN-1999 (first entry)  
 XX  
 DE CML-2 chromosomal translocation t(9;22) primer.  
 XX  
 KW CML-2 chromosomal translocation t(9;22); block splice template;  
 KW autocatalytic RNA amplification; primer; ss.  
 OS Synthetic.  
 XX  
 PN US5824518-A.  
 XX  
 PD 20-OCT-1998.  
 XX  
 PF 06-JUN-1995; 95US-00469067.  
 XX  
 PR 11-JUL-1989; 89US-00379501.  
 PR 10-JUL-1990; 90US-00550837.  
 XX  
 PA (GENP-) GEN-PROBE INC.  
 XX  
 PI Fultz TJ, Kacian DL;  
 XX  
 DR WPI; 1998-582557/49.  
 XX  
 PT Block splice template useful for amplification of nucleic acids -  
 PT comprises two nucleic acid regions, the first region located 3' of the  
 PT second region and blocked at its 3' terminus to inhibit primer extension  
 PT by a DNA polymerase.  
 XX

```
PS Example 15; Col 9; 5lpp; English.
XX
CC AAV6349-50 represent CML-2 chromosomal translocation t(9;22) primers,
CC for the (+) and (-) strands respectively. The primers are used to
CC exemplify the invention, together with probe AAV6351. The specification
CC describes methods of synthesising multiple copies of a target nucleic
CC acid sequence autocatalytically under conditions of substantially
CC constant temperature, ionic strength and pH are provided in which
CC multiple RNA copies of the target sequence autocatalytically generate
CC additional copies. The target sequence is a block splice template which
CC comprises two nucleic acid regions. The first region is located 3' of the
CC second region and is blocked at its 3' terminus to inhibit primer
CC extension by a DNA polymerase, and the second region comprises a promoter
CC sequence recognised by an RNA polymerase. The methods are used to amplify
CC nucleic acids, especially RNA, for analysis, cloning or probe production
XX
SQ Sequence 50 BP; 17 A; 12 C; 11 G; 10 T; 0 U; 0 Other;
    Query Match          90.7%; Score 49; DB 2; Length 50;
    Best Local Similarity 65.3%; Pred. No. 8.8e-17;
    Matches 32; Conservative 17; Mismatches 0; Indels 0; Gaps 0;

QY 4 GACUUUGAGCCUCACGGGUCUGAGUCUCCUUAUAGUGAGUCGUUAUAAU 52
    |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db 50 GACTTTGAGCCTCAGGGTCTGAGTCTCCCTATAGTGCATTAATT 2

RESULT 9
AAAX23191/c
ID AAAX23191 standard; DNA; 50 BP.
XX
AC AAAX23191;
XX
DT 11-JUN-1999 (first entry)
DE CML chromosomal translocation t(9;22) primer #1.
XX
KW Autocatalytic amplification; transcription-based amplification; CML;
KW thermalcycling; diagnostic; environmental testing; probe; detection;
KW genetic disease; infectious disease; microorganism; food; forensic;
KW paternity; primer; ss.
XX
OS Synthetic.
XX
PN US5888779-A.
XX
PD 30-MAR-1999.
XX
PF 05-JUN-1995; 95US-00461654.
XX
PR 11-JUL-1989; 89US-00379501.
PR 10-JUL-1990; 90US-00550837.
XX
PA (GENP-) GEN-PROBE INC.
XX
PI Fultz TJ, Kacian DL;
XX
DR WPI; 1999-253231/21.
XX
PT Kit for autocatalytic amplification of RNA targets.
XX
PS Disclosure; Col 9; 5lpp; English.
XX
CC This invention describes a novel method for the autocatalytic
CC amplification of an RNA target in a transcription-based amplification
CC system without thermalcycling. The method generates oligonucleotides for
CC diagnostic or environmental testing, for use e.g. as probes and in
CC cloning. Typical applications are the detection of genetic or infectious
CC diseases, the monitoring of responses to therapy, the quantitation or
CC detection of microorganisms in foods, forensic studies and the
CC establishment of paternity. Kits containing the products of the invention
CC provide many copies of selected RNA targets under conditions of constant
CC temperature, ionic strength and pH. Specific amplification of RNA targets
XX

CC increases sensitivity, convenience, accuracy and the reliability of
CC assays
XX
SQ Sequence 50 BP; 17 A; 12 C; 11 G; 10 T; 0 U; 0 Other;
    Query Match          90.7%; Score 49; DB 2; Length 50;
    Best Local Similarity 65.3%; Pred. No. 8.8e-17;
    Matches 32; Conservative 17; Mismatches 0; Indels 0; Gaps 0;

QY 4 GACUUUGAGCCUCACGGGUCUGAGUCUCCUUAUAGUGAGUCGUUAUAAU 52
    |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db 50 GACTTTGAGCCTCAGGGTCTGAGTCTCCCTATAGTGCATTAATT 2

RESULT 10
AAD62600/c
ID AAD62600 standard; DNA; 50 BP.
XX
AC AAD62600;
XX
DT 15-JAN-2004 (first entry)
DE CML chromosomal translocation t(9;22) PCR primer #2.
XX
KW Amplification; human immunodeficiency virus; environmental testing; HIV;
KW detection; diagnostic testing; PCR; primer; ss.
XX
OS Unidentified.
XX
PN US6589734-B1.
XX
PD 08-JUL-2003.
XX
PF 08-OCT-1998; 98US-00168947.
XX
PR 11-JUL-1989; 89US-00379501.
PR 10-JUL-1990; 90US-00550837.
XX
PA (GENP-) GEN-PROBE INC.
XX
PI Kacian DL, Fultz TJ, McDonough SH;
XX
DR WPI; 2003-810379/76.
XX
PT New oligonucleotide probe, useful in detecting HIV nucleic acid in a
PT sample and for environmental and diagnostic testing.
XX
PS Disclosure; Col 9; 62pp; English.
XX
CC The invention relates to oligonucleotides useful in amplifying and
CC detecting human immunodeficiency virus (HIV) nucleic acid in a sample.
CC The invention is used for environmental testing, diagnostic testing,
CC research studies and for the preparation of reagents or materials for
CC cloning or other purposes. The present sequence is CML chromosomal
CC translocation t(9;22) PCR primer. This sequence is used in the invention
XX
SQ Sequence 50 BP; 17 A; 12 C; 11 G; 10 T; 0 U; 0 Other;
    Query Match          90.7%; Score 49; DB 9; Length 50;
    Best Local Similarity 65.3%; Pred. No. 8.8e-17;
    Matches 32; Conservative 17; Mismatches 0; Indels 0; Gaps 0;

QY 4 GACUUUGAGCCUCACGGGUCUGAGUCUCCUUAUAGUGAGUCGUUAUAAU 52
    |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db 50 GACTTTGAGCCTCAGGGTCTGAGTCTCCCTATAGTGCATTAATT 2

RESULT 11
AAA76067/c
ID AAA76067 standard; DNA; 54 BP.
XX
AC AAA76067;
```



CC markers for prostate and breast cancer, and PCR primers and probes which  
 CC are able to detect and quantify these markers. Prostate specific antigen  
 CC (PSA), prostate-specific membrane antigen (PSMA) and glandular kallikrein  
 CC -2 (hk2) have all been linked to prostate and breast cancers, and the  
 CC primers and probes of the invention are able to detect the abnormal  
 CC presence of mRNA expressed by their coding sequences in tissues other  
 CC than the prostate. This enables the presence of cancer to be perceived  
 CC and aids in the detection of metastases

XX Sequence 50 BP; 16 A; 11 C; 11 G; 12 T; 0 U; 0 Other;

Query Match 55.6%; Score 30; DB 3; Length 50;  
 Best Local Similarity 60.0%; Pred. No. 1.5e-06;  
 Matches 18; Conservative 12; Mismatches 0; Indels 0; Gaps 0;

QY 25 AGUCUCCCUAUGAGUCGUUAUUAUUA 54

DB 30 AGTCTCCCTATAGTAGTCGTATTATTA 1

RESULT 14

AAA76211/c

ID AAA76211 standard; DNA; 52 BP.

XX

AC AAA76211;

XX

DT 25-JAN-2001 (first entry)

XX

DE Human prostate specific antigen PCR primer SEQ ID NO: 40.

XX

XX Prostate specific antigen; PSA; prostate-specific membrane antigen; PSMA;

KW glandular kallikrein-2; hk2; prostate cancer; breast cancer; probe;

KW PCR primer; ss.

XX

OS Homo sapiens.

XX

PN WO200044940-A2.

XX

PD 03-AUG-2000.

XX

PF 28-JAN-2000; 2000WO-US002270.

XX

PR 28-JAN-1999; 99US-0117640P.

XX

PA (GENP-) GEN-PROBE INC.

XX

PI Harvey RC, Clark TJ;

XX

XX WPI; 2000-505986/45.

DR

PT Detecting prostate-specific antigen (PSA), prostate specific membrane

PT antigen (PSMA) or human kallikrein 2 (hk2) nucleic acids in samples using

PT probe molecules, useful for the diagnosis of prostate and breast cancers.

XX

PS Claim 1; Page 13; 77pp; English.

XX

CC The present invention is concerned with the detection of nucleic acid  
 CC markers for prostate and breast cancer, and PCR primers and probes which  
 CC are able to detect and quantify these markers. Prostate specific antigen  
 CC (PSA), prostate-specific membrane antigen (PSMA) and glandular kallikrein  
 CC -2 (hk2) have all been linked to prostate and breast cancers, and the  
 CC primers and probes of the invention are able to detect the abnormal  
 CC presence of mRNA expressed by their coding sequences in tissues other  
 CC than the prostate. This enables the presence of cancer to be perceived  
 CC and aids in the detection of metastases

XX Sequence 52 BP; 17 A; 11 C; 11 G; 13 T; 0 U; 0 Other;

Query Match 55.6%; Score 30; DB 3; Length 52;

Best Local Similarity 60.0%; Pred. No. 1.5e-06;

Matches 18; Conservative 12; Mismatches 0; Indels 0; Gaps 0;

QY 25 AGUCUCCCUAUGAGUCGUUAUUAUUA 54

DB 30 AGTCTCCCTATAGTAGTCGTATTATTA 1

RESULT 15

ABZ59191/c

ID ABZ59191 standard; DNA; 45 BP.

XX

AC ABZ59191;

XX

DT 15-MAY-2003 (first entry)

XX

DE LacZ RNA generating primer.

XX

KW LacZ; gene expression; gene function; pharmaceutical; PCR; primer; ss.

XX

OS Synthetic.

XX

PN WO200268635-A2.

XX

PD 06-SEP-2002.

XX

PF 27-FEB-2002; 2002WO-EP002098.

XX

PR 28-FEB-2001; 2001GB-00004948.

XX

PA (NOVS ) NOVARTIS FORSCHUNGSSTIFTUNG ZWEIGNIEDERL.

XX

PI Billy E, Filipowicz W, Mueller U;

XX

DR WPI; 2002-706992/76.

XX

PT Inhibiting expression of a target gene, useful for identifying gene  
 PT function in an organism, comprises exposing a mammalian cell to a  
 PT partially double-stranded ribonucleic acid with at least 60% sequence  
 PT identity to a target gene.

XX

PS Example 1; Page 16; 31pp; English.

XX

CC The invention relates to inhibiting expression of a target gene. The  
 CC method involves exposing a renewable, mammalian cell to a partially  
 CC double-stranded ribonucleic acid and with at least 60% sequence identity  
 CC to a target gene. The method is useful for identifying gene function in  
 CC an organism, in determining potential targets for pharmaceuticals,  
 CC and determining normal and pathological events associated with development,  
 CC aging. The method may also be used to allow the inhibition of essential  
 CC genes which may be required for cell or organism viability at particular  
 CC stages of development or cellular compartments, and to allow addition or  
 CC expression of RNA at specific times of development and locations in the  
 CC organism without introducing permanent mutations into the target genome.  
 CC The present sequence represents a PCR primer for generating a lacZ RNA,  
 CC used in the preparation of dsRNA

XX Sequence 45 BP; 15 A; 10 C; 10 G; 10 T; 0 U; 0 Other;

Query Match 53.7%; Score 29; DB 6; Length 45;

Best Local Similarity 65.5%; Pred. No. 5.3e-06;

Matches 19; Conservative 10; Mismatches 0; Indels 0; Gaps 0;

QY 22 CUGAGUCCCUAUGAGUCGUUAUUA 50

DB 29 CTGAGTCTCCCTATAGTAGTCGTATTAA 1

Search completed: May 26, 2004, 16:52:13

Job time : 240.833 secs

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Result No.	Query %			DB	ID	Description
	Score	Match	Length			
C 1	49	90.7	50	4	US-09-168-947-45	Sequence 45, Appl
C 2	32	59.3	54	4	US-09-493-491-29	Sequence 29, Appl
C 3	32	59.3	54	4	US-09-493-491A-32	Sequence 32, Appl
C 4	30	55.6	49	4	US-09-493-491-35	Sequence 35, Appl
C 5	30	55.6	49	4	US-09-493-491A-38	Sequence 38, Appl
C 6	30	55.6	50	4	US-09-493-491-28	Sequence 28, Appl
C 7	30	55.6	50	4	US-09-493-491A-31	Sequence 31, Appl
C 8	30	55.6	52	4	US-09-493-491-40	Sequence 40, Appl
C 9	30	55.6	52	4	US-09-493-491A-43	Sequence 43, Appl
C 10	29	53.7	37	1	US-08-099-867-5	Sequence 5, Appl
C 11	29	53.7	50	3	US-08-972-799A-25	Sequence 25, Appl
C 12	29	53.7	50	3	US-09-506-282-25	Sequence 25, Appl
C 13	29	53.7	50	5	PCT-US95-03339-25	Sequence 25, Appl
C 14	29	53.7	51	4	US-09-944-036-40	Sequence 40, Appl
C 15	29	53.7	52	4	US-09-493-491-33	Sequence 33, Appl
C 16	29	53.7	52	4	US-09-493-491-39	Sequence 39, Appl
C 17	29	53.7	52	4	US-09-493-491A-36	Sequence 36, Appl
C 18	29	53.7	52	4	US-09-493-491A-42	Sequence 42, Appl
C 19	29	53.7	54	4	US-09-493-491-27	Sequence 27, Appl
C 20	29	53.7	54	4	US-09-493-491-49	Sequence 49, Appl
C 21	29	53.7	54	4	US-09-493-491A-30	Sequence 30, Appl
C 22	29	53.7	54	4	US-09-493-491A-49	Sequence 49, Appl
C 23	29	53.7	55	4	US-09-493-491-47	Sequence 47, Appl
C 24	29	53.7	60	4	US-09-493-491A-47	Sequence 47, Appl
C 25	29	53.7	60	1	US-08-099-867-7	Sequence 7, Appl
C 26	29	53.7	79	1	US-08-099-867-3	Sequence 3, Appl
C 27	29	53.7	80	1	US-08-099-867-1	Sequence 1, Appl

; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 29  
; LENGTH: 54  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: construct  
US-09-493-491-29

Query Match 59.3%; Score 32; DB 4; Length 54;  
Best Local Similarity 59.4%; Pred. No. 9.1e-09;  
Matches 19; Conservative 13; Mismatches 0; Indels 0; Gaps 0;

Qy 23 UGAGUCUCCUAGAGUCGUAUUAUUA 54  
||:||||:||||:||||:||||:||||:||||:  
Db 32 TGAGTCTCCCTAGTAGTGAGTCGTAATAATT 1

## RESULT 3

US-09-493-491A-32/c  
; Sequence 32, Application US/09493491A  
; Patent No. 6551778  
; GENERAL INFORMATION:  
; APPLICANT: HARVEY, Richard, C.  
; APPLICANT: CLARK, JR., Thomas, J.  
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FOR DETECTING GENETIC MARKERS  
; TITLE OF INVENTION: FOR CANCER IN A BIOLOGICAL SAMPLE  
; FILE REFERENCE: GP097-02.UT  
; CURRENT APPLICATION NUMBER: US/09/493,491A  
; PRIOR FILING DATE: 2000-01-28  
; PRIOR APPLICATION NUMBER: 60/117,640 US  
; PRIOR FILING DATE: 1999-01-28  
; NUMBER OF SEQ ID NOS: 50  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 32  
; LENGTH: 54  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: construct  
; NAME/KEY: promoter  
; LOCATION: (1)..(28)  
US-09-493-491A-32

Query Match 59.3%; Score 32; DB 4; Length 54;  
Best Local Similarity 59.4%; Pred. No. 9.1e-09;  
Matches 19; Conservative 13; Mismatches 0; Indels 0; Gaps 0;

Qy 23 UGAGUCUCCUAGAGUCGUAUUAUUA 54  
||:||||:||||:||||:||||:||||:||||:  
Db 32 TGAGTCTCCCTAGTAGTGAGTCGTAATAATT 1

## RESULT 4

US-09-493-491-35/c  
; Sequence 35, Application US/09493491  
; Patent No. 6391556  
; GENERAL INFORMATION:  
; APPLICANT: HARVEY, Richard, C.  
; APPLICANT: CLARK, JR., Thomas, J.  
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FOR DETECTING GENETIC MARKERS  
; TITLE OF INVENTION: FOR CANCER IN A BIOLOGICAL SAMPLE  
; FILE REFERENCE: GP097-02.UT  
; CURRENT APPLICATION NUMBER: US/09/493,491  
; PRIOR FILING DATE: 2000-01-28  
; PRIOR APPLICATION NUMBER: 60/117,640 US  
; PRIOR FILING DATE: 1999-01-28  
; NUMBER OF SEQ ID NOS: 50  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 35

; LENGTH: 49  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: construct  
US-09-493-491-35

Query Match 55.6%; Score 30; DB 4; Length 49;  
Best Local Similarity 60.0%; Pred. No. 1.2e-07;  
Matches 18; Conservative 12; Mismatches 0; Indels 0; Gaps 0;

Qy 25 AGUCUCCUAGAGUCGUAUUAUUA 54  
||:||||:||||:||||:||||:||||:||||:  
Db 30 AGTCTCCCTAGTAGTGAGTCGTAATAATT 1

## RESULT 5

US-09-493-491A-38/c  
; Sequence 38, Application US/09493491A  
; Patent No. 6551778  
; GENERAL INFORMATION:  
; APPLICANT: HARVEY, Richard, C.  
; APPLICANT: CLARK, JR., Thomas, J.  
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FOR DETECTING GENETIC MARKERS  
; TITLE OF INVENTION: FOR CANCER IN A BIOLOGICAL SAMPLE  
; FILE REFERENCE: GP097-02.UT  
; CURRENT APPLICATION NUMBER: US/09/493,491A  
; CURRENT FILING DATE: 2000-01-28  
; PRIOR APPLICATION NUMBER: 60/117,640 US  
; PRIOR FILING DATE: 1999-01-28  
; NUMBER OF SEQ ID NOS: 50  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 38  
; LENGTH: 49  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: construct  
; NAME/KEY: promoter  
; LOCATION: (1)..(28)  
US-09-493-491A-38

Query Match 55.6%; Score 30; DB 4; Length 49;  
Best Local Similarity 60.0%; Pred. No. 1.2e-07;  
Matches 18; Conservative 12; Mismatches 0; Indels 0; Gaps 0;

Qy 25 AGUCUCCUAGAGUCGUAUUAUUA 54  
||:||||:||||:||||:||||:||||:||||:  
Db 30 AGTCTCCCTAGTAGTGAGTCGTAATAATT 1

## RESULT 6

US-09-493-491-28/c  
; Sequence 28, Application US/09493491  
; Patent No. 6391556  
; GENERAL INFORMATION:  
; APPLICANT: HARVEY, Richard, C.  
; APPLICANT: CLARK, JR., Thomas, J.  
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FOR DETECTING GENETIC MARKERS  
; TITLE OF INVENTION: FOR CANCER IN A BIOLOGICAL SAMPLE  
; FILE REFERENCE: GP097-02.UT  
; CURRENT APPLICATION NUMBER: US/09/493,491  
; CURRENT FILING DATE: 2000-01-28  
; EARLIER APPLICATION NUMBER: 60/117,640 US  
; EARLIER FILING DATE: 1999-01-28  
; NUMBER OF SEQ ID NOS: 50  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 28  
; LENGTH: 50  
; TYPE: DNA

; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: construct  
US-09-493-491-28

Query Match 55.6%; Score 30; DB 4; Length 50;  
Best Local Similarity 60.0%; Pred. No. 1.2e-07;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 25 AGUCUCCCUAUGAGUCGUAAUUAUUA 54  
||:||||:||||:||||:||||:||||:|  
Db 30 AGTCTCCCTATAGTCGATGCTATTATTA 1

## RESULT 7

US-09-493-491A-31/c  
; Sequence 31, Application US/09493491A  
; Patent No. 6551778  
; GENERAL INFORMATION:  
; APPLICANT: HARVEY, Richard, C.  
; APPLICANT: CLARK, JR., Thomas, J.  
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FOR DETECTING GENETIC MARKERS  
; FILE REFERENCE: GP097-02.UT  
; CURRENT APPLICATION NUMBER: US/09/493,491A  
; CURRENT FILING DATE: 2000-01-28  
; PRIOR APPLICATION NUMBER: 60/117,640 US  
; PRIOR FILING DATE: 1999-01-28  
; NUMBER OF SEQ ID NOS: 50  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 31  
; LENGTH: 50  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: construct  
; FEATURE:  
; NAME/KEY: promoter  
; LOCATION: (1)..(28)  
US-09-493-491A-31

Query Match 55.6%; Score 30; DB 4; Length 50;  
Best Local Similarity 60.0%; Pred. No. 1.2e-07;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 25 AGUCUCCCUAUGAGUCGUAAUUAUUA 54  
||:||||:||||:||||:||||:||||:|  
Db 30 AGTCTCCCTATAGTCGATGCTATTATTA 1

## RESULT 8

US-09-493-491-40/c  
; Sequence 40, Application US/09493491  
; Patent No. 6391556  
; GENERAL INFORMATION:  
; APPLICANT: HARVEY, Richard, C.  
; APPLICANT: CLARK, JR., Thomas, J.  
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FOR DETECTING GENETIC MARKERS  
; FILE REFERENCE: GP097-02.UT  
; CURRENT APPLICATION NUMBER: US/09/493,491  
; CURRENT FILING DATE: 2000-01-28  
; EARLIER APPLICATION NUMBER: 60/117,640 US  
; EARLIER FILING DATE: 1999-01-28  
; NUMBER OF SEQ ID NOS: 50  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 40  
; LENGTH: 52  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: construct  
US-09-493-491-40

Query Match 55.6%; Score 30; DB 4; Length 52;  
Best Local Similarity 60.0%; Pred. No. 1.2e-07;  
Matches 18; Conservative 12; Mismatches 0; Indels 0; Gaps 0;

QY 25 AGUCUCCCUAUGAGUCGUAAUUAUUA 54  
||:||||:||||:||||:||||:||||:|  
Db 30 AGTCTCCCTATAGTCGATGCTATTATTA 1

## RESULT 9

US-09-493-491A-43/c  
; Sequence 43, Application US/09493491A  
; Patent No. 6551778  
; GENERAL INFORMATION:  
; APPLICANT: HARVEY, Richard, C.  
; APPLICANT: CLARK, JR., Thomas, J.  
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FOR DETECTING GENETIC MARKERS  
; FILE REFERENCE: GP097-02.UT  
; CURRENT APPLICATION NUMBER: US/09/493,491A  
; CURRENT FILING DATE: 2000-01-28  
; PRIOR APPLICATION NUMBER: 60/117,640 US  
; PRIOR FILING DATE: 1999-01-28  
; NUMBER OF SEQ ID NOS: 50  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 43  
; LENGTH: 52  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: construct  
; FEATURE:  
; NAME/KEY: promoter  
; LOCATION: (1)..(28)  
US-09-493-491A-43

Query Match 55.6%; Score 30; DB 4; Length 52;  
Best Local Similarity 60.0%; Pred. No. 1.2e-07;  
Matches 18; Conservative 12; Mismatches 0; Indels 0; Gaps 0;

QY 25 AGUCUCCCUAUGAGUCGUAAUUAUUA 54  
||:||||:||||:||||:||||:||||:|  
Db 30 AGTCTCCCTATAGTCGATGCTATTATTA 1

## RESULT 10

US-08-099-867-5/c  
; Sequence 5, Application US/08099867  
; Patent No. 5547862  
; GENERAL INFORMATION:  
; APPLICANT: James Meador  
; APPLICANT: Hoyt E. McElroy  
; APPLICANT: Michelle L. Herrmann  
; APPLICANT: Matthew Winkler  
; TITLE OF INVENTION: Vectors Containing Multiple Promoters  
; TITLE OF INVENTION: in the Same Orientation  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Arnold, White & Durkee  
; STREET: P.O. Box 4433  
; CITY: Houston  
; STATE: Texas  
; COUNTRY: USA  
; ZIP: 77210  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy Disk  
; COMPUTER: IBM PC Compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS



PCT-US95-03339-25/c  
; Sequence 25, Application PC/TUS9503339  
; GENERAL INFORMATION:  
; APPLICANT:  
; TITLE OF INVENTION: ISOTHERMAL STRAND DISPLACEMENT NUCLEIC ACID  
; TITLE OF INVENTION: AMPLIFICATION  
; NUMBER OF SEQUENCES: 27  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (BPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US95/03339  
; FILING DATE:  
; CLASSIFICATION:  
; INFORMATION FOR SEQ ID NO: 25:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 50 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
PCT-US95-03339-25

Query Match 53.7%; Score 29; DB 5; Length 50;  
Best Local Similarity 58.6%; Pred. No. 4.1e-07;  
Matches 17; Conservative 12; Mismatches 0; Indels 0; Gaps 0;  
QY 25 AGUCUCCCUAUGAGUCGUAAUUU 53  
Db 30 AGTCTCCCTATAGTGAGTCGTATTATTT 2

RESULT 14  
US-09-944-036-40/c  
; Sequence 40, Application US/09944036  
; Patent No. 6582920  
; GENERAL INFORMATION:  
; APPLICANT: YANG, Yeasing Y.  
; APPLICANT: BRENTANO, Steven T.  
; APPLICANT: BABOLA, Odile  
; APPLICANT: TRAN, Nathalie  
; APPLICANT: VERNET, Guy  
; TITLE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF  
; TITLE OF INVENTION: SEQUENCES ASSOCIATED WITH DRUG-RESISTANCE MUTATIONS  
; FILE REFERENCE: GP114-02.UT  
; CURRENT APPLICATION NUMBER: US/09/944,036  
; CURRENT FILING DATE: 2001-08-31  
; PRIOR APPLICATION NUMBER: US 60/229,790  
; PRIOR FILING DATE: 2000-09-01  
; NUMBER OF SEQ ID NOS: 70  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 40  
; LENGTH: 51  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:  
; OTHER INFORMATION: Oligonucleotide primer for Reverse Transcriptase  
; OTHER INFORMATION: target sequence  
; NAME/KEY: promoter  
; LOCATION: (1)..(29)  
US-09-944-036-40

Query Match 53.7%; Score 29; DB 4; Length 51;  
Best Local Similarity 58.6%; Pred. No. 4.1e-07;  
Matches 17; Conservative 12; Mismatches 0; Indels 0; Gaps 0;  
QY 25 AGUCUCCCUAUGAGUCGUAAUUU 53  
Db 29 AGTCTCCCTATAGTGAGTCGTATTATTT 1

RESULT 15  
US-09-493-491-33/c  
; Sequence 33, Application US/09493491  
; Patent No. 6391556  
; GENERAL INFORMATION:  
; APPLICANT: HARVEY, Richard, C.  
; APPLICANT: CLARK, JR., Thomas, J.  
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FOR DETECTING GENETIC MARKERS  
; TITLE OF INVENTION: FOR CANCER IN A BIOLOGICAL SAMPLE  
; FILE REFERENCE: GP097-02.UT  
; CURRENT APPLICATION NUMBER: US/09/493,491  
; CURRENT FILING DATE: 2000-01-28  
; EARLIER APPLICATION NUMBER: 60/117,640 US  
; EARLIER FILING DATE: 1999-01-28  
; NUMBER OF SEQ ID NOS: 50  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 33  
; LENGTH: 52  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: Construct  
US-09-493-491-33

Query Match 53.7%; Score 29; DB 4; Length 52;  
Best Local Similarity 58.6%; Pred. No. 4.1e-07;  
Matches 17; Conservative 12; Mismatches 0; Indels 0; Gaps 0;  
QY 26 GUCUCCCUAUGAGUCGUAAUUU 54  
Db 29 GTCTCCCTATAGTGAGTCGTATTATTT 1

Search completed: May 27, 2004, 02:25:08  
Job time : 45.5117 sec

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RESULT 2
US-10-273-707-32/c
; Sequence 32, Application US/10273707
; Publication No. US20030104448A1
; GENERAL INFORMATION:
; APPLICANT: HARVEY, Richard, C.
; APPLICANT: CLARK, JR., Thomas, J.
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FOR DETECTING GENETIC MARKERS
; TITLE OF INVENTION: FOR CANCER IN A BIOLOGICAL SAMPLE
; FILE REFERENCE: GP097-03.DV1
; CURRENT APPLICATION NUMBER: US/10/273,707
; CURRENT FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: 09/493,491
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/117,640 US
; PRIOR FILING DATE: 1999-01-28
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 32
; LENGTH: 54
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: construct
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (1)..(28)
US-10-273-707-32

Query Match          59.3%; Score 32; DB 15; Length 54;
Best Local Similarity 59.4%; Pred. No. 2e-08;
Matches 19; Conservative 13; Mismatches 0; Indels 0; Gaps 0;

QY      23 UGAGUCUCCUAGUAGUGAGUCGUAAUUUA 54
Db      32 TGAGTCTCCCTATAGTAGTGAGTCGTATTA 1

RESULT 3
US-10-273-707-38/c
; Sequence 38, Application US/10273707
; Publication No. US20030104448A1
; GENERAL INFORMATION:
; APPLICANT: HARVEY, Richard, C.
; APPLICANT: CLARK, JR., Thomas, J.
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FOR DETECTING GENETIC MARKERS
; TITLE OF INVENTION: FOR CANCER IN A BIOLOGICAL SAMPLE
; FILE REFERENCE: GP097-03.DV1
; CURRENT APPLICATION NUMBER: US/10/273,707
; CURRENT FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: 09/493,491
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/117,640 US
; PRIOR FILING DATE: 1999-01-28
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 38
; LENGTH: 49
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: construct
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (1)..(28)
US-10-273-707-38

Query Match          55.6%; Score 30; DB 15; Length 49;
Best Local Similarity 60.0%; Pred. No. 2.8e-07;
Matches 18; Conservative 12; Mismatches 0; Indels 0; Gaps 0;
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QY      25 AGUCUCCUAGUAGUGAGUCGUAAUUUA 54
Db      30 AGTCTCCCTATAGTAGTGAGTCGTATTA 1

RESULT 4
US-10-273-707-31/c
; Sequence 31, Application US/10273707
; Publication No. US20030104448A1
; GENERAL INFORMATION:
; APPLICANT: HARVEY, Richard, C.
; APPLICANT: CLARK, JR., Thomas, J.
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FOR DETECTING GENETIC MARKERS
; TITLE OF INVENTION: FOR CANCER IN A BIOLOGICAL SAMPLE
; FILE REFERENCE: GP097-03.DV1
; CURRENT APPLICATION NUMBER: US/10/273,707
; CURRENT FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: 09/493,491
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/117,640 US
; PRIOR FILING DATE: 1999-01-28
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 31
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: construct
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (1)..(28)
US-10-273-707-31

Query Match          55.6%; Score 30; DB 15; Length 50;
Best Local Similarity 60.0%; Pred. No. 2.8e-07;
Matches 18; Conservative 12; Mismatches 0; Indels 0; Gaps 0;

QY      25 AGUCUCCUAGUAGUGAGUCGUAAUUUA 54
Db      30 AGTCTCCCTATAGTAGTGAGTCGTATTA 1

RESULT 5
US-10-273-707-43/c
; Sequence 43, Application US/10273707
; Publication No. US20030104448A1
; GENERAL INFORMATION:
; APPLICANT: HARVEY, Richard, C.
; APPLICANT: CLARK, JR., Thomas, J.
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FOR DETECTING GENETIC MARKERS
; TITLE OF INVENTION: FOR CANCER IN A BIOLOGICAL SAMPLE
; FILE REFERENCE: GP097-03.DV1
; CURRENT APPLICATION NUMBER: US/10/273,707
; CURRENT FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: 09/493,491
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/117,640 US
; PRIOR FILING DATE: 1999-01-28
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 43
; LENGTH: 52
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: construct
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (1)..(28)
US-10-273-707-43
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Query Match 55.6%; Score 30; DB 15; Length 52;  
Best Local Similarity 60.0%; Pred. No. 2.8e-07;  
Matches 18; Conservative 12; Mismatches 0; Indels 0; Gaps 0;  
QY 25 AGUCUCCUUAUAGUGAGUCGUUAUUAUUUA 54  
DB 30 AGTCTCCCTATAGTGCATTAATT 1

## RESULT 6

US-09-944-036-40/c  
; Sequence 40, Application US/09944036  
; Patent No. US2002005509A1  
; GENERAL INFORMATION:  
; APPLICANT: YANG, Yeasing Y.  
; APPLICANT: BRENTANO, Steven T.  
; APPLICANT: BABOLA, Odile  
; APPLICANT: TRAN, Nathalie  
; APPLICANT: VERNET, Guy  
; TITLE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF  
; FILE REFERENCE: GP114-02.UT  
; CURRENT APPLICATION NUMBER: US/09/944,036  
; CURRENT FILING DATE: 2001-08-31  
; PRIOR APPLICATION NUMBER: US 60/229,790  
; PRIOR FILING DATE: 2000-09-01  
; NUMBER OF SEQ ID NOS: 70  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 40  
; LENGTH: 51  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:  
; OTHER INFORMATION: Oligonucleotide primer for Reverse Transcriptase  
; OTHER INFORMATION: target sequence  
; NAME/KEY: promoter  
; LOCATION: (1)..(29)  
US-09-944-036-40

Query Match 53.7%; Score 29; DB 9; Length 51;  
Best Local Similarity 58.6%; Pred. No. 1.1e-06;  
Matches 17; Conservative 12; Mismatches 0; Indels 0; Gaps 0;

QY 25 AGUCUCCUUAUAGUGAGUCGUUAUUAUU 53  
DB 29 AGTCTCCCTATAGTGCATTAATT 1

## RESULT 7

US-10-425-975-40/c  
; Sequence 40, Application US/10425975  
; Publication No. US2003022857A1  
; GENERAL INFORMATION:  
; APPLICANT: YANG, Yeasing Y.  
; APPLICANT: BRENTANO, Steven T.  
; APPLICANT: BABOLA, Odile  
; APPLICANT: TRAN, Nathalie  
; APPLICANT: VERNET, Guy  
; TITLE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF  
; FILE REFERENCE: GP114-02.UT  
; CURRENT APPLICATION NUMBER: US/10/425,975  
; CURRENT FILING DATE: 2003-04-28  
; PRIOR APPLICATION NUMBER: US/09/944,036  
; PRIOR FILING DATE: 2001-08-31  
; PRIOR APPLICATION NUMBER: US 60/229,790  
; PRIOR FILING DATE: 2000-09-01  
; NUMBER OF SEQ ID NOS: 70  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 40  
; LENGTH: 51

; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:  
; OTHER INFORMATION: Oligonucleotide primer for Reverse Transcriptase  
; OTHER INFORMATION: target sequence  
; FEATURE:  
; NAME/KEY: promoter  
; LOCATION: (1)..(29)  
US-10-425-975-40

Query Match 53.7%; Score 29; DB 16; Length 51;  
Best Local Similarity 58.6%; Pred. No. 1.1e-06;  
Matches 17; Conservative 12; Mismatches 0; Indels 0; Gaps 0;

QY 25 AGUCUCCUUAUAGUGAGUCGUUAUUAUU 53  
DB 29 AGTCTCCCTATAGTGCATTAATT 1

## RESULT 8

US-10-273-707-36/c  
; Sequence 36, Application US/10273707  
; Publication No. US2003010448A1  
; GENERAL INFORMATION:  
; APPLICANT: HARVEY, Richard, C.  
; APPLICANT: CLARK, JR., Thomas, J.  
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FOR DETECTING GENETIC MARKERS  
; FILE REFERENCE: GP097-03.DV1  
; CURRENT APPLICATION NUMBER: US/10/273,707  
; CURRENT FILING DATE: 2002-10-17  
; PRIOR APPLICATION NUMBER: 09/493,491  
; PRIOR FILING DATE: 2000-01-28  
; PRIOR APPLICATION NUMBER: 60/117,640 US  
; PRIOR FILING DATE: 1999-01-28  
; NUMBER OF SEQ ID NOS: 50  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 36  
; LENGTH: 52  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: construct  
; FEATURE:  
; NAME/KEY: promoter  
; LOCATION: (1)..(28)  
US-10-273-707-36

Query Match 53.7%; Score 29; DB 15; Length 52;  
Best Local Similarity 58.6%; Pred. No. 1.1e-06;  
Matches 17; Conservative 12; Mismatches 0; Indels 0; Gaps 0;

QY 26 GUCUCCUUAUAGUGAGUCGUUAUUAUUUA 54  
DB 29 GTCTCCCTATAGTGCATTAATT 1

## RESULT 9

US-10-273-707-42/c  
; Sequence 42, Application US/10273707  
; Publication No. US2003010448A1  
; GENERAL INFORMATION:  
; APPLICANT: HARVEY, Richard, C.  
; APPLICANT: CLARK, JR., Thomas, J.  
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FOR DETECTING GENETIC MARKERS  
; FILE REFERENCE: GP097-03.DV1  
; CURRENT APPLICATION NUMBER: US/10/273,707  
; CURRENT FILING DATE: 2002-10-17  
; PRIOR APPLICATION NUMBER: 09/493,491  
; PRIOR FILING DATE: 2000-01-28

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; FILE REFERENCE: GP097-03.DV1
; CURRENT APPLICATION NUMBER: US/10/273,707
; CURRENT FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: 09/493,491
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/117,640 US
; PRIOR FILING DATE: 1999-01-28
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 42
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: construct
; NAME/KEY: promoter
; LOCATION: (1)..(28)
US-10-273-707-42

Query Match          53.7%; Score 29; DB 15; Length 52;
Best Local Similarity 58.6%; Pred. No. 1.le-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      26 GUCUCCCUAUGAGUGUGCUUAUUUA 54
Db      29 GTCTCCCTATAGTGCATTAATTTA 1

RESULT 10
US-10-273-707-30/c
; Sequence 30, Application US/10273707
; Publication No. US20030104448A1
; GENERAL INFORMATION:
; APPLICANT: HARVEY, Richard, C.
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FOR DETECTING GENETIC MARKERS
; FILE REFERENCE: GP097-03.DV1
; CURRENT APPLICATION NUMBER: US/10/273,707
; CURRENT FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: 09/493,491
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/117,640 US
; PRIOR FILING DATE: 1999-01-28
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 30
; LENGTH: 54
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: construct
; NAME/KEY: promoter
; LOCATION: (1)..(28)
US-10-273-707-30

Query Match          53.7%; Score 29; DB 15; Length 54;
Best Local Similarity 58.6%; Pred. No. 1.le-06;
Matches 17; Conservative 12; Mismatches 0; Indels 0; Gaps 0;

QY      26 GUCUCCCUAUGAGUGUGCUUAUUUA 54
Db      29 GTCTCCCTATAGTGCATTAATTTA 1

RESULT 11
US-10-273-707-49/c
; Sequence 49, Application US/10273707
; Publication No. US20030104448A1
; GENERAL INFORMATION:
; APPLICANT: HARVEY, Richard, C.
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FOR DETECTING GENETIC MARKERS
; FILE REFERENCE: GP097-03.DV1
; CURRENT APPLICATION NUMBER: US/10/273,707
; CURRENT FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: 09/493,491
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/117,640 US
; PRIOR FILING DATE: 1999-01-28
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 49
; LENGTH: 54
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: construct
; NAME/KEY: promoter
; LOCATION: (1)..(28)
US-10-273-707-49
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; FILE REFERENCE: GP097-03.DV1
; CURRENT APPLICATION NUMBER: US/10/273,707
; CURRENT FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: 09/493,491
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/117,640 US
; PRIOR FILING DATE: 1999-01-28
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 49
; LENGTH: 54
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: construct
; NAME/KEY: promoter
; LOCATION: (1)..(28)
US-10-273-707-49

Query Match          53.7%; Score 29; DB 15; Length 54;
Best Local Similarity 58.6%; Pred. No. 1.le-06;
Matches 17; Conservative 12; Mismatches 0; Indels 0; Gaps 0;

QY      26 GUCUCCCUAUGAGUGUGCUUAUUUA 54
Db      29 GTCTCCCTATAGTGCATTAATTTA 1

RESULT 12
US-10-273-707-47/c
; Sequence 47, Application US/10273707
; Publication No. US20030104448A1
; GENERAL INFORMATION:
; APPLICANT: HARVEY, Richard, C.
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FOR DETECTING GENETIC MARKERS
; FILE REFERENCE: GP097-03.DV1
; CURRENT APPLICATION NUMBER: US/10/273,707
; CURRENT FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: 09/493,491
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/117,640 US
; PRIOR FILING DATE: 1999-01-28
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 47
; LENGTH: 55
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: construct
; NAME/KEY: promoter
; LOCATION: (1)..(28)
US-10-273-707-47

Query Match          53.7%; Score 29; DB 15; Length 55;
Best Local Similarity 58.6%; Pred. No. 1.le-06;
Matches 17; Conservative 12; Mismatches 0; Indels 0; Gaps 0;

QY      26 GUCUCCCUAUGAGUGUGCUUAUUUA 54
Db      29 GTCTCCCTATAGTGCATTAATTTA 1

RESULT 13
US-09-833-782-3/c
; Sequence 3, Application US/09833782
; Publication No. US2002040131A1
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; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Wilganowski, Nathaniel L.
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: Novel Human Metalloprotease and Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0161-USA
; CURRENT APPLICATION NUMBER: US/09/833,782
; CURRENT FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: US 60/196,319
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 6306
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-833-782-3

Query Match      53.7%; Score 29; DB 13; Length 6306;
Best Local Similarity 58.6%; Pred. No. 1.2e-06;
Matches 17; Conservative 12; Mismatches 0; Indels 0; Gaps 0;

QY 25 AGUCUCCUUAUGAGUGUGUAUUUUU 53
Db 114 AGTCTCCTATAGTAGTGATTAATTT 86

RESULT 14
US-10-273-707-44/c
; Sequence 44, Application US/10273707
; Publication No. US20030104448A1
; GENERAL INFORMATION:
; APPLICANT: HARVEY, Richard, C.
; APPLICANT: CLARK, JR., Thomas, J.
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FOR DETECTING GENETIC MARKERS
; FILE REFERENCE: GP097-03.DV1
; CURRENT APPLICATION NUMBER: US/10/273,707
; CURRENT FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: 09/493,491
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/117,640 US
; PRIOR FILING DATE: 1999-01-28
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 44
; LENGTH: 28
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: construct
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (1)..(28)
US-10-273-707-44

Query Match      51.9%; Score 28; DB 15; Length 28;
Best Local Similarity 57.1%; Pred. No. 3.9e-06;
Matches 16; Conservative 12; Mismatches 0; Indels 0; Gaps 0;

QY 27 UCUCUCCUUAUGAGUGUGUAUUUUU 54
Db 28 TCTCCCTATAGTAGTGATTAATTTA 1

RESULT 15
US-09-876-527-29/c
; Sequence 29, Application US/09876527
; Patent No. US20020102616A1
; GENERAL INFORMATION:
; APPLICANT: Kindsvogel, Wayne
; Jelinek, Laura J.
```

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; Sheppard, Paul O.
; Hagopian, William A.
; LaGasse, James M.
; TITLE OF INVENTION: ISLET CELL ANTIGEN 1851
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/876,527
; FILING DATE: 07-Jun-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/811,481
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Lingenfelter, Susan
; REGISTRATION NUMBER: P-41,156
; REFERENCE/DOCKET NUMBER: 95-36
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6675
; TELEFAX: 206-442-6678
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; IMMEDIATE SOURCE:
; CLONE: ZC11197
; SEQUENCE DESCRIPTION: SEQ ID NO: 29:
US-09-876-527-29

Query Match      51.9%; Score 28; DB 9; Length 30;
Best Local Similarity 57.1%; Pred. No. 3.9e-06;
Matches 16; Conservative 12; Mismatches 0; Indels 0; Gaps 0;

QY 26 GUUCUCCUUAUGAGUGUGUAUUUUU 53
Db 28 GTCTCCCTATAGTAGTGATTAATTT 1

Search completed: May 27, 2004, 14:58:25
Job time : 284.177 secs
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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 26, 2004, 15:22:41 ; Search time 1906.62 Seconds  
(without alignments)  
845.770 Million cell updates/sec

Title: US-09-121-239-4

Perfect score: 54

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Scoring table: OLIGO\_NUC

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Searched: 27513289 seqs, 14931090276 residues

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Minimum DB seq length: 0

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Post-processing: Listing first 45 summaries

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7: em\_estro:\*

8: em\_estc:\*

9: gb\_est1:\*

10: gb\_est2:\*

11: gb\_hic:\*

12: gb\_est3:\*

13: gb\_est4:\*

14: gb\_est5:\*

15: em\_estfun:\*

16: em\_estom:\*

17: em\_ges\_hum:\*

18: em\_ges\_inv:\*

19: em\_ges\_pin:\*

20: em\_ges\_vrt:\*

21: em\_ges\_fun:\*

22: em\_ges\_mam:\*

23: em\_ges\_mus:\*

24: em\_ges\_pro:\*

25: em\_ges\_rod:\*

26: em\_ges\_pbg:\*

27: em\_ges\_vrl:\*

28: gb\_ges1:\*

29: gb\_ges2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	29	53.7	560	29	CC966861
2	29	53.7	571	29	CC964269
3	29	53.7	585	29	CC947893
4	29	53.7	592	29	CC961654

FEATURES

Location/Qualifiers

ALIGNMENTS

RESULT 1	CC966861	CC966861	560 bp	DNA	linear	GSS 18-AUG-2003
LOCUS	BOIFL85TR	BO_1.4_1.6_KB_nuc	Brassica oleracea	genomic clone		
DEFINITION	BOIFL85, genomic survey sequence.					
ACCESSION	CC966861					
VERSION	CC966861.1	GI:33819522				
KEYWORDS	GSS.					
SOURCE	Brassica oleracea					
ORGANISM	Brassica oleracea					
REFERENCE	1 (bases 1 to 560)					
AUTHORS	Town,C.D., Van Aken,S., Utterback,T., Koo,H. and Fraser,C.M.					
TITLE	Whole genome shotgun sequencing of Brassica oleracea					
JOURNAL	Unpublished (2001)					
COMMENT	Contact: Chris Town					

TIGR  
9712 Medical Center Drive, Rockville, MD 20850, USA.  
Tel: 301-838-3523  
Fax: 301-838-0208  
Email: cdtown@tigr.org  
DNA is from a doubled haploid provided by Tom Osborn.  
Seq primer: TR  
Class: sheared ends.

CC952121 BOIB185TR  
CC948768 BOIDG32TR  
CC947463 BOIGK06TR  
CC967304 BOIFK41TR  
CC968451 BOIFB27TR  
CC944751 BOIRU81TR  
CC946396 BOICU54TR  
CC949404 BOIGZ19TR  
CC951454 BOIEA62TR  
CC962886 BOIGN54TR  
CC961061 BOICX68TR  
CC945503 BOIDK74TR  
CC948738 BOIFI28TR  
CC944195 BOIBU59TR  
CC944485 BOIHL39TR  
CC951566 BOIEJ65TR  
CC958824 BOIBM11TR  
CC954347 BOIBW60TR  
CC968802 BOICU62TR  
CC969001 BOICK93TR  
CC953502 BOIGT40TR  
CC961701 BOIDQ39TR  
CC958105 BOIGX30TR  
CC968053 BOICE19TR  
CC958532 BOIFG34TR  
BQ102727 UUGC0111  
BE391582 BO1282148  
BE262878 BO1148014  
BF976190 602245057  
BE314661 601146777  
BG475075 602491094  
BF397962 601290494  
BF974085 602240343  
BE410828 601301490  
BF398063 601290252  
BF027436 601672556  
BQ102748 UUGC0132  
BE391744 601282029  
BQ102753 UUGC0137  
BQ102710 UUGC0094  
BG425691 602448292

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/organism="Brassica oleracea"
/mol_type="genomic DNA"
/strain="TO1000DH3"
/db_xref="taxon:3712"
/clone="BOIEFL85"
/notes="Vector: PHOS2; Site 1: BatXI; 1.4-1.6 kb sheared
nuclear DNA inserted into PHOS2 using BstXI linkers"

ORIGIN
Query Match 53.7%; Score 29; DB 29; Length 560;
Best Local Similarity 62.1%; Pred. No. 8.1e-06;
Matches 18; Conservative 11; Mismatches 0; Indels 0; Gaps 0;

QY 24 GAGUCUCCUAGAGUCGUAUAUUAU 52
||||:||||:||||:||||:||||:||||:
Db 149 GAGTCCTCCATAGTGCATTAATT 177

RESULT 2
CC964269
LOCUS
DEFINITION
BOIEN76TR BO_1.4_1.6_KB_nuc Brassica oleracea genomic clone
ACCESSION
CC964269
VERSION
CC964269.1 GI:33814428
KEYWORDS
GSS.
SOURCE
Brassica oleracea
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE
1 (bases 1 to 571)
TOWN,C.D., Van Aken,S., Utterback,T., Koo,H. and Fraser,C.M.
Whole genome shotgun sequencing of Brassica oleracea
Unpublished (2001)
Contact: Chris Town
Seq primer: TR
Class: sheared ends.
FEATURES
Location/Qualifiers
1. .571
/organism="Brassica oleracea"
/mol_type="genomic DNA"
/strain="TO1000DH3"
/db_xref="taxon:3712"
/clone="BOIEN76"
/notes="Vector: PHOS2; Site 1: BatXI; 1.4-1.6 kb sheared
nuclear DNA inserted into PHOS2 using BstXI linkers"

ORIGIN
Query Match 53.7%; Score 29; DB 29; Length 571;
Best Local Similarity 62.1%; Pred. No. 8.1e-06;
Matches 18; Conservative 11; Mismatches 0; Indels 0; Gaps 0;

QY 24 GAGUCUCCUAGAGUCGUAUAUUAU 52
||||:||||:||||:||||:||||:||||:
Db 151 GAGTCCTCCATAGTGCATTAATT 179

RESULT 3
CC947693
LOCUS
DEFINITION
BOIEQ41TR BO_1.4_1.6_KB_nuc Brassica oleracea genomic clone
BOIEQ41, genomic survey sequence.
ACCESSION
CC947693

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VERSION
KEYWORDS
SOURCE
ORGANISM
CC947693.1 GI:33781675
GSS.
Brassica oleracea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE
1 (bases 1 to 585)
TOWN,C.D., Van Aken,S., Utterback,T., Koo,H. and Fraser,C.M.
Whole genome shotgun sequencing of Brassica oleracea
Unpublished (2001)
Contact: Chris Town
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TR
Class: sheared ends.
FEATURES
Location/Qualifiers
1. .585
/organism="Brassica oleracea"
/mol_type="genomic DNA"
/strain="TO1000DH3"
/db_xref="taxon:3712"
/clone="BOIEQ41"
/notes="Vector: PHOS2; Site 1: BatXI; 1.4-1.6 kb sheared
nuclear DNA inserted into PHOS2 using BstXI linkers"

ORIGIN
Query Match 53.7%; Score 29; DB 29; Length 585;
Best Local Similarity 62.1%; Pred. No. 8.2e-06;
Matches 18; Conservative 11; Mismatches 0; Indels 0; Gaps 0;

QY 24 GAGUCUCCUAGAGUCGUAUAUUAU 52
||||:||||:||||:||||:||||:||||:
Db 149 GAGTCCTCCATAGTGCATTAATT 177

RESULT 4
CC961654
LOCUS
DEFINITION
BOIDB28TR BO_1.4_1.6_KB_nuc Brassica oleracea genomic clone
BOIDB28, genomic survey sequence.
ACCESSION
CC961654
VERSION
CC961654.1 GI:33809231
KEYWORDS
GSS.
SOURCE
Brassica oleracea
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE
1 (bases 1 to 592)
TOWN,C.D., Van Aken,S., Utterback,T., Koo,H. and Fraser,C.M.
Whole genome shotgun sequencing of Brassica oleracea
Unpublished (2001)
Contact: Chris Town
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TR
Class: sheared ends.
FEATURES
Location/Qualifiers
1. .592
/organism="Brassica oleracea"
/mol_type="genomic DNA"
/strain="TO1000DH3"
/db_xref="taxon:3712"

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/clone="BOIDB28"
/clone_lib="BO_1.4_1.6_KB_nuc"
/note="Vector: pHOS2; Site 1: BstXI; 1.4-1.6 kb sheared
nuclear DNA inserted into pHOS2 using BstXI linkers"

ORIGIN
Query Match      53.7%; Score 29; DB 29; Length 592;
Best Local Similarity 62.1%; Pred. No. 8.2e-06;
Matches 18; Conservative 11; Mismatches 0; Indels 0; Gaps 0;

QY 24 GAGUCUCCUAGUGAGUGUCGUUAUUAU 52
||||:||||:||||:||||:||||:||||:
DB 156 GAGTCTCCTATAGTGCCTATTAAATT 184

RESULT 5
LOCUS CC952121 604 bp DNA linear GSS 18-AUG-2003
DEFINITION BOIB185TR BO_1.4_1.6_KB_nuc Brassica oleracea genomic clone
ACCESSION CC952121
VERSION CC952121.1 GI:33790560
KEYWORDS GSS.
SOURCE Brassica oleracea
ORGANISM Brassica oleracea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE 1 (bases 1 to 604)
AUTHORS Town,C.D., Van Aken,S., Utterback,T., Koo,H. and Fraser,C.M.
TITLE Whole genome shotgun sequencing of Brassica oleracea
JOURNAL Unpublished (2001)
COMMENT Other GSSs: BOIB185TF
Contact: Chris Town
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TR
Class: sheared ends.

FEATURES
source
Location/Qualifiers
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/organism="Brassica oleracea"
/mol_type="genomic DNA"
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/db_xref="taxon:3712"
/clone_lib="BO_1.4_1.6_KB_nuc"

ORIGIN
Query Match      53.7%; Score 29; DB 29; Length 604;
Best Local Similarity 62.1%; Pred. No. 8.2e-06;
Matches 18; Conservative 11; Mismatches 0; Indels 0; Gaps 0;

QY 24 GAGUCUCCUAGUGAGUGUCGUUAUUAU 52
||||:||||:||||:||||:||||:||||:
DB 157 GAGTCTCCTATAGTGCCTATTAAATT 185

RESULT 6
LOCUS CC948768 610 bp DNA linear GSS 18-AUG-2003
DEFINITION BOIDG32TR BO_1.4_1.6_KB_nuc Brassica oleracea genomic clone
ACCESSION CC948768
VERSION CC948768.1 GI:33783814
KEYWORDS GSS.
SOURCE Brassica oleracea
ORGANISM Brassica oleracea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE 1 (bases 1 to 610)
AUTHORS Town,C.D., Van Aken,S., Utterback,T., Koo,H. and Fraser,C.M.
TITLE Whole genome shotgun sequencing of Brassica oleracea
JOURNAL Unpublished (2001)
COMMENT Other GSSs: BOIDG32TF
Contact: Chris Town
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TR
Class: sheared ends.

FEATURES
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Location/Qualifiers
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/strain="T01000DH3"
/db_xref="taxon:3712"
/clone_lib="BO_1.4_1.6_KB_nuc"

ORIGIN
Query Match      53.7%; Score 29; DB 29; Length 604;
Best Local Similarity 62.1%; Pred. No. 8.2e-06;
Matches 18; Conservative 11; Mismatches 0; Indels 0; Gaps 0;

QY 24 GAGUCUCCUAGUGAGUGUCGUUAUUAU 52
||||:||||:||||:||||:||||:||||:
DB 157 GAGTCTCCTATAGTGCCTATTAAATT 185

RESULT 7
LOCUS CC947463 612 bp DNA linear GSS 18-AUG-2003
DEFINITION BOIGK06TR BO_1.4_1.6_KB_nuc Brassica oleracea genomic clone
ACCESSION CC947463
VERSION CC947463.1 GI:33781217
KEYWORDS GSS.
SOURCE Brassica oleracea
ORGANISM Brassica oleracea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE 1 (bases 1 to 612)
AUTHORS Town,C.D., Van Aken,S., Utterback,T., Koo,H. and Fraser,C.M.
TITLE Whole genome shotgun sequencing of Brassica oleracea
JOURNAL Unpublished (2001)
COMMENT Other GSSs: BOIGK06TF
Contact: Chris Town
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TR
Class: sheared ends.

FEATURES
source
Location/Qualifiers
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/mol_type="genomic DNA"
/strain="T01000DH3"
/db_xref="taxon:3712"
/clone_lib="BO_1.4_1.6_KB_nuc"

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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE 1 (bases 1 to 610)
AUTHORS Town,C.D., Van Aken,S., Utterback,T., Koo,H. and Fraser,C.M.
TITLE Whole genome shotgun sequencing of Brassica oleracea
JOURNAL Unpublished (2001)
COMMENT Other GSSs: BOIDG32TF
Contact: Chris Town
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TR
Class: sheared ends.

FEATURES
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Best Local Similarity 62.1%; Pred. No. 8.2e-06;
Matches 18; Conservative 11; Mismatches 0; Indels 0; Gaps 0;

QY 24 GAGUCUCCUAGUGAGUGUCGUUAUUAU 52
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DB 242 GAGTCTCCTATAGTGCCTATTAAATT 270

RESULT 7
LOCUS CC947463 612 bp DNA linear GSS 18-AUG-2003
DEFINITION BOIGK06TR BO_1.4_1.6_KB_nuc Brassica oleracea genomic clone
ACCESSION CC947463
VERSION CC947463.1 GI:33781217
KEYWORDS GSS.
SOURCE Brassica oleracea
ORGANISM Brassica oleracea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE 1 (bases 1 to 612)
AUTHORS Town,C.D., Van Aken,S., Utterback,T., Koo,H. and Fraser,C.M.
TITLE Whole genome shotgun sequencing of Brassica oleracea
JOURNAL Unpublished (2001)
COMMENT Other GSSs: BOIGK06TF
Contact: Chris Town
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TR
Class: sheared ends.

FEATURES
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Location/Qualifiers
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/mol_type="genomic DNA"
/strain="T01000DH3"
/db_xref="taxon:3712"
/clone_lib="BO_1.4_1.6_KB_nuc"

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/note="Vector: PHOS2; Site 1: BstXI; 1.4-1.6 kb sheared
nuclear DNA inserted into PHOS2 using BstXI linkers"

ORIGIN

Query Match      53.7%; Score 29; DB 29; Length 612;
Best Local Similarity 62.1%; Pred. No. 8.2e-06;
Matches 18; Conservative 11; Mismatches 0; Indels 0; Gaps 0;

QY 24 GAGUCUCCUAGUGAGUGAGUGUAUAUU 52
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Db 289 GAGTCCTCCCTATAGTCGATTAATT 317

RESULT 8
CC967304 617 bp DNA linear GSS 18-AUG-2003
LOCUS BOIFK41TR BO 1.4-1.6 KB nuc Brassica oleracea genomic clone
DEFINITION BOIFK41, genomic survey sequence.
ACCESSION CC967304
VERSION CC967304.1 GI:33820392
KEYWORDS GSS.
SOURCE Brassica oleracea
ORGANISM Brassica oleracea
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
TITLE rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
JOURNAL 1 (bases 1 to 617)
COMMENT Town,C.D., Van Aken,S., Utterback,T., Koo,H. and Fraser,C.M.
Whole genome shotgun sequencing of Brassica oleracea
Contact: Chris Town
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TR
Class: sheared ends.

FEATURES
Location/Qualifiers
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/note="Vector: PHOS2; Site 1: BstXI; 1.4-1.6 kb sheared
nuclear DNA inserted into PHOS2 using BstXI linkers"

ORIGIN

Query Match      53.7%; Score 29; DB 29; Length 612;
Best Local Similarity 62.1%; Pred. No. 8.3e-06;
Matches 18; Conservative 11; Mismatches 0; Indels 0; Gaps 0;

QY 24 GAGUCUCCUAGUGAGUGAGUGUAUAUU 52
    |||:|||||:|||||:|||||:|||||:
Db 159 GAGTCCTCCCTATAGTCGATTAATT 187

RESULT 10
CC944751 642 bp DNA linear GSS 18-AUG-2003
LOCUS BOIBU81TR BO 1.4-1.6 KB nuc Brassica oleracea genomic clone
DEFINITION BOIBU81, genomic survey sequence.
ACCESSION CC944751
VERSION CC944751.1 GI:33777617
KEYWORDS GSS.
SOURCE Brassica oleracea
ORGANISM Brassica oleracea
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
TITLE rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
JOURNAL 1 (bases 1 to 642)
COMMENT Town,C.D., Van Aken,S., Utterback,T., Koo,H. and Fraser,C.M.
Whole genome shotgun sequencing of Brassica oleracea
Contact: Chris Town
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TR
Class: sheared ends.

FEATURES
Location/Qualifiers
source
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/clone_lib="BO1.4-1.6 KB nuc"
/note="Vector: PHOS2; Site 1: BstXI; 1.4-1.6 kb sheared
nuclear DNA inserted into PHOS2 using BstXI linkers"

ORIGIN

Query Match      53.7%; Score 29; DB 29; Length 612;
Best Local Similarity 62.1%; Pred. No. 8.3e-06;
Matches 18; Conservative 11; Mismatches 0; Indels 0; Gaps 0;

QY 24 GAGUCUCCUAGUGAGUGAGUGUAUAUU 52
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Db 296 GAGTCCTCCCTATAGTCGATTAATT 324

RESULT 9
CC968451 621 bp DNA linear GSS 18-AUG-2003
LOCUS BOIFB27TR BO 1.4-1.6 KB nuc Brassica oleracea genomic clone
DEFINITION BOIFB27, genomic survey sequence.
ACCESSION CC968451
VERSION CC968451.1 GI:33822676
KEYWORDS GSS.
SOURCE Brassica oleracea
ORGANISM Brassica oleracea
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
TITLE rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

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1 (bases 1 to 621)
Town,C.D., Van Aken,S., Utterback,T., Koo,H. and Fraser,C.M.
Whole genome shotgun sequencing of Brassica oleracea
Unpublished (2001)
COMMENT TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TR
Class: sheared ends.

FEATURES
Location/Qualifiers
source
1..621
/organism="Brassica oleracea"
/mol_type="genomic DNA"
/strain="TO1000DH3"
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/note="Vector: PHOS2; Site 1: BstXI; 1.4-1.6 kb sheared
nuclear DNA inserted into PHOS2 using BstXI linkers"

ORIGIN

Query Match      53.7%; Score 29; DB 29; Length 621;
Best Local Similarity 62.1%; Pred. No. 8.3e-06;
Matches 18; Conservative 11; Mismatches 0; Indels 0; Gaps 0;

QY 24 GAGUCUCCUAGUGAGUGAGUGUAUAUU 52
    |||:|||||:|||||:|||||:|||||:
Db 159 GAGTCCTCCCTATAGTCGATTAATT 187

RESULT 10
CC944751 642 bp DNA linear GSS 18-AUG-2003
LOCUS BOIBU81TR BO 1.4-1.6 KB nuc Brassica oleracea genomic clone
DEFINITION BOIBU81, genomic survey sequence.
ACCESSION CC944751
VERSION CC944751.1 GI:33777617
KEYWORDS GSS.
SOURCE Brassica oleracea
ORGANISM Brassica oleracea
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
TITLE rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
JOURNAL 1 (bases 1 to 642)
COMMENT Town,C.D., Van Aken,S., Utterback,T., Koo,H. and Fraser,C.M.
Whole genome shotgun sequencing of Brassica oleracea
Contact: Chris Town
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TR
Class: sheared ends.

FEATURES
Location/Qualifiers
source
1..642
/organism="Brassica oleracea"
/mol_type="genomic DNA"
/strain="TO1000DH3"
/db_xref="taxon:3712"
/clone_lib="BO1.4-1.6 KB nuc"
/note="Vector: PHOS2; Site 1: BstXI; 1.4-1.6 kb sheared
nuclear DNA inserted into PHOS2 using BstXI linkers"

ORIGIN

Query Match      53.7%; Score 29; DB 29; Length 642;

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Best Local Similarity 62.1%; Pred. No. 8.3e-06; Indels 0; Gaps 0;
Matches 18; Conservative 11; Mismatches 0;

QY 24 GAGUCUCCCUAUGAGUCGUUAUUAU 52
    |||:||||:||||:||||:||||:||||:
Db 295 GAGTCTCCCTATAGTGAGTCGTATTATT 323

RESULT 11
CC946396 642 bp DNA linear GSS 18-AUG-2003
LOCUS BOICQ54TR BO.1.4.1.6_KB_nuc Brassica oleracea genomic clone
DEFINITION BOICQ54, genomic survey sequence.
ACCESSION CC946396
VERSION CC946396.1 GI:33779262
KEYWORDS GSS.
SOURCE Brassica oleracea
ORGANISM Brassica oleracea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
1 (bases 1 to 642)
Town,C.D., Van Aken,S., Utterback,T., Koo,H. and Fraser,C.M.
Whole genome shotgun sequencing of Brassica oleracea
Unpublished (2001)
COMMENT Other_GSSs: BOICQ54TF
Contact: Chris Town
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TR
Class: sheared ends.

FEATURES
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ORIGIN
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Best Local Similarity 62.1%; Pred. No. 8.3e-06;
Matches 18; Conservative 11; Mismatches 0; Indels 0; Gaps 0;

QY 24 GAGUCUCCCUAUGAGUCGUUAUUAU 52
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Db 156 GAGTCTCCCTATAGTGAGTCGTATTATT 184

RESULT 12
CC949404 644 bp DNA linear GSS 18-AUG-2003
LOCUS BOIGZ19TR BO.1.4.1.6_KB_nuc Brassica oleracea genomic clone
DEFINITION BOIGZ19, genomic survey sequence.
ACCESSION CC949404
VERSION CC949404.1 GI:33785090
KEYWORDS GSS.
SOURCE Brassica oleracea
ORGANISM Brassica oleracea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
1 (bases 1 to 644)
Town,C.D., Van Aken,S., Utterback,T., Koo,H. and Fraser,C.M.
Whole genome shotgun sequencing of Brassica oleracea
Unpublished (2001)

FEATURES
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ORIGIN
Query Match 53.7%; Score 29; DB 29; Length 644;
Best Local Similarity 62.1%; Pred. No. 8.3e-06;
Matches 18; Conservative 11; Mismatches 0; Indels 0; Gaps 0;

QY 24 GAGUCUCCCUAUGAGUCGUUAUUAU 52
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Db 156 GAGTCTCCCTATAGTGAGTCGTATTATT 184

RESULT 13
CC951454 644 bp DNA linear GSS 18-AUG-2003
LOCUS BOIEA62TR BO.1.4.1.6_KB_nuc Brassica oleracea genomic clone
DEFINITION BOIEA62, genomic survey sequence.
ACCESSION CC951454
VERSION CC951454.1 GI:33789233
KEYWORDS GSS.
SOURCE Brassica oleracea
ORGANISM Brassica oleracea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
1 (bases 1 to 644)
Town,C.D., Van Aken,S., Utterback,T., Koo,H. and Fraser,C.M.
Whole genome shotgun sequencing of Brassica oleracea
Unpublished (2001)
COMMENT Contact: Chris Town
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TR
Class: sheared ends.

FEATURES
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ORIGIN
Query Match 53.7%; Score 29; DB 29; Length 644;
Best Local Similarity 62.1%; Pred. No. 8.3e-06;
Matches 18; Conservative 11; Mismatches 0; Indels 0; Gaps 0;

QY 24 GAGUCUCCCUAUGAGUCGUUAUUAU 52
    |||:||||:||||:||||:||||:||||:
Db 149 GAGTCTCCCTATAGTGAGTCGTATTATT 177

RESULT 14
CC951454 644 bp DNA linear GSS 18-AUG-2003
LOCUS BOIEA62TR BO.1.4.1.6_KB_nuc Brassica oleracea genomic clone
DEFINITION BOIEA62, genomic survey sequence.
ACCESSION CC951454
VERSION CC951454.1 GI:33789233
KEYWORDS GSS.
SOURCE Brassica oleracea
ORGANISM Brassica oleracea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
1 (bases 1 to 644)
Town,C.D., Van Aken,S., Utterback,T., Koo,H. and Fraser,C.M.
Whole genome shotgun sequencing of Brassica oleracea
Unpublished (2001)
COMMENT Contact: Chris Town
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TR
Class: sheared ends.

FEATURES
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        /note="Vector: BO.1.4.1.6_KB_nuc"
        /note="nuclear DNA inserted into pHOS2 using BstXI linkers"

ORIGIN
Query Match 53.7%; Score 29; DB 29; Length 644;
Best Local Similarity 62.1%; Pred. No. 8.3e-06;
Matches 18; Conservative 11; Mismatches 0; Indels 0; Gaps 0;

QY 24 GAGUCUCCCUAUGAGUCGUUAUUAU 52
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Db 149 GAGTCTCCCTATAGTGAGTCGTATTATT 177
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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: May 26, 2004, 16:00:31 ; Search time 510.783 Seconds  
(without alignments)  
2036.547 Million cell updates/sec

Title: US-09-121-239-6

Perfect score: 24

Sequence: 1 GACCAACUCGUGUGAAACUCCA 24

Scoring table: OLIGO\_NUC  
Gapop\_60.0 , Gapext 60.0

Searched: 3470272 seqs, 21671516995 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

GenEmbl:

1: gb\_ba:

2: gb\_hgt:

3: gb\_in:

4: gb\_om:

5: gb\_ov:

6: gb\_pat:

7: gb\_ph:

8: gb\_pl:

9: gb\_pr:

10: gb\_ro:

11: gb\_scs:

12: gb\_sy:

13: gb\_un:

14: gb\_vi:

15: em\_ba:

16: em\_fun:

17: em\_hum:

18: em\_in:

19: em\_mu:

20: em\_om:

21: em\_or:

22: em\_ov:

23: em\_pat:

24: em\_ph:

25: em\_pi:

26: em\_ro:

27: em\_scs:

28: em\_un:

29: em\_vi:

30: em\_hgt\_hum:

31: em\_hgt\_inv:

32: em\_hgt\_other:

33: em\_hgt\_mus:

34: em\_hgt\_pln:

35: em\_hgt\_rod:

36: em\_hgt\_mam:

37: em\_hgt\_vrt:

38: em\_sy:

39: em\_hgtgo\_hum:

40: em\_hgtgo\_mus:

41: em\_hgtgo\_other:

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	24	100.0	24	6	E61323	E61323 Probe for d
2	24	100.0	24	6	AR352049	AR352049 Sequence
3	24	100.0	24	6	BD140611	BD140611 Direct RT
4	24	100.0	24	6	BD222527	BD222527 Methods f
5	24	100.0	24	6	BD222528	BD222528 Methods f
6	24	100.0	24	6	BD222529	BD222529 Methods f
7	24	100.0	24	6	BD222530	BD222530 Methods f
8	24	100.0	210	9	AY043457	AY043457 Homo sapi
9	24	100.0	250	9	AF321981	AF321981 Homo sapi
10	24	100.0	305	9	AF192533	AF192533 Homo sapi
11	24	100.0	350	6	BD222546	BD222546 Methods f
12	24	100.0	561	9	HUMMK562B	M19695 Human myelo
13	24	100.0	679	9	HUMABLB	M30832 Human bcr/a
14	24	100.0	854	9	HUMABLB	M30829 Human bcr/a
15	24	100.0	922	9	HSAL131467	AJ131467 Homo sapi
16	24	100.0	997	9	HSAL131466	AJ131466 Homo sapi
17	24	100.0	1078	6	A92081	A92081 Sequence 5
18	24	100.0	1078	6	AR230688	AR230688 Sequence
19	24	100.0	1157	6	BD177069	BD177069 Standard
20	24	100.0	2255	6	E00984	E00984 Probe detec
21	24	100.0	2255	6	I04527	I04527 Sequence 1
22	24	100.0	2541	9	HUMBCRX	M55395 Human break
23	24	100.0	2811	6	AX780333	AX780333 Sequence
24	24	100.0	3481	9	AK128501	AK128501 Homo sapi
25	24	100.0	4714	9	HSBCR	Y00661 Human bcr m
26	24	100.0	4739	6	AX331144	AX331144 Sequence
27	24	100.0	4739	9	HSBCR	X02596 Human mRNA
28	24	100.0	5000	9	HUMBCRE	L02935 Human major
29	24	100.0	111249	9	AP000343	AP000343 Homo sapi
30	24	100.0	152141	9	HSU07000	U07000 Human break
31	24	100.0	219210	2	AC145066	AC145066 Pan trogl
32	24	100.0	240115	2	AC138021	AC138021 Pan trogl
33	21	87.5	40	6	AR100696	AR100696 Sequence
34	20	83.3	20	6	I83631	I83631 Sequence 5
35	18	75.0	209030	2	AC122318	AC122318 Mus muscu
36	17	70.8	201752	2	AC113044	AC113044 Mus muscu
37	17	70.8	232458	2	AC099934	AC099934 Mus muscu
38	16	66.7	22	6	BD133933	BD133933 Method of
39	16	66.7	22	6	BD143900	BD143900 Method of
40	16	66.7	40	6	E16986	E16986 Sense prime
41	16	66.7	93172	9	AL357872	AL357872 Human DNA
42	16	66.7	110000	2	AC105546	Continuation (5 of
43	16	66.7	114450	2	AC019287	AC019287 Homo sapi
44	16	66.7	122418	5	AL592306	AL592306 Zebrafish
45	16	66.7	134976	8	AP004968	AP004968 Lotus cor

ALIGNMENTS

RESULT 1	E61323	Probe for detecting oligonucleotide.	24 bp	DNA	linear	PAT 18-JUN-2001
LOCUS	E61323	Probe for detecting oligonucleotide.				
DEFINITION	E61323	Probe for detecting oligonucleotide.				
ACCESSION	E61323	Probe for detecting oligonucleotide.				
VERSION	E61323.1	GI:13025885				
KEYWORDS	JP 1999046778-A/37.					
SOURCE		synthetic construct				
ORGANISM		artificial sequences.				
REFERENCE		1 (bases 1 to 24)				
AUTHORS		Daniel L.K. and Timothy J.F.				
TITLE		Probe for detecting oligonucleotide				
JOURNAL		Patent: JP 1999046778-A 37 23-FEB-1999;				
		GEN-PROBE INC				



Qy	1	GACCAACUCGUGUGAGAAACUCCA	24
Db	24	GACCAACTCGTGTGGAACCTCCA	1
RESULT 7			
BD222530/c			
LOCUS	BD222530	24 bp RNA linear	PAT 17-JUL-2003
DEFINITION	Methods for detecting and measuring spliced nucleic acids.		
ACCESSION	BD222530		
VERSION	BD222530.1	GI:33032300	
KEYWORDS	JP 2002521037-A/8.		
SOURCE	synthetic construct		
ORGANISM	artificial sequences.		
REFERENCE	1 (bases 1 to 24)		
AUTHORS	Harvey, R.C. and Eastman, P.S.		
TITLE	Methods for detecting and measuring spliced nucleic acids		
JOURNAL	Patent: JP 2002521037-A 8 16-JUL-2002;		
COMMENT	GEN PROBE INC		
	OS Artificial Sequence		
	PN JP 2002521037-A/8		
	PD 16-JUL-2002		
	PF 23-JUL-1999 JP 2000561364		
	PR 23-JUL-1998 US 09/121239		
	PI RICHARD C HARVEY, PAUL S EASTMAN		
	PC 12Q1/68, C12N15/09, C12N15/00		
	CC Description of Artificial Sequence: RNA version of SEQ ID NO:7		
	FH Key Location/Qualifiers		
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FEATURES	source		
	1..24		
	Location/Qualifiers		
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Best Local Similarity	79.2%;	Pred. No. 0.049;	
Matches	19;	Conservative 5;	Mismatches 0; Indels 0; Gaps 0;
Qy	1	GACCAACUCGUGUGAGAAACUCCA	24
Db	24	GACCAACTCGTGTGGAACCTCCA	1
RESULT 8			
AY043457			
LOCUS	AY043457	210 bp mRNA linear	PRI 27-JUN-2003
DEFINITION	Homo sapiens BCR-ABL fusion protein (BCR-ABL fusion) mRNA, partial cds.		
ACCESSION	AY043457		
VERSION	AY043457.1	GI:22073966	
KEYWORDS	Homo sapiens (human)		
SOURCE	Homo sapiens		
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
REFERENCE	1 (bases 1 to 210)		
AUTHORS	Otazu, I.B., Belen Rivero, M., Olcio, R., Pinto, A., Zalcberg, I. and Suarez, H.N.		
TITLE	A rare, in-frame BCR-ABL fusion (e13a3) in a patient with an aggressive chronic myeloid leukaemia		
JOURNAL	Acta Haematol. 108 (3), 150-153 (2002)		
MEDLINE	22259050		
PUBMED	12373087		
REFERENCE	2 (bases 1 to 210)		
AUTHORS	Otazu, I.B., Rivero, M.B. and Olcio, R.		
TITLE	Direct Submission		
JOURNAL	Submitted (03-JUL-2001) Genetics Division, Instituto Nacional de Cancer, Praca da Cruz Vermelha, 23, sexto andar, Rio de Janeiro, Brazil		

BD222546	350 bp	DNA	linear	PAT 17-JUL-2003
LOCUS				
DEFINITION				Methods for detecting and measuring spliced nucleic acids.
ACCESSION				BD222546
VERSION				BD222546.1 GI:33032316
KEYWORDS				JP 2002521037-A/24.
SOURCE				Homo sapiens (human)
ORGANISM				Homo sapiens
				Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE AUTHORS JOURNAL COMMENT	Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.	RESULT 13 HUMABLB LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL MEDLINE PUBMED COMMENT FEATURES source	Human bcr/abl fusion protein, partial cds, clone E3. 679 bp mRNA linear PRI 13-FEB-1996 M30832.1 GI:177944 Philadelphia chromosome; abl proto-oncogene; translocation. Homo sapiens (human) Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo. Shivelman, E., Lifshitz, B., Gale, R.P. and Canaani, E. Fused transcript of abl and bcr genes in chronic myelogenous leukemia Nature 315 (6020), 550-554 (1985) 85240529 2989692 Original Location/Qualifiers source text: Homo sapiens (clone: E3.) cDNA to mRNA. Location/Qualifiers 1. 679 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="E3." /cell_lines="chronic myelogenous leukemia cell line EM2" <1..>679 /note="putative" /codon_start=3 /product="bcr/abl fusion protein" /protein_id="AAA87612.1" /db_xref="GI:1185071" /translation="ISQIKSDIOREKANKGSKATERLKKLSSEOSLLILMSPSNAP RVHRSNGSYFLISSDYERAWRENIREQKKCFRSLASVELQMLTNSCVKQTV HSIPITNKEDDESGLYFLNIVHSATGFKQSKLQRPVADPEPQGLSAAARWNS KENLAAPSENDPNLFVALYDFVAGSDNTLSITKGEKLVGLNGENGEAQTQIGQ GWVPSNY"
	1 (bases 1 to 350)		
	Harvey, R.C. and Eastman, P.S.		
	Methods for detecting and measuring spliced nucleic acids		
	Patent: JP 2002521037-A 24 16-JUL-2002;		
	GEN PROBE INC		
	OS Homo sapiens (human)		
	PN JP 2002521037-A/24		
	PD 16-JUL-2002		
	PF 23-JUL-1998 US 09/121239		
FEATURES source	PI RICHARD C HARVEY, PAUL S EASTMAN		
	PC C12Q1/68, C12N15/09, C12N15/00		
	CC Methods for detecting and measuring spliced nucleic acids FH		
	Key Location/Qualifiers		
	FT source 1..350		
	Location/Qualifiers		
	1..350		
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ORIGIN	Query Match 100.0%; Score 24; DB 6; Length 350;	RESULT 14 HUMABLD LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL MEDLINE PUBMED COMMENT FEATURES source	Human bcr/abl fusion protein mRNA, partial cds, clone K28. 854 bp mRNA linear PRI 14-FEB-1996 M30829.1 GI:177953 Philadelphia chromosome; abl proto-oncogene; translocation. Homo sapiens (human) Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo. Shivelman, E., Lifshitz, B., Gale, R.P. and Canaani, E. Fused transcript of abl and bcr genes in chronic myelogenous leukemia Nature 315 (6020), 550-554 (1985) 85240529 2989692 Original Location/Qualifiers source text: Homo sapiens (clone: K28.) cDNA to mRNA. Location/Qualifiers 1. 854 /organism="Homo sapiens" /mol_type="mRNA"
	Best Local Similarity 79.2%; Pred. No. 0.019;		
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	QY 1 GACCAACUCGUGUGAACUCCA 24		
	: : : : : : : : :		
	DB 65 GACCAACTCGTGTGTGAACCTCCA 88		
	: : : : : : : : :		
	RESULT 12		
	HUMMK562B		
	LOCUS		
FEATURES source	DEFINITION		
	ACCESSION		
	VERSION		
	KEYWORDS		
	SOURCE		
	ORGANISM		
	REFERENCE		
	AUTHORS		
	TITLE		
	JOURNAL		
FEATURES source	MEDLINE		
	PUBMED		
	COMMENT		
	Original source text: Human myelocytic Ph(1)-positive CML K562 cell line, cDNA to mRNA, clone 8E.		
	The bcr region of the fusion protein is located on chromosome 22q11; the abl region was translocated from chromosome 9q34.		
	Location/Qualifiers		
	1..561		
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ORIGIN	<1..>561		
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	Chromosome 22q11.		
	Query Match 100.0%; Score 24; DB 9; Length 561;		
	Best Local Similarity 79.2%; Pred. No. 0.016;		
	Matches 19; Conservative 5; Mismatches 0; Indels 0; Gaps 0;		
	QY 1 GACCAACUCGUGUGAACUCCA 24		
	: : : : : : : : :		
	DB 60 GACCAACTCGTGTGTGAACCTCCA 83		
	: :~ :~ :~ :~ :~ :~ :~		

CDS

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/clone="K28."

/cell\_line="chronic myelogenous leukemia cell line K562"

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/notes="putative"

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/db\_xref="GI:1196396"

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IPLVDEELNALKIQSKDIQREKRNKSGKATERLKXLSQESLILLMSPSMA  
FVHSGNSGYTFLISSDYERAERENIREQKKCFRSLASVELQMTNCSVKLQT  
VHSIPLTINKEDDESGLYFLNVIHVSATGKQSKLQRPVASFQPOGLSEARWN  
SKENLAGSPENDPNLFVALYDFVSGDNTLSITKGEKLRVLGYNHNGEWCEAQTKNG  
QGWVPSNY"

ORIGIN

Query Match 100.0%; Score 24; DB 9; Length 854;

Best Local Similarity 79.2%; Pred. No. 0.014;

Matches 19; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 GACCAACUCUGUGUCAAACUCCA 24

|||||:|:|:|:|:|:|

Db 453 GACCAACTCGTGTGAAACTCCA 476

RESULT 15

HSAL131467

LOCUS Homo sapiens mRNA for BCR/ABL chimeric fusion peptide, partial.

DEFINITION AJ131467

ACCESSION AJ131467.1 GI:4033556

VERSION BCR/ABL chimeric fusion peptide; bcr/abl gene.

KEYWORDS Homo sapiens (human)

SOURCE Homo sapiens

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Burmeister T., Maurer J., Aivado M., Elmaagacli A.H., Grunebach F., Held K.R., Hess G., Hochhaus A., Hoppner W., Lences K.U., Lubbert M., Schafer K.L., Schafhausen P., Schmidt C.A., Schuler F., Seeger K., Seelig R., Thiede C., Viehmann S., Weber C., Wilhelm S., Christmann A., Clement J.H., Ebener U., Enczmann J., Leo R., Schleuning M., Schoch R. and Thiel E.

TITLE Quality assurance in RT-PCR-based BCR/ABL diagnostics--results of an interlaboratory test and a standardization approach

JOURNAL Leukemia 14 (10), 1850-1856 (2000)

MEDLINE 20471781

PUBMED 11021760

REFERENCE 2 (bases 1 to 922)

AUTHORS Burmeister T.

TITLE Direct Submission

JOURNAL Submitted (04-DEC-1998) Burmeister T., Medizinische Klinik III, FU Berlin, Hindenburgdamm 30, Berlin, Germany 12200, Germany

FEATURES

source

1..922

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/notes="the BCR/ABL fusion gene results from the chromosomal translocation t(9;22)(q34;q11) (Philadelphia translocation)"

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ORIGIN

Query Match 100.0%; Score 24; DB 9; Length 922;

Best Local Similarity 79.2%; Pred. No. 0.013;

Matches 19; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 GACCAACUCUGUGUCAAACUCCA 24

|||||:|:|:|:|:|:|

Db 237 GACCAACTCGTGTGAAACTCCA 260

Search completed: May 27, 2004, 02:16:37

Job time : 513.783 secs



GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: May 26, 2004, 14:55:11 ; Search time 107.037 Seconds  
(without alignments)  
952.539 Million cell updates/sec

Title: US-09-121-239-6  
Perfect score: 24  
Sequence: 1 GACCAACUGUGUGAAACUCCA 24

Scoring table: OLIGO\_NUC  
Gapop\_60.0 , Gapext 60.0

Searched: 3373863 seqs, 2124099041 residues

Word size : 0-

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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1: Geneseqn1980s.\*  
2: Geneseqn1990s.\*  
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5: Geneseqn2001bs.\*  
6: Geneseqn2002s.\*  
7: Geneseqn2003as.\*  
8: Geneseqn2003bs.\*  
9: Geneseqn2003cs.\*  
10: Geneseqn2004s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	24	100.0	24	2	AAQ86635 Modified
2	24	100.0	24	2	AAV66353 CML-2 chr
3	24	100.0	24	2	AAV66353 CML-2 chr
4	24	100.0	24	2	AAV66353 CML-2 chr
5	24	100.0	24	2	AAV66353 CML-2 chr
6	24	100.0	24	3	AAZ60844 Oligonucle
7	24	100.0	24	3	AAZ60845 Oligonucle
8	24	100.0	24	3	AAZ60846 Oligonucle
9	24	100.0	24	9	AAZ60847 Oligonucle
10	24	100.0	24	9	AAZ60848 Oligonucle
11	24	100.0	250	6	ABST8785 Leukemic
12	24	100.0	305	6	ABST73174 Human tra
13	24	100.0	350	6	ABST73174 DNA encod
14	24	100.0	504	5	AAZ60863 Region su
15	24	100.0	504	8	AAZ60863 DNA encod
16	24	100.0	561	6	ABST3169 Human end
17	24	100.0	679	6	ABST3169 Human tra
18	24	100.0	766	5	ABST29306 Human pro
19	24	100.0	766	5	ABST29306 Human pro
20	24	100.0	854	6	ABST3449 Human pro
21	24	100.0	921	5	AAZ60848 DNA encod
22	24	100.0	922	6	ABST3180 DNA encod
23	24	100.0	997	6	ABST3173 DNA encod

24	24	100.0	1097	2	AAQ86635	Chimeric
25	24	100.0	1157	9	AAQ86635	Hepatitis
26	24	100.0	1212	5	AAQ86635	DNA encod
27	24	100.0	2255	1	AAQ86635	Sequence
28	24	100.0	4725	5	AAQ86635	DNA encod
29	24	100.0	4739	6	AAQ86635	Breast ca
30	24	100.0	4739	7	AAQ86635	Human Bcr
31	24	100.0	4756	5	AAQ86635	DNA encod
32	24	100.0	4775	5	AAQ86635	DNA encod
33	24	100.0	5795	5	AAQ86635	DNA encod
34	24	100.0	152141	7	AAQ86635	Human BCR
35	21	87.5	40	2	AAQ86635	L6 bcr ex
36	20	83.3	20	2	AAQ86635	bcn mRNA
37	19	79.2	47	2	AAQ86635	Primer BB
38	17	70.8	47	2	AAQ86635	Primer BB
39	16	66.7	22	6	AAQ86635	Human leu
40	16	66.7	40	2	AAQ86635	Forward p
41	15	62.5	47	2	AAQ86635	3SR prime
42	15	62.5	47	2	AAQ86635	Primer BB
43	15	62.5	2097	7	AAQ86635	Rice gene
44	15	62.5	2674	4	AAQ86635	ABL18554
45	15	62.5	3125	9	AAQ86635	C. neofo

#### ALIGNMENTS

RESULT 1  
AAQ86635  
ID AAQ86635 standard; DNA; 24 BP.  
AC AAQ86635;  
XX  
DT 25-MAR-2003 (revised)  
DT 16-NOV-1995 (first entry)  
XX  
DE Modified non-promoter primer for the CML major breakpoint region.  
XX  
KW Primer; autocatalytic; PCR; target; sequence; ss.  
XX  
OS Synthetic.  
XX  
PN US5399491-A.  
XX  
PD 21-MAR-1995.  
XX  
PF 19-MAR-1992; 92US-00855732.  
XX  
PR 11-JUL-1989; 89US-00379501.  
PR 10-JUL-1990; 90US-00550837.  
(GENP-) GEN-PROBE INC.  
Fultz TJ, Kacian DL;  
WPI; 1995-130686/17.  
Amplification of nucleic acid targets - using a reverse transcriptase with RNase H activity and a RNA polymerase at constant temp.

Example 18; Col 47; 58pp; English.  
The oligonucleotide AAQ86635 is a non-promoter primer for the CML major breakpoint amplification region. It is used to illustrate that small changes in the NA sequence result in large changes in the amplification efficiency. AAQ86635 is capable of serving as a primer for the synthesis of autocatalytic oligonucleotides which require no change in the PCR conditions i.e. constant temperature, pH and ionic strength. This sequence is useful in generating multiple copies of specific nucleic acid target sequences. (Updated on 25-MAR-2003 to correct PF field.)  
Sequence 24 BP; 7 A; 7 C; 5 G; 5 T; 0 U; 0 Other;

ID	AAX23204 standard; DNA; 24 BP.
XX	
AC	AAX23204;
DT	11-JUN-1999 (first entry)
DE	CML t(14; 18) non-promoter primer #2.
XX	
KW	Autocatalytic amplification; transcription-based amplification; CML;
KW	thermalcycling; diagnostic; environmental testing; probe; detection;
KW	genetic disease; infectious disease; microorganism; food; forensic;
XX	paternity; primer; ss.
OS	Synthetic.
XX	
PN	US5888779-A.
XX	
PD	30-MAR-1999.
XX	
PF	05-JUN-1995; 95US-00461654.
XX	
PR	11-JUL-1989; 89US-00379501.
PR	10-JUL-1990; 90US-00550837.
XX	
PA	(GENP-) GEN-PROBE INC.
XX	
PI	Fultz TJ, Kacian DL;
XX	
XX	WPI; 1999-253231/21.
DR	Kit for autocatalytic amplification of RNA targets.
PT	
XX	
PS	Example 18; Col 43; 51pp; English.
XX	
CC	This invention describes a novel method for the autocatalytic
CC	amplification of an RNA target in a transcription-based amplification
CC	system without thermalcycling. The method generates oligonucleotides for
CC	diagnostic or environmental testing, for use e.g. as probes and in
CC	cloning. Typical applications are the detection of genetic or infectious
CC	diseases, the monitoring of responses to therapy, the quantitation or
CC	detection of microorganisms in foods, forensic studies and the
CC	establishment of paternity. Kits containing the products of the invention
CC	provide many copies of selected RNA targets under conditions of constant
CC	temperature, ionic strength and pH. Specific amplification of RNA targets
CC	increases sensitivity, convenience, accuracy and the reliability of
CC	assays
XX	
SQ	Sequence 24 BP; 7 A; 7 C; 5 G; 5 T; 0 U; 0 Other;
XX	
Query Match	100.0%; Score 24; DB 2; Length 24;
Best Local Similarity	79.2%; Pred. No. 0.00042;
Matches	19; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
QY	1 GACCAACUCGUGUGAAGAACUCCA 24
DB	1 GACCAACTCGTGTGTGAAGACTCCA 24
RESULT 4	
AAX83985	
ID	AAX83985 standard; DNA; 24 BP.
XX	
AC	AAX83985;
DT	08-SEP-1999 (first entry)
XX	
DE	bcr-abl sense primer.
XX	
KW	Reverse transcription PCR; oligonucleotide-immobilised microplate;
KW	polypropylene; thermal cycle; solid phase; cell lysate; research;
KW	gene expression analysis; diagnostic; drug screening; primer; ss.
XX	
OS	Synthetic.

Query Match	100.0%; Score 24; DB 2; Length 24;
Best Local Similarity	79.2%; Pred. No. 0.00042;
Matches	19; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
QY	1 GACCAACUCGUGUGAAGAACUCCA 24
DB	1 GACCAACTCGTGTGTGAAGACTCCA 24
RESULT 2	
AAX66353	
ID	AAV66353 standard; DNA; 24 BP.
XX	
AC	AAV66353;
DT	06-JAN-1999 (first entry)
XX	
DE	CML-2 chromosomal translocation major breakpoint non-promoter primer.
XX	
KW	CML-2 chromosomal translocation t(14; 18) major breakpoint;
KW	block splice template; autocatalytic RNA amplification; primer; ss.
XX	
OS	Synthetic.
XX	
PN	US5824518-A.
XX	
PD	20-OCT-1998.
XX	
PF	06-JUN-1995; 95US-00469067.
XX	
PR	11-JUL-1989; 89US-00379501.
PR	10-JUL-1990; 90US-00550837.
XX	
PA	(GENP-) GEN-PROBE INC.
XX	
PI	Fultz TJ, Kacian DL;
XX	
XX	WPI; 1998-582557/49.
DR	Block splice template useful for amplification of nucleic acids -
PT	comprises two nucleic acid regions, the first region located 3' of the
PT	second region and blocked at its 3' terminus to inhibit primer extension
PT	by a DNA polymerase.
XX	
PS	Example 18; Col 43; 51pp; English.
XX	
CC	AAV6352-55 represent CML-2 chromosomal translocation t(14;18) major
CC	breakpoint amplification region non-promoter primers. The primers are
CC	used to exemplify the invention. The specification describes methods of
CC	synthesising multiple copies of a target nucleic acid sequence
CC	autocatalytically under conditions of substantially constant temperature,
CC	ionic strength and pH are provided in which multiple RNA copies of the
CC	target sequence autocatalytically generate additional copies. The target
CC	sequence is a block splice template which comprises two nucleic acid
CC	regions. The first region is located 3' of the second region and is
CC	blocked at its 3' terminus to inhibit primer extension by a DNA
CC	polymerase, and the second region comprises a promoter sequence
CC	recognised by an RNA polymerase. The methods are used to amplify nucleic
CC	acids, especially RNA, for analysis, cloning or probe production
XX	
SQ	Sequence 24 BP; 7 A; 7 C; 5 G; 5 T; 0 U; 0 Other;
XX	
Query Match	100.0%; Score 24; DB 2; Length 24;
Best Local Similarity	79.2%; Pred. No. 0.00042;
Matches	19; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
QY	1 GACCAACUCGUGUGAAGAACUCCA 24
DB	1 GACCAACTCGTGTGTGAAGACTCCA 24
RESULT 3	
AAX23204	
ID	AAX23204 standard; DNA; 24 BP.
XX	
AC	AAX23204;
DT	11-JUN-1999 (first entry)
DE	CML t(14; 18) non-promoter primer #2.
XX	
KW	Autocatalytic amplification; transcription-based amplification; CML;
KW	thermalcycling; diagnostic; environmental testing; probe; detection;
KW	genetic disease; infectious disease; microorganism; food; forensic;
XX	paternity; primer; ss.
OS	Synthetic.
XX	
PN	US5888779-A.
XX	
PD	30-MAR-1999.
XX	
PF	05-JUN-1995; 95US-00461654.
XX	
PR	11-JUL-1989; 89US-00379501.
PR	10-JUL-1990; 90US-00550837.
XX	
PA	(GENP-) GEN-PROBE INC.
XX	
PI	Fultz TJ, Kacian DL;
XX	
XX	WPI; 1999-253231/21.
DR	Kit for autocatalytic amplification of RNA targets.
PT	
XX	
PS	Example 18; Col 43; 51pp; English.
XX	
CC	This invention describes a novel method for the autocatalytic
CC	amplification of an RNA target in a transcription-based amplification
CC	system without thermalcycling. The method generates oligonucleotides for
CC	diagnostic or environmental testing, for use e.g. as probes and in
CC	cloning. Typical applications are the detection of genetic or infectious
CC	diseases, the monitoring of responses to therapy, the quantitation or
CC	detection of microorganisms in foods, forensic studies and the
CC	establishment of paternity. Kits containing the products of the invention
CC	provide many copies of selected RNA targets under conditions of constant
CC	temperature, ionic strength and pH. Specific amplification of RNA targets
CC	increases sensitivity, convenience, accuracy and the reliability of
CC	assays
XX	
SQ	Sequence 24 BP; 7 A; 7 C; 5 G; 5 T; 0 U; 0 Other;
XX	
Query Match	100.0%; Score 24; DB 2; Length 24;
Best Local Similarity	79.2%; Pred. No. 0.00042;
Matches	19; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
QY	1 GACCAACUCGUGUGAAGAACUCCA 24
DB	1 GACCAACTCGTGTGTGAAGACTCCA 24
RESULT 3	
AAX23204	
ID	AAX23204 standard; DNA; 24 BP.
XX	
AC	AAX23204;
DT	11-JUN-1999 (first entry)
DE	CML t(14; 18) non-promoter primer #2.
XX	
KW	Autocatalytic amplification; transcription-based amplification; CML;
KW	thermalcycling; diagnostic; environmental testing; probe; detection;
KW	genetic disease; infectious disease; microorganism; food; forensic;
XX	paternity; primer; ss.
OS	Synthetic.
XX	
PN	US5888779-A.
XX	
PD	30-MAR-1999.
XX	
PF	05-JUN-1995; 95US-00461654.
XX	
PR	11-JUL-1989; 89US-00379501.
PR	10-JUL-1990; 90US-00550837.
XX	
PA	(GENP-) GEN-PROBE INC.
XX	
PI	Fultz TJ, Kacian DL;
XX	
XX	WPI; 1999-253231/21.
DR	Kit for autocatalytic amplification of RNA targets.
PT	
XX	
PS	Example 18; Col 43; 51pp; English.
XX	
CC	This invention describes a novel method for the autocatalytic
CC	amplification of an RNA target in a transcription-based amplification
CC	system without thermalcycling. The method generates oligonucleotides for
CC	diagnostic or environmental testing, for use e.g. as probes and in
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CC	diseases, the monitoring of responses to therapy, the quantitation or
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CC	temperature, ionic strength and pH. Specific amplification of RNA targets
CC	increases sensitivity, convenience, accuracy and the reliability of
CC	assays
XX	
SQ	Sequence 24 BP; 7 A; 7 C; 5 G; 5 T; 0 U; 0 Other;
XX	
Query Match	100.0%; Score 24; DB 2; Length 24;
Best Local Similarity	79.2%; Pred. No. 0.00042;
Matches	19; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
QY	1 GACCAACUCGUGUGAAGAACUCCA 24
DB	1 GACCAACTCGTGTGTGAAGACTCCA 24
RESULT 3	
AAX23204	
ID	AAX23204 standard; DNA; 24 BP.
XX	
AC	AAX23204;
DT	11-JUN-1999 (first entry)
DE	CML t(14; 18) non-promoter primer #2.
XX	
KW	Autocatalytic amplification; transcription-based amplification; CML;
KW	thermalcycling; diagnostic; environmental testing; probe; detection;
KW	genetic disease; infectious disease; microorganism; food; forensic;
XX	paternity; primer; ss.
OS	Synthetic.
XX	
PN	US5888779-A.
XX	
PD	30-MAR-1999.
XX	
PF	05-JUN-1995; 95US-00461654.
XX	
PR	11-JUL-1989; 89US-00379501.
PR	10-JUL-1990; 90US-00550837.
XX	
PA	(GENP-) GEN-PROBE INC.
XX	
PI	Fultz TJ, Kacian DL;
XX	
XX	WPI; 1999-253231/21.
DR	Kit for autocatalytic amplification of RNA targets.
PT	
XX	
PS	Example 18; Col 43; 51pp; English.
XX	
CC	This invention describes a novel method for the autocatalytic
CC	amplification of an RNA target in a transcription-based amplification
CC	system without thermalcycling. The method generates oligonucleotides for
CC	diagnostic or environmental testing, for use e.g. as probes and in
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CC	detection of microorganisms in foods, forensic studies and the
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CC	temperature, ionic strength and pH. Specific amplification of RNA targets
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CC	assays
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SQ	Sequence 24 BP; 7 A; 7 C; 5 G; 5 T; 0 U; 0 Other;
XX	
Query Match	100.0%; Score 24; DB 2; Length 24;
Best Local Similarity	79.2%; Pred. No. 0.00042;
Matches	19; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
QY	1 GACCAACUCGUGUGAAGAACUCCA 24
DB	1 GACCAACTCGTGTGTGAAGACTCCA 24
RESULT 3	
AAX23204	
ID	AAX23204 standard; DNA; 24 BP.
XX	
AC	AAX23204;
DT	11-JUN-1999 (first entry)
DE	CML t(14; 18) non-promoter primer #2.
XX	
KW	Autocatalytic amplification; transcription-based amplification; CML;
KW	thermalcycling; diagnostic; environmental testing; probe; detection;
KW	genetic disease; infectious disease; microorganism; food; forensic;
XX	paternity; primer; ss.
OS	Synthetic.
XX	
PN	US5888779-A.
XX	
PD	30-MAR-1999.
XX	
PF	05-JUN-1995; 95US-00461654.
XX	
PR	11-JUL-1989; 89US-00379501.
PR	10-JUL-1990; 90US-00550837.
XX	
PA	(GENP-) GEN-PROBE INC.
XX	
PI	Fultz TJ, Kacian DL;
XX	
XX	WPI; 1999-253231/21.
DR	Kit for autocatalytic amplification of RNA targets.
PT	
XX	
PS	Example 18; Col 43; 51pp; English.
XX	
CC	This invention describes a novel method for the autocatalytic
CC	amplification of an RNA target in a transcription-based amplification
CC	system without thermalcycling. The method generates oligonucleotides for
CC	diagnostic or environmental testing, for use e.g. as probes and in
CC	cloning. Typical applications are the detection of genetic or infectious
CC	diseases, the monitoring of responses to therapy, the quantitation or
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CC	temperature, ionic strength and pH. Specific amplification of RNA targets
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XX	
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Best Local Similarity	79.2%; Pred. No. 0.00042;
Matches	19; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
QY	1 GACCAACUCGUGUGAAGAACUCCA 24
DB	1 GACCAACTCGTGTGTGAAGACTCCA 24
RESULT 3	
AAX23204	
ID	AAX23204 standard; DNA; 24 BP.
XX	
AC	AAX23204;
DT	11-JUN-1999 (first entry)
DE	CML t(14; 18) non-promoter primer #2.
XX	
KW	Autocatalytic amplification; transcription-based amplification; CML;
KW	thermalcycling; diagnostic; environmental testing; probe; detection;
KW	genetic disease; infectious disease; microorganism; food; forensic;
XX	paternity; primer; ss.
OS	Synthetic.
XX	
PN	US5888779-A.
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PD	30-MAR-1999.
XX	
PF	05-JUN-1995; 95US-00461654.
XX	
PR	11-JUL-1989; 89US-00379501.
PR	10-JUL-1990; 90US-00550837.
XX	
PA	(GENP-) GEN-PROBE INC.
XX	
PI	Fultz TJ, Kacian DL;
XX	
XX	WPI; 1999-253231/21.
DR	Kit for autocatalytic amplification of RNA targets.
PT	
XX	
PS	Example 18; Col 43; 51pp; English.
XX	
CC	This invention describes a novel method for the autocatalytic
CC	amplification of an RNA target in a transcription-based amplification
CC	system without thermalcycling. The method generates oligonucleotides for
CC	diagnostic or environmental testing, for use e.g. as probes and in
CC	cloning. Typical applications are the detection of genetic or infectious
CC	diseases, the monitoring of responses to therapy, the quantitation or
CC	detection of microorganisms in foods, forensic studies and the
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XX	
SQ	Sequence 24 BP; 7 A; 7 C; 5 G; 5 T; 0 U; 0 Other;
XX	
Query Match	100.0%; Score 24; DB 2; Length 24;
Best Local Similarity	79.2%; Pred. No. 0.00042;
Matches	19; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
QY	1 GACCAACUCGUGUGAAGAACUCCA 24
DB	1 GACCAACTCGTGTGTGAAGACTCCA 24
RESULT 3	
AAX23204	
ID	AAX23204 standard; DNA; 24 BP.
XX	
AC	AAX23204;
DT	11-JUN-1999 (first entry)
DE	CML t(14; 18) non-promoter primer #2.
XX	
KW	Autocatalytic amplification; transcription-based amplification; CML;
KW	thermalcycling; diagnostic; environmental testing; probe; detection;
KW	genetic disease; infectious disease; microorganism; food; forensic;
XX	paternity; primer; ss.
OS	Synthetic.
XX	
PN	US5888779-A.
XX	
PD	30-MAR-1999.
XX	
PF	05-JUN-1995; 95US-00461654.
XX	
PR	11-JUL-1989; 89US-00379501.
PR	10-JUL-1990; 90US-00550837.
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PA	(GENP-) GEN-PROBE INC.
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PI	Fultz TJ, Kacian DL;
XX	
XX	WPI; 1999-253231/21.
DR	Kit for autocatalytic amplification of RNA targets.
PT	
XX	
PS	Example 18; Col 43; 51pp; English.
XX	
CC	This invention describes a novel method for the autocatalytic
CC	amplification of an RNA target in a transcription-based amplification
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CC	diagnostic or environmental testing, for use e.g. as probes and in
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CC	establishment of paternity. Kits containing the products of the invention
CC	provide many copies of selected RNA targets under conditions of constant
CC	temperature, ionic strength and pH. Specific amplification of RNA targets
CC	increases sensitivity, convenience, accuracy and the reliability of
CC	assays
XX	
SQ	Sequence 24 BP; 7 A; 7 C; 5 G; 5 T; 0 U; 0 Other;
XX	
Query Match	100.0%; Score 24; DB 2; Length 24;
Best Local Similarity	79.2%; Pred. No. 0.00042;
Matches	19; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
QY	1 GACCAACUCGUGUGAAGAACUCCA 24
DB	1 GACCAACTCGTGTGTGAAGACTCCA 24
RESULT 3	
AAX23204	
ID	AAX23204 standard; DNA; 24 BP.
XX	
AC	AAX23204;
DT	11-JUN-1999 (first entry)
DE	CML t(14; 18) non-promoter primer #2.
XX	
KW	Autocatalytic amplification; transcription-based amplification; CML;
KW	thermalcycling; diagnostic; environmental testing; probe; detection;
KW	genetic disease; infectious disease; microorganism; food; forensic;
XX	paternity; primer; ss.
OS	Synthetic.
XX	
PN	US5888779-A.
XX	
PD	30-MAR-1999.
XX	
PF	05-JUN-1995; 95US-00461654.
XX	
PR	11-JUL-1989; 89US-00379501.
PR	10-JUL-1990; 90US-00550837.
XX	
PA	(GENP-) GEN-PROBE INC.
XX	
PI	Fultz TJ, Kacian DL;
XX	
XX	WPI; 1999-253231/21.
DR	Kit for autocatalytic amplification of RNA targets.
PT	
XX	
PS	Example 18; Col 43; 51pp; English.
XX	
CC	This invention describes a novel method for the autocatalytic
CC	amplification of an RNA target in a transcription-based amplification
CC	system without thermalcycling. The method generates oligonucleotides for
CC	diagnostic or environmental testing, for use e.g. as probes and in
CC	cloning. Typical applications are the detection of genetic or infectious
CC	diseases, the monitoring of responses to therapy, the quantitation or
CC	detection of microorganisms in foods, forensic studies and the
CC	establishment of paternity. Kits containing the products of the invention
CC	provide many copies of selected RNA targets under conditions of constant
CC	temperature, ionic strength and pH. Specific amplification of RNA targets
CC	increases sensitivity, convenience, accuracy and the reliability of
CC	assays
XX	
SQ	Sequence 24 BP; 7 A; 7 C; 5 G; 5 T; 0 U; 0 Other;
XX	
Query Match	100.0%; Score 24; DB 2; Length 24;
Best Local Similarity	79.2%; Pred. No. 0.00042;
Matches	19; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
QY	1 GACCAACUCGUGUGAAGAACUCCA 24
DB	1 GACCAACTCGTGTGTGAAGACTCCA 24
RESULT 3	
AAX23204	
ID	AAX23204 standard; DNA; 24 BP.
XX	
AC	AAX23204;
DT	11-JUN-1999 (first entry)
DE	CML t(14; 18) non-promoter primer #2.
XX	
KW	Autocatalytic amplification; transcription-based amplification; CML;
K	



```

XX (GENP-) GEN-PROBE INC.
XX Harvey RC, Eastman PS;
XX WPI; 2000-182730/16.
XX
XX Novel methods for preparing RNA from biological samples, used for the
XX detection and measurement of nucleic acids and fusion nucleic acids.
XX
XX Claim 19; Page 40; 49pp; English.
XX
XX Oligonucleotides AAZ60840-62 and AAZ60865-66 are used in the method of
XX the invention to detect fusion transcripts produced from a translocation
XX between the bcr b3 region and the abl gene. The specification describes a
XX method for detecting a fusion nucleic acid (particularly chimeric mRNA
XX species), in a biological sample. The method comprises contacting a
XX sample of fusion nucleic acid with primers, amplifying the hybridized
XX fusion nucleic acid, and detecting the target hybrid. The method is used
XX for the simple and rapid preparation of RNA from a biological sample,
XX particularly from the cytoplasm of eukaryotic cells, which is suitable
XX for use in an amplification and detection assay. The methods are used for
XX the analysis and detection of nucleic acids in biological samples. The
XX methods are useful in the human medical and veterinary fields, for
XX medical diagnoses and clinical monitoring of a patient's response to
XX therapy where a disease or medical condition is associated with a
XX particular type and/or level of mRNA present in the sample. The methods
XX are also useful for detecting or quantifying fusion or chimeric RNA
XX species, and for detecting a translocation as a marker for a given
XX condition or disease, e.g. translocations associate with cancers,
XX particularly forms of leukemia
XX
XX Sequence 24 BP; 7 A; 7 C; 5 G; 0 T; 5 U; 0 Other;
XX
XX Query Match 100.0%; Score 24; DB 3; Length 24;
XX Best Local Similarity 100.0%; Pred. NO. 0.00042;
XX Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 GACCAACUCGUGUGAAGAACUCCA 24
XX Db |||||:|||||:|||||:|||||:|||||:
XX 24 GACCAACTCGTGTGAAACTCCA 1
XX
XX RESULT 8
XX AAZ60847/c
XX ID AAZ60847 standard; RNA; 24 BP.
XX AC AAZ60847;
XX DT 16-MAY-2000 (first entry)
XX DE Oligonucleotide used to detect bcr b3-abl fusion transcripts.
XX
XX Fusion transcript; translocation; bcr b3 region; abl gene;
XX amplification assay; detection assay; medical diagnosis;
XX clinical monitoring; chimeric RNA; fusion RNA; condition marker;
XX disease marker; cancer; leukemia; ss.
XX
XX Synthetic.
XX
XX WO200005418-A1.
XX
XX 03-FEB-2000.
XX
XX 23-JUL-1999; 99WO-US016832.
XX
XX 23-JUL-1998; 98US-00121239.
XX
XX (GENP-) GEN-PROBE INC.
XX Harvey RC, Eastman PS;
XX WPI; 2000-182730/16.
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XX Novel methods for preparing RNA from biological samples, used for the
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XX fusion nucleic acid, and detecting the target hybrid. The method is used
XX for the simple and rapid preparation of RNA from a biological sample,
XX particularly from the cytoplasm of eukaryotic cells, which is suitable
XX for use in an amplification and detection assay. The methods are used for
XX the analysis and detection of nucleic acids in biological samples. The
XX methods are useful in the human medical and veterinary fields, for
XX medical diagnoses and clinical monitoring of a patient's response to
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XX particular type and/or level of mRNA present in the sample. The methods
XX are also useful for detecting or quantifying fusion or chimeric RNA
XX species, and for detecting a translocation as a marker for a given
XX condition or disease, e.g. translocations associate with cancers,
XX particularly forms of leukemia
XX
XX Sequence 24 BP; 7 A; 7 C; 5 G; 0 T; 5 U; 0 Other;
XX
XX Query Match 100.0%; Score 24; DB 3; Length 24;
XX Best Local Similarity 100.0%; Pred. NO. 0.00042;
XX Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 GACCAACUCGUGUGAAGAACUCCA 24
XX Db |||||:|||||:|||||:|||||:|||||:
XX 1 GACCAACUCGUGUGAAGAACUCCA 24
XX
XX RESULT 7
XX AAZ60846/c
XX ID AAZ60846 standard; DNA; 24 BP.
XX AC AAZ60846;
XX DT 16-MAY-2000 (first entry)
XX DE Oligonucleotide used to detect bcr b3-abl fusion transcripts.
XX
XX Fusion transcript; translocation; bcr b3 region; abl gene;
XX amplification assay; detection assay; medical diagnosis;
XX clinical monitoring; chimeric RNA; fusion RNA; condition marker;
XX disease marker; cancer; leukemia; ss.
XX
XX Synthetic.
XX
XX WO200005418-A1.
XX
XX 03-FEB-2000.
XX
XX 23-JUL-1999; 99WO-US016832.
XX
XX 23-JUL-1998; 98US-00121239.
XX
XX (GENP-) GEN-PROBE INC.
XX Harvey RC, Eastman PS;
XX WPI; 2000-182730/16.
XX

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XX Novel methods for preparing RNA from biological samples, used for the
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XX
XX Claim 19; Page 40; 49pp; English.
XX
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XX particularly from the cytoplasm of eukaryotic cells, which is suitable
XX for use in an amplification and detection assay. The methods are used for
XX the analysis and detection of nucleic acids in biological samples. The
XX methods are useful in the human medical and veterinary fields, for
XX medical diagnoses and clinical monitoring of a patient's response to
XX therapy where a disease or medical condition is associated with a
XX particular type and/or level of mRNA present in the sample. The methods
XX are also useful for detecting or quantifying fusion or chimeric RNA
XX species, and for detecting a translocation as a marker for a given
XX condition or disease, e.g. translocations associate with cancers,
XX particularly forms of leukemia
XX
XX Sequence 24 BP; 5 A; 5 C; 7 G; 7 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 24; DB 3; Length 24;
XX Best Local Similarity 79.2%; Pred. NO. 0.00042;
XX Matches 19; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 GACCAACUCGUGUGAAGAACUCCA 24
XX Db |||||:|||||:|||||:|||||:|||||:
XX 24 GACCAACTCGTGTGAAACTCCA 1
XX
XX RESULT 8
XX AAZ60847/c
XX ID AAZ60847 standard; RNA; 24 BP.
XX AC AAZ60847;
XX DT 16-MAY-2000 (first entry)
XX DE Oligonucleotide used to detect bcr b3-abl fusion transcripts.
XX
XX Fusion transcript; translocation; bcr b3 region; abl gene;
XX amplification assay; detection assay; medical diagnosis;
XX clinical monitoring; chimeric RNA; fusion RNA; condition marker;
XX disease marker; cancer; leukemia; ss.
XX
XX Synthetic.
XX
XX WO200005418-A1.
XX
XX 03-FEB-2000.
XX
XX 23-JUL-1999; 99WO-US016832.
XX
XX 23-JUL-1998; 98US-00121239.
XX
XX (GENP-) GEN-PROBE INC.
XX Harvey RC, Eastman PS;
XX WPI; 2000-182730/16.
XX
XX Novel methods for preparing RNA from biological samples, used for the
XX detection and measurement of nucleic acids and fusion nucleic acids.
XX
XX Claim 19; Page 41; 49pp; English.
XX

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The invention relates to oligonucleotides useful in amplifying and detecting human immunodeficiency virus (HIV) nucleic acid in a sample. The invention is used for environmental testing, diagnostic testing, research studies and for the preparation of reagents or materials for cloning or other purposes. The present sequence is CMV chromosomal translocation t(9;22) PCR primer. This sequence is used in the invention

```

XX AC ABS73175;
XX XX
XX DT 04-DEC-2002 (first entry)
XX DE
XX DE Human translocation (9: 22) (q34: q11) #3.
XX XX
XX KW Chromosome aberration; oncogenic fusion protein; cancer;
XX KW proliferative disease; cellular protein isoform; heat shock protein 90;
XX KW HSP-90; rheumatoid arthritis; cancer; haematopoietic disorder;
XX KW T cell lymphoma; B cell lymphoma; chronic myeloid leukaemia; CML;
XX KW acute myeloid leukaemia; AML; chronic myelomonocytic leukaemia; CMML;
XX KW acute lymphoblastic leukaemia; ALL; APL; NHL; solid tumour;
XX KW papillary thyroid carcinoma; Ewing's sarcoma; melanoma; liposarcoma;
XX KW rhabdomyosarcoma; synovial sarcoma; viral infection; gene; ds.
XX OS
XX OS Homo sapiens.
XX PN WO200269900-A2.
XX PD 12-SEP-2002.
XX XX
XX PF 01-MAR-2002; 2002WO-US006518.
XX XX
XX PR 01-MAR-2001; 2001US-0272751P.
XX XX
XX PA (CONF-) CONFORMA THERAPEUTICS CORP.
XX XX
XX PI Fritz LC, Burrows FJ;
XX DR WPI; 2002-698710/75.
XX XX
XX PT Treating genetically-defined disease associated with chromosomal
XX PT aberrations yielding oncogenic fusion proteins, e.g. cell proliferative
XX PT diseases, involves administering an inhibitor of heat shock protein 90.
XX PS Disclosure; Page 97; 389pp; English.
XX CC
XX CC The invention describes a method of treating genetically-defined disease
XX CC associated with chromosomal aberrations yielding oncogenic fusion
XX CC proteins (I), treating cancerous cells containing (I) in a heterogeneous
XX CC cell population, treating proliferative diseases associated with mutant
XX CC protein or cellular protein isoforms (II) dependent on heat shock protein
XX CC (HSP)-90, or selectively treating cells expressing (II) involving
XX CC administering HSP90-inhibitor. The method is useful for treating
XX CC genetically-defined disease with chromosomal aberration yielding
XX CC oncogenic fusion protein, treating cancerous cells containing fusion
XX CC protein in heterogeneous cell population, treating proliferative disease
XX CC (e.g. rheumatoid arthritis or cancer) associated with mutant protein or
XX CC cellular protein isoform dependent on heat shock protein (HSP)-90 (e.g.
XX CC p53), or selectively treating cells expressing mutant protein or cellular
XX CC protein isoform in a patient heterozygous for (II). The method is useful
XX CC for treating a disease e.g. haematopoietic disorder such as T or B cell
XX CC lymphoma, chronic myeloid leukaemia (CML), APL, ALL, NHL and CMML,
XX CC or a disease characterised by a solid tumour such as papillary thyroid
XX CC carcinoma, Ewing's sarcoma, melanoma, liposarcoma, rhabdomyosarcoma and
XX CC synovial sarcoma. The method is also useful for treating viral
XX CC infections. This represents the DNA sequence of a chromosome aberration
XX SQ Sequence 250 BP; 65 A; 62 C; 63 G; 60 T; 0 U; 0 Other;

Query Match 100.0%; Score 24; DB 6; Length 250;
Best Local Similarity 79.2%; Pred. No. 0.00039;
Matches 19; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 GACCAACUCGUGUGAGAAACUCCA 24
Db 17 GACCAACTCGTGTGAAACTCCA 40

RESULT 12
ABS73174
ID ABS73174 standard; DNA; 305 BP.

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XX AC ABS73174;
XX XX
XX DT 04-DEC-2002 (first entry)
XX DE
XX DE DNA encoding human translocation (9: 22) (q34: q11) protein #5.
XX XX
XX KW Chromosome aberration; oncogenic fusion protein; cancer;
XX KW proliferative disease; cellular protein isoform; heat shock protein 90;
XX KW HSP-90; rheumatoid arthritis; cancer; haematopoietic disorder;
XX KW T cell lymphoma; B cell lymphoma; chronic myeloid leukaemia; CML;
XX KW acute myeloid leukaemia; AML; chronic myelomonocytic leukaemia; CMML;
XX KW acute lymphoblastic leukaemia; ALL; APL; NHL; solid tumour;
XX KW papillary thyroid carcinoma; Ewing's sarcoma; melanoma; liposarcoma;
XX KW rhabdomyosarcoma; synovial sarcoma; viral infection; gene; ds.
XX OS
XX OS Homo sapiens.
XX PN WO200269900-A2.
XX PD 12-SEP-2002.
XX XX
XX PF 01-MAR-2002; 2002WO-US006518.
XX XX
XX PR 01-MAR-2001; 2001US-0272751P.
XX XX
XX PA (CONF-) CONFORMA THERAPEUTICS CORP.
XX XX
XX PI Fritz LC, Burrows FJ;
XX DR WPI; 2002-698710/75.
XX XX
XX PT Treating genetically-defined disease associated with chromosomal
XX PT aberrations yielding oncogenic fusion proteins, e.g. cell proliferative
XX PT diseases, involves administering an inhibitor of heat shock protein 90.
XX PS Disclosure; Page 97; 389pp; English.
XX CC
XX CC The invention describes a method of treating genetically-defined disease
XX CC associated with chromosomal aberrations yielding oncogenic fusion
XX CC proteins (I), treating cancerous cells containing (I) in a heterogeneous
XX CC cell population, treating proliferative diseases associated with mutant
XX CC protein or cellular protein isoforms (II) dependent on heat shock protein
XX CC (HSP)-90, or selectively treating cells expressing (II) involving
XX CC administering HSP90-inhibitor. The method is useful for treating
XX CC genetically-defined disease with chromosomal aberration yielding
XX CC oncogenic fusion protein, treating cancerous cells containing fusion
XX CC protein in heterogeneous cell population, treating proliferative disease
XX CC (e.g. rheumatoid arthritis or cancer) associated with mutant protein or
XX CC cellular protein isoform dependent on heat shock protein (HSP)-90 (e.g.
XX CC p53), or selectively treating cells expressing mutant protein or cellular
XX CC protein isoform in a patient heterozygous for (II). The method is useful
XX CC for treating a disease e.g. haematopoietic disorder such as T or B cell
XX CC lymphoma, chronic myeloid leukaemia (CML), APL, ALL, NHL and CMML,
XX CC or a disease characterised by a solid tumour such as papillary thyroid
XX CC carcinoma, Ewing's sarcoma, melanoma, liposarcoma, rhabdomyosarcoma and
XX CC synovial sarcoma. The method is also useful for treating viral
XX CC infections. This represents the DNA sequence of a chromosome aberration
XX SQ Sequence 305 BP; 77 A; 79 C; 77 G; 72 T; 0 U; 0 Other;

Query Match 100.0%; Score 24; DB 6; Length 305;
Best Local Similarity 79.2%; Pred. No. 0.00039;
Matches 19; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 GACCAACUCGUGUGAGAAACUCCA 24
Db 64 GACCAACTCGTGTGAAACTCCA 87

RESULT 13
AAZ60863

```

ID	AAZ60863 standard; DNA; 350 BP.	DE	DNA encoding novel human diagnostic protein #20827.
XX		XX	
AC	AAZ60863;	KW	Human; chromosome mapping; gene mapping; gene therapy; forensic;
XX		KW	food supplement; medical imaging; diagnostic; genetic disorder; ss.
DT	16-MAY-2000 (first entry)	XX	
XX		OS	Homo sapiens.
DE	Region surrounding a bcr-able splice junction.	XX	
XX		PN	WO200175067-A2.
KW	Fusion transcript; translocation; bcr b3 region; abl gene;	XX	
KW	amplification assay; detection assay; medical diagnosis;	PD	11-OCT-2001.
KW	clinical monitoring; chimeric RNA; fusion RNA; condition marker;	XX	
KW	disease marker; cancer; leukemia; ss.	PF	30-MAR-2001; 2001WO-US008631.
XX		XX	
OS	Unidentified.	PR	31-MAR-2000; 2000US-00540217.
XX		PR	23-AUG-2000; 2000US-00649167.
PN	WO200005418-A1.	XX	
XX		PA	(HYSE-) HYSEQ INC.
PD	03-FEB-2000.	XX	
XX		PI	Drmanac RT, Liu C, Tang YT;
PF	23-JUL-1999; 99WO-US016832.	XX	
XX		DR	WPI; 2001-639362/73.
PR	23-JUL-1998; 98US-00121239.	DR	P-PSDB; ABG20836.
XX		XX	
PA	(GENP-) GEN-PROBE INC.	XX	
XX		PT	New isolated polynucleotide and encoded polypeptides, useful in
PI	Harvey RC, Eastman PS;	PT	diagnostics, forensics, gene mapping, identification of mutations
XX		PT	responsible for genetic disorders or other traits and to assess
XX		PT	biodiversity.
DR	WPI; 2000-182730/16.	XX	
XX		PS	Claim 1; SEQ ID NO 20827; 103pp; English.
PT	Novel methods for preparing RNA from biological samples, used for the	XX	
PT	detection and measurement of nucleic acids and fusion nucleic acids.	CC	The invention relates to isolated polynucleotide (I) and polypeptide (II)
XX		CC	sequences. (I) is useful as hybridisation probes, polymerase chain
PS	Disclosure; Fig 2; 49pp; English.	CC	reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
XX		CC	and in recombinant production of (II). The polynucleotides are also used
CC	The present sequence represents a region surrounding a bcr-able splice	CC	in diagnostics as expressed sequence tags for identifying expressed
CC	junction. The specification describes oligonucleotides which are used to	CC	genes. (I) is useful in gene therapy techniques to restore normal
CC	detect fusion transcripts produced from a translocation between the bcr	CC	activity of (II) or to treat disease states involving (II). (II) is
CC	b3 region and the abl gene. The specification also describes a method for	CC	useful for generating antibodies against it, detecting or quantitating a
CC	detecting a fusion nucleic acid (particularly chimeric mRNA species), in	CC	polypeptide in tissue, as molecular weight markers and as a food
CC	a biological sample. The method comprises contacting a sample of fusion	CC	supplement. (II) and its binding partners are useful for treating disorders
CC	nucleic acid with primers, amplifying the hybridized fusion nucleic acid,	CC	of sites expressing (II). (I) and (II) are useful for treating disorders
CC	and detecting the target hybrid. The method is used for the simple and	CC	involving aberrant protein expression or biological activity. The
CC	rapid preparation of RNA from a biological sample, particularly from the	CC	polypeptide and polynucleotide sequences have applications in
CC	cytoplasm of eukaryotic cells, which is suitable for use in an	CC	diagnostics, forensics, gene mapping, identification of mutations
CC	amplification and detection assay. The methods are used for the analysis	CC	responsible for genetic disorders or other traits to assess biodiversity
CC	and detection of nucleic acids in biological samples. The methods are	CC	and to produce other types of data and products dependent on DNA and
CC	useful in the human medical and veterinary fields, for medical diagnoses	CC	amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic
CC	and clinical monitoring of a patient's response to therapy where a disease	CC	coding sequences of the invention. Note: The sequence data for this
CC	or medical condition is associated with a particular type and/or level of	CC	patent did not appear in the printed specification, but was obtained in
CC	mRNA present in the sample. The methods are also useful for detecting or	CC	electronic format directly from WIPO at
CC	quantifying fusion or chimeric RNA species, and for detecting a	CC	ftp.wipo.int/pub/published_pct_sequences
CC	translocation as a marker for a given condition or disease, e.g.	XX	
CC	translocations associate with cancers, particularly forms of leukemia	XX	
XX		SQ	Sequence 504 BP; 119 A; 122 C; 144 G; 117 T; 0 U; 2 Other;
SQ	Sequence 350 BP; 85 A; 92 C; 89 G; 84 T; 0 U; 0 Other;		
	Query Match 100.0%; Score 24; DB 3; Length 350;		Query Match 100.0%; Score 24; DB 5; Length 504;
	Best Local Similarity 79.2%; Pred. No. 0.00039;		Best Local Similarity 79.2%; Pred. No. 0.00039;
	Matches 19; Conservative 5; Mismatches 0; Indels 0; Gaps 0;		Matches 19; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
QY	1 GACCAACUCGUGUGAACAUCCA 24	QY	1 GACCAACUCGUGUGAACAUCCA 24
	: : : : : : : : :		: : : : : : : : :
DB	65 GACCAACTCGTGTGGAACCTCCA 88	DB	215 GACCAACTCGTGTGGAACCTCCA 238
RESULT 14		RESULT 15	
AAS85023		ACH38242	
ID	AAS85023 standard; cDNA; 504 BP.	ID	ACH38242 standard; cDNA; 504 BP.
XX		XX	
AC	AAS85023;	AC	ACH38242;
XX		XX	
DT	13-FEB-2002 (first entry)	DT	13-OCT-2003 (first entry)
XX		XX	
DE	Human endothelial cell cDNA #6375.	DE	Human endothelial cell cDNA #6375.
XX		XX	

KW Human; ss; sequencing by hybridisation; SBH; expressed sequence tag; EST;  
 KW genome mapping; biodiversity; genetic disorder.

OS Homo sapiens.

XX US2003073623-A1.

XX 17-APR-2003.

XX 30-JUL-2001; 2001US-00918995.

XX 30-JUL-2001; 2001US-00918995.

XX (DRMA/) DRMANAC R T.

XX (LABA/) LABAT I.

XX (STAC/) STACHE-CRAIN B.

XX (DICK/) DICKSON M C.

XX (JONE/) JONES L W.

PI Drmanac RT, Labat I, Stache-Crain B, Dickson MC, Jones LW;

XX WPI; 2003-615964/58.

XX New polynucleotide sequences obtained from various cDNA libraries, useful  
 PT as hybridization probes, as oligomers for PCR, for chromosome and gene  
 PT mapping, in the recombinant production of protein, or in generating  
 PT antisense DNA or RNA.

XX Claim 1; SEQ ID NO 25454; 44pp; English.

XX The invention relates to an isolated polynucleotide comprising any one of  
 CC 38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence was  
 CC determined by the technique of SBH (sequencing by hybridisation). Also  
 CC included is a purified polypeptide comprising a sequence corresponding to  
 CC a reading frame of the novel polynucleotide. The nucleic acid sequences  
 CC are useful in diagnostics as expressed sequence tags (EST) for  
 CC identifying expressed genes or for physical mapping of the human genome,  
 CC in forensics, in assessing biodiversity, or in identifying mutations  
 CC responsible for genetic disorders and other traits. The nucleotide  
 CC sequences are also useful as hybridisation probes, as oligomers for PCR,  
 CC for chromosome and gene mapping, in the recombinant production of  
 CC protein, or in generating antisense DNA or RNA. The purified polypeptide  
 CC is useful for generating antibodies specific for it. The present sequence  
 CC is one of the 38043 isolated cDNA/EST sequences. Note: The sequence data  
 CC for this patent did not form part of the printed specification, but was  
 CC obtained in electronic format directly from USPTO at  
 CC seqdata.uspto.gov/sequence.html?docID=20030073623

XX Sequence 504 BP; 119 A; 122 C; 144 G; 117 T; 0 U; 2 Other;

Query Match 100.0%; Score 24; DB 8; Length 504;

Best Local Similarity 79.2%; Pred. No. 0.00039;

Matches 19; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

OY 1 GACCAACUCGUGUGAAGACUCCA 24

DB 215 GACCAACTCGTGTGAACTCCA 238

Search completed: May 26, 2004, 16:52:16

Job time : 110.037 secs



Result No.	Query			DB	ID	Description
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1	24	100.0	24	4	US-09-168-947-37	Sequence 37, Appl
2	24	100.0	1078	4	US-09-310-843-1	Sequence 1, Appli
3	21	87.5	40	3	US-08-448-4468-16	Sequence 16, Appl
4	20	83.3	20	1	US-08-363-233B-5	Sequence 5, Appli
5	15	62.5	486	4	US-09-621-976-19145	Sequence 19145, A
6	14	58.3	264	4	US-09-313-294A-3357	Sequence 3357, Ap
7	14	58.3	1821	4	US-09-149-476-90	Sequence 90, Appl
8	13	54.2	1638	1	US-08-253-155A-1	Sequence 1, Appli
9	13	54.2	1689	4	US-08-851-567B-29	Sequence 29, Appl
10	13	54.2	2234	3	US-08-993-088A-8	Sequence 8, Appli
11	13	54.2	2234	4	US-08-993-424B-8	Sequence 8, Appli
12	13	54.2	2234	4	US-09-603-680-8	Sequence 8, Appli
13	13	54.2	2692	1	US-08-036-210-14	Sequence 14, Appl
14	13	54.2	2692	2	US-08-449-603-14	Sequence 14, Appl
15	13	54.2	2692	4	US-09-361-096A-14	Sequence 14, Appl
16	13	54.2	3825	6	5310678-2	Patent No. 5310678
17	13	54.2	3900	4	US-09-976-594-569	Sequence 569, App
18	13	54.2	6055	4	US-08-851-567B-25	Sequence 25, Appl
19	13	54.2	6527	4	US-09-492-308A-3	Sequence 3, Appli
20	13	54.2	8931	3	US-09-051-019-1	Sequence 1, Appli
21	13	54.2	10878	4	US-09-911-842A-1	Sequence 1, Appli
22	12	50.0	20	3	US-09-513-729B-81	Sequence 81, Appl
23	12	50.0	36	1	US-08-403-762A-155	Sequence 155, App
24	12	50.0	207	4	US-09-511-625B-42	Sequence 42, Appl
25	12	50.0	349	4	US-09-621-976-15221	Sequence 15221, A
26	12	50.0	418	4	US-09-257-179-36	Sequence 36, Appl
27	12	50.0	444	4	US-09-621-976-12314	Sequence 12314, A

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; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1078
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Gene
; LOCATION: (1)..(1078)
; OTHER INFORMATION: bcr3=abl2; Oligo DNA Dumbbell
; FEATURE:
; NAME/KEY: misc_binding
; LOCATION: (1)..(2)
; OTHER INFORMATION: Intramolecular binding site; the T-nucleotides at position 1 to
; OTHER INFORMATION: 2 can be modified with amino or caroxy features
; FEATURE:
; NAME/KEY: misc_binding
; LOCATION: (1077)..(1078)
; OTHER INFORMATION: Intramolecular binding site; the T-nucleotides at position 1077
; OTHER INFORMATION: to 1078 can be modified with amino or caroxy features
; FEATURE:
; NAME/KEY: Description of Artificial Sequence: Strandness: both; nucleic
; OTHER INFORMATION: acid (linear), hypothetical: No. 6451593 anti-sense: NO
US-09-310-842-1

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RESULT 5

US-09-621-976-19145/c  
 ; Sequence 19145, Application US/09621976  
 ; Patent No. 6639063  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Dumas Milne Edwards, J.B.  
 ; APPLICANT: Jobert, S.  
 ; APPLICANT: Giordano, J.Y.  
 ; TITLE OF INVENTION: ESTs and Encoded Human Proteins.  
 ; FILE REFERENCE: GENSET.054PR2  
 ; CURRENT APPLICATION NUMBER: US/09/621,976  
 ; CURRENT FILING DATE: 2000-07-21  
 ; NUMBER OF SEQ ID NOS: 19335  
 ; SOFTWARE: Patent.pm  
 ; SEQ ID NO 19145  
 ; LENGTH: 486  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; US-09-621-976-19145

Query Match 62.5%; Score 15; DB 4; Length 486;  
 Best Local Similarity 73.3%; Pred. No. 3.7;  
 Matches 11; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 2 ACCAACUCGUGUG 16  
 |||||:|:|:|:  
 Db 16 ACCAACTCGTGTG 2

RESULT 6

US-09-313-294A-3357  
 ; Sequence 3357, Application US/09313294A  
 ; Patent No. 6476212  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Lalgudi, Raghunath V.  
 ; APPLICANT: Ito, Laura Y.  
 ; APPLICANT: Sherman, Bradley K.  
 ; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR  
 ; FILE REFERENCE: PL-0017 US  
 ; CURRENT APPLICATION NUMBER: US/09/313,294A  
 ; CURRENT FILING DATE: 1999-05-14  
 ; NUMBER OF SEQ ID NOS: 7600  
 ; SOFTWARE: PERL Program  
 ; SEQ ID NO 3357  
 ; LENGTH: 264  
 ; TYPE: DNA  
 ; ORGANISM: Zea mays  
 ; FEATURE:  
 ; NAME/KEY: misc\_feature  
 ; OTHER INFORMATION: Incyte ID No. 6476212 700611411H1  
 ; US-09-313-294A-3357

Query Match 58.3%; Score 14; DB 4; Length 264;  
 Best Local Similarity 71.4%; Pred. No. 14;  
 Matches 10; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 11 UGUGUGAACUCCA 24  
 :|:|:|:|:|:  
 Db 35 TGTGTGAARACTCCA 48

RESULT 7

US-09-149-476-90/c  
 ; Sequence 90, Application US/09149476  
 ; Patent No. 6420526  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Rosen et al.  
 ; TITLE OF INVENTION: 186 Human Secreted proteins  
 ; FILE REFERENCE: P2002P1  
 ; CURRENT APPLICATION NUMBER: US/09/149,476  
 ; CURRENT FILING DATE: 1998-09-08  
 ; EARLIER APPLICATION NUMBER: PCT/US98/04493  
 ; EARLIER FILING DATE: 1998-03-06

; EARLIER APPLICATION NUMBER: 60/040,162  
 ; EARLIER FILING DATE: 1997-03-07  
 ; EARLIER APPLICATION NUMBER: 60/040,333  
 ; EARLIER FILING DATE: 1997-03-07  
 ; EARLIER APPLICATION NUMBER: 60/038,621  
 ; EARLIER FILING DATE: 1997-03-07  
 ; EARLIER APPLICATION NUMBER: 60/040,626  
 ; EARLIER FILING DATE: 1997-03-07  
 ; EARLIER APPLICATION NUMBER: 60/040,334  
 ; EARLIER FILING DATE: 1997-03-07  
 ; EARLIER APPLICATION NUMBER: 60/040,336  
 ; EARLIER FILING DATE: 1997-03-07  
 ; EARLIER APPLICATION NUMBER: 60/040,163  
 ; EARLIER FILING DATE: 1997-03-07  
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 ; EARLIER FILING DATE: 1997-05-23  
 ; EARLIER APPLICATION NUMBER: 60/047,615  
 ; EARLIER FILING DATE: 1997-05-23  
 ; EARLIER APPLICATION NUMBER: 60/047,597  
 ; EARLIER FILING DATE: 1997-05-23  
 ; EARLIER APPLICATION NUMBER: 60/047,502  
 ; EARLIER FILING DATE: 1997-05-23  
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 ; EARLIER FILING DATE: 1997-05-23  
 ; EARLIER APPLICATION NUMBER: 60/047,583  
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 ; EARLIER FILING DATE: 1997-05-23  
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 ; EARLIER APPLICATION NUMBER: 60/047,613  
 ; EARLIER FILING DATE: 1997-05-23  
 ; EARLIER APPLICATION NUMBER: 60/047,582  
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 ; EARLIER APPLICATION NUMBER: 60/047,596  
 ; EARLIER FILING DATE: 1997-05-23  
 ; EARLIER APPLICATION NUMBER: 60/047,601  
 ; EARLIER FILING DATE: 1997-05-23  
 ; EARLIER APPLICATION NUMBER: 60/043,580  
 ; EARLIER FILING DATE: 1997-04-11  
 ; EARLIER APPLICATION NUMBER: 60/043,568  
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 ; EARLIER APPLICATION NUMBER: 60/043,311  
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 ; EARLIER APPLICATION NUMBER: 60/043,671  
 ; EARLIER FILING DATE: 1997-04-11  
 ; EARLIER APPLICATION NUMBER: 60/043,674  
 ; EARLIER FILING DATE: 1997-04-11  
 ; EARLIER APPLICATION NUMBER: 60/043,869

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EARLIER APPLICATION NUMBER: 60/043,312  
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EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/043,315  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/048,974  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/056,886  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,877  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,889  
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EARLIER APPLICATION NUMBER: 60/056,893  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,630  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,878  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,662  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,872  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,882  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,637  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,903  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,888  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,879  
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EARLIER APPLICATION NUMBER: 60/056,911  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,636  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,874  
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EARLIER APPLICATION NUMBER: 60/056,910  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,864  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,631  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,845  
EARLIER FILING DATE: 1997-08-22  
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EARLIER APPLICATION NUMBER: 60/057,761  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/047,595  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,599  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,588  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,585  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,586  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,590  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,594  
EARLIER FILING DATE: 1997-05-23

EARLIER APPLICATION NUMBER: 60/047,589  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,593  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,614  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/043,578  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/043,576  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/047,501  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/043,670  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/056,632  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,664  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,876  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,881  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,909  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,875  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,862  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,887  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,908  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/048,964  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/057,650  
EARLIER FILING DATE: 1997-09-05  
EARLIER APPLICATION NUMBER: 60/056,884  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/057,669  
EARLIER FILING DATE: 1997-09-05  
EARLIER APPLICATION NUMBER: 60/049,610  
EARLIER FILING DATE: 1997-06-13  
EARLIER APPLICATION NUMBER: 60/061,060  
EARLIER FILING DATE: 1997-10-02

Query Match 58.3%; Score 14; DB 4; Length 1821;  
Best Local Similarity 71.4%; Pred. No. 15;  
Matches 10; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 10 GUGUGUGAAACUCC 23  
Db 194 GTGTGTGAACCTCC 181  
|.:|.:|.:|.:|.:|

RESULT 8  
US-08-253-155A-1  
Sequence 1, Application US/08253155A  
Patent No. 5691147  
GENERAL INFORMATION:  
APPLICANT: Gyuris, Jeno  
APPLICANT: Draetta, Giulio  
TITLE OF INVENTION: CDK4 Binding Proteins  
NUMBER OF SEQUENCES: 95  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD  
STREET: 60 State Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible

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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII(text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/253,155A
; FILING DATE: 02-JUN-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: M11-028
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1638 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-08-253-155A-1

Query Match 54.2%; Score 13; DB 1; Length 1638;
Best Local Similarity 76.9%; Pred. No. 56;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 12 GUGGAAACUCCA 24
DB 452 GTGTGAACCTCCA 464

RESULT 9
US-08-551-567B-29/c
; Sequence 29, Application US/08851567B
; Patent No. 6528484
; GENERAL INFORMATION:
; APPLICANT: Ensign, Gerald C
; APPLICANT: Bowen, David J
; APPLICANT: Petell, James
; APPLICANT: Fatig, Raymond
; APPLICANT: Schoonover, Sue
; APPLICANT: French-Constant, Richard
; APPLICANT: Rocheleau, Thomas A.
; APPLICANT: Blackburn, Michael B.
; APPLICANT: Hey, Timothy D.
; APPLICANT: Merlo, Donald J.
; APPLICANT: Orr, Gregory L.
; APPLICANT: Roberts, Jean L.
; APPLICANT: Strickland, James A.
; APPLICANT: Guo, Lining
; APPLICANT: Ciche, Todd A.
; TITLE OF INVENTION: Insecticidal Protein Toxins From Photorhabdus
; NUMBER OF SEQUENCES: 88
; CORRESPONDENCE ADDRESS:
; ADDRESS: Dow Agrosciences Patent Department
; STREET: 9330 Zionsville Road
; CITY: Indianapolis
; STATE: IN
; COUNTRY: US
; ZIP: 46268
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/851,567B
; FILING DATE: 05-MAY-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/063,615
; FILING DATE: 18-MAY-1993

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/395,497
; FILING DATE: 28-FEB-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/007,255
; FILING DATE: 06-NOV-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/608,423
; FILING DATE: 28-FEB-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/705,484
; FILING DATE: 28-AUG-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Seay, Nicholas J
; REGISTRATION NUMBER: 27386
; REFERENCE/DOCKET NUMBER: 960296.93804
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 608-251-5000
; TELEFAX: 608-251-9166
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1689 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1689
; US-08-851-567B-29

Query Match 54.2%; Score 13; DB 4; Length 1689;
Best Local Similarity 76.9%; Pred. No. 56;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 GACCAACUCUGU 13
DB 1635 GACCAACTCGTGT 1623

RESULT 10
US-08-993-088A-8
; Sequence 8, Application US/08993088A
; Patent No. 6287855
; GENERAL INFORMATION:
; APPLICANT: Tan, Carina
; APPLICANT: Sullivan, Kathleen
; TITLE OF INVENTION: GALANIN RECEPTOR GALR2 AND
; TITLE OF INVENTION: NUCLEOTIDES ENCODING SAME
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Metck & Co., Inc.
; STREET: P.O. Box 2000, 126 B. Lincoln Ave.
; CITY: Rahway
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065-0900
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/993,088A
; FILING DATE: 18-DEC-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/033,851
; FILING DATE: 27-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Heber, Sheldon O.
; REGISTRATION NUMBER: 38,179
; REFERENCE/DOCKET NUMBER: 19846

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TELECOMMUNICATION INFORMATION:  
TELEPHONE: 732-594-1958  
TELEFAX: 732-594-4720  
TELEX:  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2234 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
US-08-993-088A-8

Query Match 54.2%; Score 13; DB 3; Length 2234;  
Best Local Similarity 69.2%; Pred. No. 57;  
Matches 9; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 3 CCAACUCGUGUGU 15  
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DB 1928 CCAACTCGTGTT 1940

RESULT 11  
US-08-993-424B-8  
Sequence 8, Application US/08993424B  
Patent No. 6337206  
GENERAL INFORMATION:  
APPLICANT: Tan, Carina  
APPLICANT: Kolakowski, Lee F., Jr.  
TITLE OF INVENTION: MOUSE GALANIN RECEPTOR GALR2 AND  
TITLE OF INVENTION: NUCLEOTIDES ENCODING SAME  
NUMBER OF SEQUENCES: 18  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Merck & Co., Inc.  
STREET: P.O. Box 2000, 126 E. Lincoln Ave.  
CITY: Rahway  
STATE: NJ  
COUNTRY: USA  
ZIP: 07065-0900  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows  
SOFTWARE: FastSeq for Windows Version 2.0b  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/993,424B  
FILING DATE: 18-DEC-1997  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/033,851  
FILING DATE: 27-DEC-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Heber, Sheldon O.  
REGISTRATION NUMBER: 38,179  
REFERENCE/DOCKET NUMBER: 19846N2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 732-594-1958  
TELEFAX: 732-594-4720  
TELEX:

INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2234 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
US-08-993-424B-8

Query Match 54.2%; Score 13; DB 4; Length 2234;  
Best Local Similarity 69.2%; Pred. No. 57;  
Matches 9; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 3 CCAACUCGUGUGU 15

DB 1928 CCAACTCGTGTT 1940  
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RESULT 12  
US-09-603-680-8  
Sequence 8, Application US/09603680  
Patent No. 6544753  
GENERAL INFORMATION:  
APPLICANT: Tan, Carina  
APPLICANT: Sullivan, Kathleen  
TITLE OF INVENTION: GALANIN RECEPTOR GALR2 AND  
NUCLEOTIDES ENCODING SAME  
NUMBER OF SEQUENCES: 20  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Merck & Co., Inc.  
STREET: P.O. Box 2000, 126 E. Lincoln Ave.  
CITY: Rahway  
STATE: NJ  
COUNTRY: USA  
ZIP: 07065-0900  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows  
SOFTWARE: FastSeq for Windows Version 2.0b  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/603,680  
FILING DATE: 26-Jun-2000  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/033,851  
FILING DATE: 27-DEC-1996  
APPLICATION NUMBER: 08/993,088  
FILING DATE: 18-DEC-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Heber, Sheldon O.  
REGISTRATION NUMBER: 38,179  
REFERENCE/DOCKET NUMBER: 19846 CA  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 732-594-1958  
TELEFAX: 732-594-4720  
TELEX: <Unknown>  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2234 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
SEQUENCE DESCRIPTION: SEQ ID NO: 8:  
US-09-603-680-8

Query Match 54.2%; Score 13; DB 4; Length 2234;  
Best Local Similarity 69.2%; Pred. No. 57;  
Matches 9; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 3 CCAACUCGUGUGU 15  
|||||:|:|:  
DB 1928 CCAACTCGTGTT 1940

RESULT 13  
US-08-036-210-14  
Sequence 14, Application US/08036210  
Patent No. 5585233  
GENERAL INFORMATION:  
APPLICANT: Moller, Niels P.H.  
APPLICANT: Moller, Karin B.  
APPLICANT: Ullrich, Axel  
TITLE OF INVENTION: PTP-S31: A NOVEL PROTEIN TYROSINE  
PHOSPHATASE  
TITLE OF INVENTION: PHOSPHATASE  
NUMBER OF SEQUENCES: 45

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; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/036,210
; FILING DATE: 23-MAR-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7683-025
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2692 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: unknown
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 2149
; OTHER INFORMATION: /note= "N=x=unknown nucleotide"
; US-08-036-210-14

Query Match 54.2%; Score 13; DB 1; Length 2692;
Best Local Similarity 69.2%; Pred. No. 57;
Matches 9; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 11 UGUGUGAAACUCC 23
Db 216 TGTGTGAAACTCC 228

RESULT 14
US-08-449-609-14
; Sequence 14, Application US/08449609
; Patent No. 5952212
; GENERAL INFORMATION:
; APPLICANT: Moller, Nils P.H.
; APPLICANT: Moller, Karin B.
; APPLICANT: Ullrich, Axel
; TITLE OF INVENTION: PTP-S31: A NOVEL PROTEIN TYROSINE
; PHOSPHATASE
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/449,609
; FILING DATE: 24-MAY-1995
; CLASSIFICATION: 435
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/036,210
; FILING DATE: 23-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7683-025
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2692 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: unknown
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 2149
; OTHER INFORMATION: /note= "N=x=unknown nucleotide"
; US-08-449-609-14

Query Match 54.2%; Score 13; DB 2; Length 2692;
Best Local Similarity 69.2%; Pred. No. 57;
Matches 9; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 11 UGUGUGAAACUCC 23
Db 216 TGTGTGAAACTCC 228

RESULT 15
US-09-361-096A-14
; Sequence 14, Application US/09361096A
; Patent No. 6492495
; GENERAL INFORMATION:
; APPLICANT: MOLLER, NIELS P.H.
; APPLICANT: MOLLER, KARIN B.
; APPLICANT: ULLRICH, AXEL
; TITLE OF INVENTION: PTP-S31: A NOVEL PROTEIN TYROSINE PHOSPHATASE
; FILE REFERENCE: 038602/0686
; CURRENT APPLICATION NUMBER: US/09/361,096A
; CURRENT FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: 08/449,609
; PRIOR FILING DATE: 1995-05-24
; PRIOR APPLICATION NUMBER: 08/036,210
; PRIOR FILING DATE: 1995-03-23
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 14
; LENGTH: 2692
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified base
; LOCATION: (1)..(2692)
; OTHER INFORMATION: n = unknown nucleotide
; NAME/KEY: CDS
; LOCATION: (92...139, 259..1414)
; US-09-361-096A-14

Query Match 54.2%; Score 13; DB 4; Length 2692;
Best Local Similarity 69.2%; Pred. No. 57;
Matches 9; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 11 UGUGUGAAACUCC 23
Db 216 TGTGTGAAACTCC 228

Search completed: May 27, 2004, 02:25:09
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3	24	100.0	24	15	US-10-404-988-5
4	24	100.0	504	10	US-09-918-995-25454
5	24	100.0	542	9	US-09-796-692-8117
6	24	100.0	542	15	US-10-040-862-8117
7	24	100.0	542	16	US-10-057-475B-8117
8	24	100.0	542	16	US-10-154-884B-8117
9	24	100.0	596	9	US-09-796-692-8967
10	24	100.0	596	15	US-10-040-862-8967
11	24	100.0	596	16	US-10-057-475B-8967
12	24	100.0	596	16	US-10-154-884B-8967
13	24	100.0	1078	15	US-10-228-811-1
14	24	100.0	4739	9	US-09-954-531-586

BEST LOCAL SIMILARITY 79.2%; PRED. NO. 6.5E-03;  
Matches 19; Conservative 5; Mismatches 0; Indels 0; Gaps 0;







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Query Match      100.0%; Score 24; DB 9; Length 596;
Best Local Similarity 79.2%; Pred. No. 6.2e-05;
Matches 19; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY      1  GACCAACUCGUGUGAAGAAUCCA 24
         |||||:|:|:|:|:|:|:|:|
Db      409  GACCAACTCGTGTGAACTCCA 432

RESULT 10
US-10-040-862-8967
; Sequence 8967, Application US/10040862
; Publication No. US20030078396A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; FILE OF INVENTION: Hematological Malignancies
; FILE REFERENCE: 014058-013520US
; CURRENT APPLICATION NUMBER: US/10/040,862
; CURRENT FILING DATE: 2001-11-06
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: US 60/223,416
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: US 60/223,378
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: US 09/796,692
; PRIOR FILING DATE: 2001-03-01
; NUMBER OF SEQ ID NOS: 10467
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8967
; LENGTH: 596
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (13)
; OTHER INFORMATION: n=A, T, C or G
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (47)
; OTHER INFORMATION: n=A, T, C or G
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (49)
; OTHER INFORMATION: n=A, T, C or G
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (58)
; OTHER INFORMATION: n=A, T, C or G
; FEATURE:

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5

/ AFFRICANI: weaver, ZOE  
 ; TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Cand

FILE REFERENCE: 689290-77  
CURRENT APPLICATION NUMBER: US/09/954.531

Query Match 100.0%; Score 24; DB 9; Length 4739;

QY 1 GACCAACUCGUGUGAAACUCCA 24

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US/10/193-651-22
:
: Sequence 22, Application US/10193651
: Publication No. US20030064061A1
:
: GENERAL INFORMATION:
:
: APPLICANT: Zhao, Xun
: APPLICANT: Ghaffari, Saghi
: APPLICANT: Lodish, Harvey F.
: APPLICANT: Malashkevich, Vladimir N.
: APPLICANT: Kim, Peter S.
:
: TITLE OF INVENTION: Bcr-Abl Oligomerization Domain
:
: TITLE OF INVENTION: Polypeptides and Uses Therefor
: FILE REFERENCE: 0399,2031-001
: CURRENT APPLICATION NUMBER: US/10/193.651
:

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CURRENT APPLICATION NUMBER: US/10/193,651

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OM nucleic - nucleic search, using sw model

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10: gb\_est2:\*\*

11: gb\_htc:\*\*

12: gb\_est3:\*\*

13: gb\_est4:\*\*

14: gb\_est5:\*\*

15: em\_estfun:\*\*

16: em\_estom:\*\*

17: em\_gas\_hum:\*\*

18: em\_gas\_inv:\*\*

19: em\_gas\_pin:\*\*

20: em\_gas\_vrt:\*\*

21: em\_gas\_fun:\*\*

22: em\_gas\_mam:\*\*

23: em\_gas\_mus:\*\*

24: em\_gas\_pro:\*\*

25: em\_gas\_rod:\*\*

26: em\_gas\_pbg:\*\*

27: em\_gas\_vrl:\*\*

28: gb\_ges1:\*\*

29: gb\_ges2:\*\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	24	100.0	181	14	H55545	H55545 CHR220484 C
2	24	100.0	314	14	D79153	D79153 HUM532H11B
3	24	100.0	377	10	BF800308	BF800308 CM4-C1006
4	24	100.0	401	14	R54267	R54267 yg74h05.r1

5	24	100.0	417	9	AA126116	AA126116 z185904.r
6	24	100.0	437	10	BF873838	BF873838 IL3-ET011
c	24	100.0	438	10	BE938059	BE938059 MR1-TN004
8	24	100.0	443	10	AW452440	AW452440 UI-H-B13-D
9	24	100.0	531	12	BG927169	BG927169 HNC18-1-D
10	24	100.0	588	10	BF380221	BF380221 MR3-UT005
11	24	100.0	588	10	BF094682	BF094682 MR3-UT005
12	24	100.0	597	10	BE396942	BE396942 601290652
13	24	100.0	599	9	AU132798	AU132798 AU132798
14	24	100.0	605	9	AW961897	AW961897 EST373970
15	24	100.0	621	10	BE267891	BE267891 601125452
16	24	100.0	637	14	CB267185	CB267185 1006091.H
17	24	100.0	642	10	BE019411	BE019411 bbs5b12.y
18	24	100.0	653	12	BG829045	BG829045 602753375
19	24	100.0	665	10	BE514596	BE514596 601316940
20	24	100.0	684	10	BF530440	BF530440 602071562
21	24	100.0	686	10	BE397010	BE397010 601289812
22	24	100.0	712	10	BE397695	BE397695 601289802
23	24	100.0	734	10	BE513555	BE513555 601315079
24	24	100.0	741	10	BE265121	BE265121 601193661
25	24	100.0	750	10	BE513994	BE513994 601315851
26	24	100.0	770	12	BI226004	BI226004 602950455
27	24	100.0	785	12	BG93462	BG93462 602411828
28	24	100.0	813	12	BM050194	BM050194 603632367
29	24	100.0	819	14	CF242964	CF242964 AGENCOURT
30	24	100.0	844	14	CD652568	CD652568 AGENCOURT
31	24	100.0	853	13	BQ227532	BQ227532 AGENCOURT
32	24	100.0	875	10	BF241073	BF241073 601880612
33	24	100.0	878	10	BF338795	BF338795 602036226
34	24	100.0	880	13	BQ422888	BQ422888 AGENCOURT
35	24	100.0	880	13	BUS39742	BUS39742 AGENCOURT
36	24	100.0	888	13	BUS40933	BUS40933 AGENCOURT
c	24	100.0	895	13	EX368536	EX368536 60368536
38	24	100.0	903	13	BQ441890	BQ441890 AGENCOURT
39	24	100.0	918	13	BQ212925	BQ212925 AGENCOURT
40	24	100.0	936	13	EX350695	EX350695 60350695
41	24	100.0	955	13	BQ945725	BQ945725 AGENCOURT
42	24	100.0	975	12	BG392048	BG392048 602410011
43	24	100.0	1021	13	BQ896733	BQ896733 AGENCOURT
44	19	79.2	544	10	BF901573	BF901573 IL0-MT030
c	19	79.2	725	29	AG178980	AG178980 Pan trogl

ALIGNMENTS

RESULT 1	H55545	CHR220484	Chromosome 22	181 bp	mRNA	linear	EST 07-DEC-1995
LOCUS	H55545						
DEFINITION							mRNA sequence.
ACCESSION	H55545						
VERSION	H55545.1						GI:1108411
KEYWORDS	EST.						
SOURCE							Homo sapiens (human)
ORGANISM							Homo sapiens
REFERENCE							Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS							Trofater,J.A., Long,K.R., Murrell,J.R., Stotler,C.J., Guealla,J.F. and Buckler,A.J.
TITLE							An expression-independent catalog of genes from human chromosome 22
JOURNAL							Genome Res. 5 (3), 214-224 (1995)
MEDLINE							96159527
PUBMED							8593609
COMMENT							Contact: Buckler AJ Molecular Neurogenetics Unit Massachusetts General Hospital Building 149, 13th St., Charlestown MA 02129 Tel: 6177249616 Fax: 6177265736 Email: buckler@helix.mgh.harvard.edu Seq primer: T3.

[illegible]



Email: [asimpson@ludwig.org.br](mailto:asimpson@ludwig.org.br)  
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL  
(<http://www.ludwig.org.br/scripts/gethtml2.pl?t=IL3-ET0114-071100-338-C02&t=2000-11-01&t&t=1>)  
Seq primer: puc 18 forward  
High quality sequence stop: 390.

## FEATURES

source

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/organism="Homo sapiens"
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/dev_stage="Adult"
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QY 1 GACCAACUGUGUGAAACUCCA 24
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Db 168 GACCAACTCGTGTGAAACTCCA 145
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Matches 19; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY      1  GACCAACUCGUGUGUGAAACUCCA 24
Db      342  GACCAACTCGTGTGAAACTCCA 319

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## FEATURES

source

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1. .438
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/mol type="mRNA"

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(IMAGE Clonoids 985608-986759, 1101192-1101959, 1217928-1220651); NCI\_CGAP\_Co10 pool 1 LUAM 2644-2653, 2871-2872 (IMAGE Clonoids 1057416-1061925, 1144594-1145351). (10% of the driver population), plus a pool of 3,840 arrayed clones from NCI CGAP Sub1 (IMAGE Clonoids 27108516-27110535) and NCI CGAP Sub2 (IMAGE Clonoids 2710536-2712455) (10% of the driver population), plus a pool of 17,136 clones from NCI CGAP Sub3 (IMAGE Clonoids 2712456-2723591) (10% of the driver population), plus a pool of 5,472 clones from NCI CGAP Sub4 (IMAGE Clonoids 2723592-2728969) (70% of the driver population). Subtraction was performed as previously described [Bonaldo, Lennon & Soares (1996) : Normalization and Subtraction: Two Approaches To Facilitate Gene Discovery. Genome Research 6, 791-806. TAG TISSUE=germ cell TAG LIB=NCI CGAP TAG\_SEQ=AAATC"

## ORIGIN

Query Match	100.0%	Score 24;	DB 10;
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			Indels 0;
			Gaps 0;

Qy 1 GACCAACUCGUGUGAGAAACUCCA 24  
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Db 332 GACCAACTCGTGTGTGAAACTCCA 355

## RESULT 9

BG927169	BG927169	531 bp	linear	EST 06-NOV-2001
LOCUS	HNC18-1-D3.R HNC (Human Normal Cartilage)	mRNA		
DEFINITION	sequence.			
ACCESSION	BG927169			
VERSION	BG927169.1	GI:14321692		
KEYWORDS	EST.			

SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
	Mammalia; Theria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE	1 (bases 1 to 531)
AUTHORS	Kumar S., Connor J.R., Dadds R.A., Halsey W., Van Horn M., Mao J., Sathes G., Mui P., Agarwal P., Badger A.M., Lee J.C., Gowen M. and Lark M.W.

**TITLE** Identification and initial characterization of 5000 expressed sequenced tags (ESTs) each from adult human normal and osteoarthritic cartilage cDNA libraries  
**JOURNAL** Osteoarthr. Cartil. 9 (7), 641-653 (2001)  
**AUTHOR(S)** Liakou, M.W.

MEDLINE 21482651  
 PUBMED 11597177  
 COMMENT Contact: Sanjay Kumar  
 UW2109  
 GlaxoSmithKline  
 709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA  
 Tel: 610-270-7245  
 Fax: 610-270-5598  
 Email: sanjay.kumar-l@gsk.com  
 Seg primer: T7

## FEATURES

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location/Qualifiers
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Directional"

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## ORIGIN

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Best Local Similarity 79.2%; Pred. No. 0.00089;

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Db	415	GACCAACTCGTGTGAACCTCCA	438								

RESULT 10	
BF380221	
LOCUS	
DEFINITION	
ACCESSION	
VERSION	
KEYWORDS	
SOURCE	
ORGANISM	

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

1 (bases 1 to 586)

DIAS NETO, E., Garcia Correa, R., Verjowski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, Jr., Zago, M.A., Bordin, S., Cosca, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P.S., Jengoneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.

REFERENCE

AUTHORS

**TITLE** Shotgun sequencing of the human transcriptome with ORF expressed  
sequence tags  
**JOURNAL** Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
**MEDLINE** 20202663  
**PUBMED** 10737800  
**COMMENT** Contact: Simpson A.J.G.

Contact: Sampson A.O.B.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: asimpson@ludwig.org.br  
This sequence was derived from the FAPESP/LICR Human Cancer Genome  
Project. This entry can be seen in the following URL  
(<http://www.ludwig.org.br/scripts/gethtml2.p1?tl=MR3&t2=MR3-UT0050-250900-03-q03&t3=2000-09-25&t4=1>)

Seq primer: puc 18 forward  
High quality sequence stop: 586.

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Site 2: Smal; A mini-lib
derived from ORESTES PCRs
No. 196,716 - Ludwig Institute
profiles into the pUC 19
tissue mRNA and cDNA amp
low stringency condition

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## ORIGIN

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Best Local Similarity	79.2%;	Pred. No. 0.00092;		
Matches 19;	Conservative	5;	Mismatches 0;	Indels 0;
				Gaps 0;

QY 1 GACCAACUCGUGUGGAAACUCCA 24  
|||||:|:|:|:|:|:|:  
Db 429 GACCAACTCGTGTGTGAAACTCCA 452

RESULT 11  
BF094682  
LOCUS  
DEFINITION

LOCUS	BF094682	588 bp	mRNA	linear	EST 19-OCT-2000
DEFINITION	MR3-UT0050-130900-003-g03	UT0050	Homo sapiens	cdNA, mRNA	sequence.





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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 26, 2004, 16:00:31 ; Search time 510.783 Seconds  
(without alignments)  
2036.547 Million cell updates/sec

Title: US-09-121-239-7  
Perfect score: 24  
Sequence: 1 TGGAGTTTCACACGAGTTGGTC 24

Scoring table: OLIGO NUC  
Gapop 60.0 , Gapext 60.0

Searched: 3470272 seqs, 21671516995 residues

Word size : 0  
Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Listing first 45 summaries

Database : GenEmbl.\*

- 1: gb\_ba.\*
- 2: gb\_hgt.\*
- 3: gb\_in.\*
- 4: gb\_om.\*
- 5: gb\_ov.\*
- 6: gb\_pat.\*
- 7: gb\_ph.\*
- 8: gb\_pl.\*
- 9: gb\_pr.\*
- 10: gb\_ro.\*
- 11: gb\_sta.\*
- 12: gb\_sy.\*
- 13: gb\_un.\*
- 14: gb\_vi.\*
- 15: em\_ba.\*
- 16: em\_fun.\*
- 17: em\_hum.\*
- 18: em\_in.\*
- 19: em\_mu.\*
- 20: em\_om.\*
- 21: em\_or.\*
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- 24: em\_ph.\*
- 25: em\_pl.\*
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- 27: em\_sta.\*
- 28: em\_un.\*
- 29: em\_vi.\*
- 30: em\_hgt\_hum.\*
- 31: em\_hgt\_inv.\*
- 32: em\_hgt\_other.\*
- 33: em\_hgt\_mus.\*
- 34: em\_hgt\_pln.\*
- 35: em\_hgt\_rod.\*
- 36: em\_hgt\_mam.\*
- 37: em\_hgt\_vrt.\*
- 38: em\_sy.\*
- 39: em\_hgtgo\_hum.\*
- 40: em\_hgtgo\_mus.\*
- 41: em\_hgtgo\_other.\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
C 1	24	100.0	24	6	E61323	E61323 Probe for d
C 2	24	100.0	24	6	AR352049	AR352049 Sequence
C 3	24	100.0	24	6	BD140611	BD140611 Direct RT
C 4	24	100.0	24	6	BD222527	BD222527 Methods f
C 5	24	100.0	24	6	BD222528	BD222528 Methods f
C 6	24	100.0	24	6	BD222529	BD222529 Methods f
C 7	24	100.0	24	6	BD222530	BD222530 Methods f
C 8	24	100.0	210	9	AY043457	AY043457 Homo sapi
C 9	24	100.0	250	9	AF321981	AF321981 Homo sapi
C 10	24	100.0	305	9	AF192533	AF192533 Homo sapi
C 11	24	100.0	350	6	BD222546	BD222546 Methods f
C 12	24	100.0	561	9	HUMMK562B	M19695 Human myelo
C 13	24	100.0	679	9	HUMABLD	M30832 Human bcr/a
C 14	24	100.0	854	9	HUMABLD	M30829 Human bcr/a
C 15	24	100.0	922	9	HSA131467	AJ131467 Homo sapi
C 16	24	100.0	997	9	HSA131466	AJ131466 Homo sapi
C 17	24	100.0	1078	6	A92081	A92081 Sequence 5
C 18	24	100.0	1078	6	AR230688	AR230688 Sequence
C 19	24	100.0	1157	6	BD177069	BD177069 Standard
C 20	24	100.0	2255	6	E00984	E00984 Probe detec
C 21	24	100.0	2255	6	I04527	I04527 Sequence 1
C 22	24	100.0	2541	9	HUMBCRX	M55395 Human break
C 23	24	100.0	2811	6	AX780333	AX780333 Sequence
C 24	24	100.0	3481	9	AK128501	AK128501 Homo sapi
C 25	24	100.0	4714	9	HSECR	Y00661 Human bcr m
C 26	24	100.0	4739	6	AX331144	AX331144 Sequence
C 27	24	100.0	4739	9	HSECR	X02596 Human mRNA
C 28	24	100.0	5000	9	HUMBCRE	L02335 Human major
C 29	24	100.0	11249	9	AP000343	AP000343 Homo sapi
C 30	24	100.0	152141	9	HSU07000	U07000 Human break
C 31	24	100.0	219210	2	AC145066	AC145066 Pan trogl
C 32	24	100.0	240115	2	AC138021	AC138021 Pan trogl
C 33	21	87.5	40	6	AR100696	AR100696 Sequence
C 34	20	83.3	20	6	I83631	I83631 Sequence 5
C 35	18	75.0	209030	2	AC122318	AC122318 Mus muscu
C 36	17	70.8	201752	2	AC113044	AC113044 Mus muscu
C 37	17	70.8	232458	2	AC099334	AC099334 Mus muscu
C 38	16	66.7	22	6	BD133933	BD133933 Method of
C 39	16	66.7	22	6	BD143900	BD143900 Method of
C 40	16	66.7	40	6	E16986	E16986 Sense prime
C 41	16	66.7	93172	9	AL357872	AL357872 Human DNA
C 42	16	66.7	110000	2	AC105546_4	Continuation (5 of
C 43	16	66.7	114450	2	AC019287	AC019287 Homo sapi
C 44	16	66.7	122418	5	AL592306	AL592306 Zebrafish
C 45	16	66.7	134976	8	AP004968	AP004968 Lotus cor

ALIGNMENTS

RESULT 1	E61323	24 bp	DNA	linear	PAT 18-JUN-2001
LOCUS	E61323/c				
DEFINITION	Probe for detecting oligonucleotide.				
ACCESSION	E61323				
VERSION	E61323.1 GI:13025885				
KEYWORDS	JP 1999046778-A/37.				
SOURCE	synthetic construct				
ORGANISM	artificial sequences.				
REFERENCE	1 (bases 1 to 24)				
AUTHORS	Daniel L.K. and Timothy, J.F.				
TITLE	Probe for detecting oligonucleotide				
JOURNAL	Patent: JP 1999046778-A 37 23-FEB-1999;				
	GEN-PROBE INC				

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COMMENT OS Artificial Sequence
PN JP 1999046778-A/37
PD 23-FEB-1999
PR 14-JAN-1998 JP 1998005607
PI DANIEL LOUIS KASHIAN,TIMOTHY J FURUTSU
PC C12N15/09,C12Q1/68,C12N15/00
CC
FH Key Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 0.049;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TGGAGTTTCACACGAGTTGGTC 24
DB 24 TGGAGTTTCACACGAGTTGGTC 1
RESULT 2
AR352049/c
LOCUS AR352049 24 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 37 from patent US 6589734.
ACCESSION AR352049
VERSION AR352049.1 GI:33757012
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 24)
AUTHORS Kacian,D.L., Fultz,T.J. and McDonough,S.H.
TITLE Detection of HIV
JOURNAL Patent: US 6589734-A 37 08-JUL-2003;
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QY 1 TGGAGTTTCACACGAGTTGGTC 24
DB 24 TGGAGTTTCACACGAGTTGGTC 1
RESULT 3
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LOCUS BD140611 24 bp DNA linear PAT 18-SEP-2002
DEFINITION Direct RT-PCR on oligonucleotide-immobilized PCR microplate.
ACCESSION BD140611
VERSION BD140611.1 GI:23233556
KEYWORDS JP 2002505080-A/5.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 24)
AUTHORS Mitsuhashi,M.
TITLE Direct RT-PCR on oligonucleotide-immobilized PCR microplate
JOURNAL Patent: JP 2002505080-A 5 19-FEB-2002;
COMMENT HITACHI CHEMICAL CO LTD
OS Artificial Sequence
OS Unknown

PN JP 2002505080-A/5
PD 19-FEB-2002
PR 22-DEC-1998 JP 2000525571
PR 60/068394,16-JAN-1998 US 60/071627 PI
MASATO MITSUHASHI
PC C12P19/34,C12M1/00,C12Q1/68/C12N15/09,C12N15/00 CC primer
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DB 24 TGGAGTTTCACACGAGTTGGTC 1
RESULT 4
BD222527/c
LOCUS BD222527 24 bp DNA linear PAT 17-JUL-2003
DEFINITION Methods for detecting and measuring spliced nucleic acids.
ACCESSION BD222527
VERSION BD222527.1 GI:33032297
KEYWORDS JP 2002521037-A/5.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 24)
AUTHORS Harvey,R.C. and Eastman,P.S.
TITLE Methods for detecting and measuring spliced nucleic acids
JOURNAL Patent: JP 2002521037-A 5 16-JUL-2002;
COMMENT GEN PROBE INC
OS Artificial Sequence
PN JP 2002521037-A/5
PD 16-JUL-2002
PR 23-JUL-1999 JP 2000561364
PR 09/121239
PR RICHARD C HARVEY, PAUL S EASTMAN
PC C12Q1/68,C12N15/09,C12N15/00
CC Description of Artificial Sequence: Synthetic Primer FH Key
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DB 24 TGGAGTTTCACACGAGTTGGTC 1
RESULT 5
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LOCUS BD222528 24 bp RNA linear PAT 17-JUL-2003
DEFINITION Methods for detecting and measuring spliced nucleic acids.
ACCESSION BD222528
VERSION BD222528.1 GI:33032298
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KEYWORDS JP 2002521037-A/6.  
 SOURCE synthetic construct  
 ORGANISM synthetic construct  
 REFERENCE 1 (bases 1 to 24)  
 AUTHORS Harvey, R.C. and Eastman, P.S.  
 JOURNAL Methods for detecting and measuring spliced nucleic acids  
 COMMENT Patent: JP 2002521037-A 6 16-JUL-2002;  
 GEN PROBE INC  
 LOCUS JP 2002521037-A/6  
 ACCESSION PD 16-JUL-2002  
 VERSION PF 23-JUL-1999 JP 2000561364  
 KEYWORDS PI RICHARD C HARVEY, PAUL S EASTMAN  
 ORGANISM PC C12Q1/68, C12N15/09, C12N15/00  
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 LOCUS 24 bp DNA linear PAT 17-JUL-2003  
 DEFINITION Methods for detecting and measuring spliced nucleic acids.  
 ACCESSION BD222529  
 VERSION BD222529.1 GI:33032299  
 KEYWORDS JP 2002521037-A/7.  
 ORGANISM synthetic construct  
 SOURCE synthetic construct  
 REFERENCE 1 (bases 1 to 24)  
 AUTHORS Harvey, R.C. and Eastman, P.S.  
 JOURNAL Methods for detecting and measuring spliced nucleic acids  
 COMMENT Patent: JP 2002521037-A 7 16-JUL-2002;  
 GEN PROBE INC  
 LOCUS JP 2002521037-A/7  
 ACCESSION PD 16-JUL-2002  
 VERSION PF 23-JUL-1999 JP 2000561364  
 KEYWORDS PI RICHARD C HARVEY, PAUL S EASTMAN  
 ORGANISM PC C12Q1/68, C12N15/09, C12N15/00  
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 JOURNAL Location/Qualifiers  
 COMMENT 1. .24  
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 PN /mol\_type='genomic DNA'  
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 DB 1 TGGAGTTTCACACGAGTTGGTC 24  
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 LOCUS 24 bp RNA linear PAT 17-JUL-2003  
 DEFINITION Methods for detecting and measuring spliced nucleic acids.  
 ACCESSION BD222530  
 VERSION BD222530.1 GI:33032300  
 KEYWORDS JP 2002521037-A/8.  
 ORGANISM synthetic construct  
 SOURCE synthetic construct  
 REFERENCE 1 (bases 1 to 24)  
 AUTHORS Harvey, R.C. and Eastman, P.S.  
 JOURNAL Methods for detecting and measuring spliced nucleic acids  
 COMMENT Patent: JP 2002521037-A 8 16-JUL-2002;  
 GEN PROBE INC  
 LOCUS JP 2002521037-A/8  
 ACCESSION PD 16-JUL-2002  
 VERSION PF 23-JUL-1999 JP 2000561364  
 KEYWORDS PI RICHARD C HARVEY, PAUL S EASTMAN  
 ORGANISM PC C12Q1/68, C12N15/09, C12N15/00  
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 JOURNAL Location/Qualifiers  
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 DB 1 TGGAGTTTCACACGAGTTGGTC 24  
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 AY043457  
 LOCUS 210 bp mRNA linear PRI 27-JUN-2003  
 DEFINITION Homo sapiens BCR-ABL fusion protein (BCR-ABL fusion) mRNA, partial cds.  
 ACCESSION AY043457  
 VERSION AY043457.1 GI:22073966  
 KEYWORDS Homo sapiens (human)  
 ORGANISM Homo sapiens  
 REFERENCE Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 TITLE Otazu, I.B., Belen Rivero, M., Olicio, R., Pinto, A., Zalberg, I. and  
 JOURNAL A rare, in-frame BCR-ABL fusion (e13a3) in a patient with an  
 MEDLINE aggressive chronic myeloid leukaemia  
 PUBMED 22259050  
 REFERENCE 2 (bases 1 to 210)  
 AUTHORS Otazu, I.B., Rivero, M.B. and Olicio, R.  
 TITLE Direct Submission  
 JOURNAL Submitted (03-JUL-2001) Genetics Division, Instituto Nacional de  
 Cancer, Praca da Cruz Vermelha, 23, sexto andar, Rio de Janeiro, RJ

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  DEFINITION Homo sapiens BCR-ABL fusion transcript el15a2 mRNA sequence.
  ACCESSION AF3211981
  VERSION AF3211981.1 GI:13021894
  KEYWORDS
  SOURCE Homo sapiens (human)
  ORGANISM
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  REFERENCE
    1 (bases 1 to 250)
    Moreno,M.P., Cortinas,M.N., Bonomi,R., Cardeza,A. and Uriarte,M.R.
    A novel BCR-ABL fusion transcript (el15a2) in two patients with
    atypical Chronic Myeloproliferative Syndrome
  JOURNAL
    2 (bases 1 to 250)
    Moreno,M.P., Cortinas,M.N., Bonomi,R., Cardeza,A. and Uriarte,M.R.
    Direct Submission
  TITLE
    Submitted (16-NOV-2000) Biologia Molecular, Asociacion Espanola,
    Bulevar Artigas 1465, Montevideo 11200, Uruguay
  JOURNAL
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RESULT 10
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LOCUS 305 bp mRNA linear PRI 04-APR-2000
DEFINITION Homo sapiens BCR-ABL fusion protein (BCR-ABL fusion) mRNA, partial
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ACCESSION AF192533
VERSION AF192533.1 GI:7406986
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
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  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  REFERENCE
    1 (bases 1 to 305)
    Cortinas,M.N., Uriarte,M.R. and Moreno,M.P.
    Identification of a novel BCR ABL fusion transcript in two patients
    with persistent neutrophilia in absence of Philadelphia chromosome
    Unpublished
  JOURNAL
    2 (bases 1 to 305)
    Cortinas,M.N., Uriarte,M.R. and Moreno,M.P.
    Direct Submission
  TITLE
    Submitted (06-OCT-1999) Biologia Molecular, Asociacion Espanola
    Primera de Socorros Mutuos, Bvar. Artigas 1465, Montevideo 11200,
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  JOURNAL
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  DEFINITION Methods for detecting and measuring spliced nucleic acids.
  ACCESSION BD222546
  VERSION BD222546.1 GI:33032316
  KEYWORDS
  SOURCE Homo sapiens (human)
  ORGANISM
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 350)
REFERENCE
AUTHORS Harvey,R.C. and Eastman,P.S.
TITLE Methods for detecting and measuring spliced nucleic acids
JOURNAL Patent: JP 2002521037-A 24 16-JUL-2002;
COMMENT
GEN PROBE INC
OS Homo sapiens (human)
PN JP 2002521037-A/24
PD 16-JUL-2002
PF 23-JUL-1999 JP 2000561364
PR RICHARD C HARVEY, PAUL S EASTMAN
PC C12Q1/68, C12N15/09, C12N15/00
CC Methods for detecting and measuring spliced nucleic acids FH
Key Location/Qualifiers
FT source 1..350
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RESULT 12
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DEFINITION Human myelocytic chimeric bcr and chromosome 9 fusion gene, exons 1-4.
ACCESSION M19695
VERSION M19695.1 GI:1188567
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 561)
REFERENCE
AUTHORS Grosveld,G., Verwoerd,T., van Agthoven,T., de Klein,A.,
Ranachandran,K.L., Heisterkamp,N., Stam,K. and Groffen,J.
TITLE The chronic myelocytic cell line K562 contains a breakpoint in bcr
and produces a chimeric bcr/c-abl transcript
JOURNAL Mol. Cell. Biol. 6 (2), 607-616 (1986)
MEDLINE 87064346
PUBMED 3023859
COMMENT Original source text: Human myelocytic Ph(1)-positive CML K562 cell
line, cDNA to mRNA, clone 8E.
The bcr region of the fusion protein is located on chromosome
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 350)
REFERENCE
AUTHORS Harvey,R.C. and Eastman,P.S.
TITLE Methods for detecting and measuring spliced nucleic acids
JOURNAL Patent: JP 2002521037-A 24 16-JUL-2002;
COMMENT
GEN PROBE INC
OS Homo sapiens (human)
PN JP 2002521037-A/24
PD 16-JUL-2002
PF 23-JUL-1999 JP 2000561364
PR RICHARD C HARVEY, PAUL S EASTMAN
PC C12Q1/68, C12N15/09, C12N15/00
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RESULT 13
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DEFINITION Human bcr/abl fusion protein, partial cds, clone E3.
ACCESSION M30832
VERSION M30832.1 GI:177944
KEYWORDS Philadelphia chromosome; abl proto-oncogene; translocation.
SOURCE Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 679)
REFERENCE
AUTHORS Shivelman,E., Lifshitz,B., Gale,R.P. and Canaanani,E.
TITLE Fused transcript of abl and bcr genes in chronic myelogenous
leukaemia
JOURNAL Nature 315 (6020), 550-554 (1985)
MEDLINE 85240529
PUBMED 2989692
COMMENT Original source text: Homo sapiens (clone: E3.) cDNA to mRNA.
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DEFINITION Human bcr/abl fusion protein mRNA, partial cds, Clone K28.
ACCESSION M30829
VERSION M30829.1 GI:177953
KEYWORDS Philadelphia chromosome; abl proto-oncogene; translocation.
SOURCE Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 854)
REFERENCE
AUTHORS Shivelman,E., Lifshitz,B., Gale,R.P. and Canaanani,E.
TITLE Fused transcript of abl and bcr genes in chronic myelogenous
leukaemia
JOURNAL Nature 315 (6020), 550-554 (1985)
MEDLINE 85240529
PUBMED 2989692
COMMENT Original source text: Homo sapiens (clone: K28.) cDNA to mRNA.
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LOCUS Homo sapiens mRNA for BCR/ABL chimeric fusion peptide, partial.
DEFINITION
ACCESSION AJ131467
VERSION AJ131467.1 GI:4033556
KEYWORDS BCR/ABL chimeric fusion peptide; bcr/abl gene.
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Burmeister T., Maurer J., Alvaro M., Elmaagacli A.H., Grunebach F.,
Held K.R., Hess G., Hochhaus A., Hoppper W., Lentes K.U.,
Lubbert M., Schafer K.L., Schafhausen P., Schmidt C.A., Schuler F.,
Seeger K., Seelig R., Thiede C., Viehmann S., Weber C., Wilhelm S.,
Christmann A., Clement J.H., Ebener U., Enczmann J., Leo R.,
Schleuning M., Schoch R. and Thiel E.
TITLE Quality assurance in RT-PCR-based BCR/ABL diagnostics--results of
an interlaboratory test and a standardization approach
JOURNAL Leukemia 14 (10), 1850-1856 (2000)
MEDLINE 20471781
PUBMED 11021760
REFERENCE 2 (bases 1 to 922)
AUTHORS Burmeister T.
TITLE Direct Submission
JOURNAL Submitted (04-DEC-1998) Burmeister T., Medizinische Klinik III, FU
Berlin, Hindenburgdamm 30, Berlin, Germany 12200, Germany
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GenCore version 5.1.1.6  
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OM nucleic - nucleic search, using sw model

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Sequence: 1 TGGAGTTTCACACAGCTGGTC 24

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Word size : 0

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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C 4	24	100.0	24	2	AAZ83985	AAZ83985 bcr-abl s
C 5	24	100.0	24	3	AAZ60844	AAZ60844 Oligonucle
C 6	24	100.0	24	3	AAZ60845	AAZ60845 Oligonucle
C 7	24	100.0	24	3	AAZ60847	AAZ60847 Oligonucle
C 8	24	100.0	24	3	AAZ60846	AAZ60846 Oligonucle
C 9	24	100.0	24	9	AAZ62592	AAZ62592 CML chrom
C 10	24	100.0	200	2	AAZ8785	AAZ8785 Leukemic
C 11	24	100.0	250	6	ABS73175	ABS73175 Human tra
C 12	24	100.0	305	6	ABS73174	ABS73174 DNA encod
C 13	24	100.0	350	3	AAZ60863	AAZ60863 Region su
C 14	24	100.0	504	5	AAZ85023	AAZ85023 DNA encod
C 15	24	100.0	504	8	ACH38242	ACH38242 Human end
C 16	24	100.0	561	6	ABS73169	ABS73169 Human tra
C 17	24	100.0	679	6	ABS73172	ABS73172 DNA encod
C 18	24	100.0	766	5	ABV29306	ABV29306 Human pro
C 19	24	100.0	766	5	ABV23449	ABV23449 Human pro
C 20	24	100.0	854	6	ABS73170	ABS73170 DNA encod
C 21	24	100.0	921	5	AAZ85025	AAZ85025 DNA encod
C 22	24	100.0	922	6	ABS73180	ABS73180 DNA encod
C 23	24	100.0	997	6	ABS73173	ABS73173 DNA encod

C 24	24	100.0	1097	2	AAT91764	AAT91764 Chimeric
C 25	24	100.0	1157	9	ADC64640	ADC64640 Hepatitis
C 26	24	100.0	1212	5	AAZ85028	AAZ85028 DNA encod
C 27	24	100.0	2255	1	AAZ60228	AAZ60228 Sequence
C 28	24	100.0	4725	5	AAZ76375	AAZ76375 DNA encod
C 29	24	100.0	4739	6	ABL63316	ABL63316 Breat ca
C 30	24	100.0	4739	7	ACC00031	ACC00031 Human Bcr
C 31	24	100.0	4756	5	AAZ85030	AAZ85030 DNA encod
C 32	24	100.0	4775	5	AAZ76377	AAZ76377 DNA encod
C 33	24	100.0	5795	5	AAZ85031	AAZ85031 DNA encod
C 34	24	100.0	152141	7	ACA64961	ACA64961 Human BCR
C 35	21	87.5	40	2	AAQ66789	AAQ66789 L6 bcr ex
C 36	20	83.3	20	2	AAQ51829	AAQ51829 bcr mRNA
C 37	19	79.2	47	2	AAT91751	AAT91751 Primer BB
C 38	17	70.8	47	2	AAT91749	AAT91749 Primer BB
C 39	16	66.7	22	6	ABQ92608	ABQ92608 Human leu
C 40	16	66.7	40	2	AAV58775	AAV58775 Forward p
C 41	15	62.5	47	2	AAT03636	AAT03636 3SR prime
C 42	15	62.5	47	2	AAT91753	AAT91753 Primer BB
C 43	15	62.5	2097	7	ADA70851	ADA70851 Rice gene
C 44	15	62.5	2674	4	ABL18554	ABL18554 Drosophil
C 45	15	62.5	3125	9	ADB68966	ADB68966 C. neofor

# ALIGNMENTS

RESULT 1  
AAQ86635/c  
ID AAQ86635 standard; DNA; 24 BP.  
XX  
AC AAQ86635;  
XX  
DT 25-MAR-2003 (revised)  
DT 16-NOV-1995 (first entry)  
XX  
DE Modified non-promoter primer for the CML major breakpoint region.  
XX  
KW Primer; autocatalytic; PCR; target; sequence; ss.  
XX  
OS Synthetic.  
XX  
PN US5399491-A.  
PD  
PD 21-MAR-1995.  
XX  
PF 19-MAR-1992; 92US-00855732.  
XX  
PR 11-JUL-1989; 89US-00379501.  
PR 10-JUL-1990; 90US-00550837.  
(GENP-) GEN-PROBE INC.  
Fultz TJ, Kacian DL;  
WPI; 1995-130686/17.  
Amplification of nucleic acid targets - using a reverse transcriptase with RNase H activity and a RNA polymerase at constant temp.  
Example 18; Col 47; 58pp; English.

The oligonucleotide AAQ86635 is a non-promoter primer for the CML major breakpoint amplification region. It is used to illustrate that small changes in the NA sequence result in large changes in the amplification efficiency. AAQ86635 is capable of serving as a primer for the synthesis of autocatalytic oligonucleotides which require no change in the PCR conditions i.e. constant temperature, pH and ionic strength. This sequence is useful in generating multiple copies of specific nucleic acid target sequences. (Updated on 25-MAR-2003 to correct PF field.)  
Sequence 24 BP; 7 A; 7 C; 5 G; 5 T; 0 U; 0 Other;

Query Match 100.0%; Score 24; DB 2; Length 24;  
 Best Local Similarity 100.0%; Pred. No. 0.00042;  
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGGAGTTTCACACACGAGTTGGTC 24  
 |||||  
 Db 24 TGGAGTTTCACACACGAGTTGGTC 1

RESULT 2  
 AAV66353/c  
 ID AAV66353 standard; DNA; 24 BP.  
 XX  
 AC AAV66353;  
 XX  
 XX  
 DT 06-JAN-1999 (first entry)  
 XX  
 DE CML-2 chromosomal translocation major breakpoint non-promoter primer.  
 XX  
 KW CML-2 chromosomal translocation t(14; 18) major breakpoint;  
 KW block splice template; autocatalytic RNA amplification; primer; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN US5824518-A.  
 XX  
 XX 20-OCT-1998.  
 XX  
 PF 06-JUN-1995; 95US-00469067.  
 XX  
 PR 11-JUL-1989; 89US-00379501.  
 PR 10-JUL-1990; 90US-00550837.  
 XX  
 PA (GENP-) GEN-PROBE INC.  
 XX  
 PI Fultz TJ, Kacian DL;  
 XX  
 DR WPI; 1998-582557/49.  
 XX  
 XX Block splice template useful for amplification of nucleic acids -  
 PT comprises two nucleic acid regions, the first region located 3' of the  
 PT second region and blocked at its 3' terminus to inhibit primer extension  
 PT by a DNA polymerase.  
 XX  
 PS Example 18; Col 43; 5lpp; English.  
 XX  
 CC AAV66352-55 represent CML-2 chromosomal translocation t(14;18) major  
 CC breakpoint amplification region non-promoter primers. The primers are  
 CC used to amplify the invention. The specification describes methods of  
 CC synthesising multiple copies of a target nucleic acid sequence  
 CC autocatalytically under conditions of substantially constant temperature,  
 CC ionic strength and pH are provided in which multiple RNA copies of the  
 CC target sequence autocatalytically generate additional copies. The target  
 CC sequence is a block splice template which comprises two nucleic acid  
 CC regions. The first region is located 3' of the second region and is  
 CC blocked at its 3' terminus to inhibit primer extension by a DNA  
 CC polymerase, and the second region comprises a promoter sequence  
 CC recognised by an RNA polymerase. The methods are used to amplify nucleic  
 CC acids, especially RNA, for analysis, cloning or probe production  
 XX  
 SQ Sequence 24 BP; 7 A; 7 C; 5 G; 5 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 24; DB 2; Length 24;  
 Best Local Similarity 100.0%; Pred. No. 0.00042;  
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGGAGTTTCACACACGAGTTGGTC 24  
 |||||  
 Db 24 TGGAGTTTCACACACGAGTTGGTC 1

RESULT 3  
 AAX23204/c  
 ID AAX23204 standard; DNA; 24 BP.  
 XX  
 AC AAX23204;  
 XX  
 XX  
 DT 08-SEP-1999 (first entry)  
 XX  
 DE bcr-abl sense primer.  
 XX  
 KW Reverse transcription PCR; oligonucleotide-immobilised microplate;  
 KW polypropylene; thermal cycle; solid phase; cell lysate; research;  
 KW gene expression analysis; diagnostic; drug screening; primer; ss.  
 XX  
 OS Synthetic.

ID AAX23204 standard; DNA; 24 BP.  
 XX  
 AC AAX23204;  
 XX  
 DT 11-JUN-1999 (first entry)  
 XX  
 DE CML t(14; 18) non-promoter primer #2.  
 XX  
 KW Autocatalytic amplification; transcription-based amplification; CML;  
 KW thermalcycling; diagnostic; environmental testing; probe; detection;  
 KW genetic disease; infectious disease; microorganism; food; forensic;  
 KW paternity; primer; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN US5888779-A.  
 XX  
 PD 30-MAR-1999.  
 XX  
 PF 05-JUN-1995; 95US-00461654.  
 XX  
 PR 11-JUL-1989; 89US-00379501.  
 PR 10-JUL-1990; 90US-00550837.  
 XX  
 PA (GENP-) GEN-PROBE INC.  
 XX  
 XX Fultz TJ, Kacian DL;  
 XX  
 DR WPI; 1999-253231/21.  
 XX  
 PT Kit for autocatalytic amplification of RNA targets.  
 XX  
 PS Example 18; Col 43; 5lpp; English.  
 XX  
 CC This invention describes a novel method for the autocatalytic  
 CC amplification of an RNA target in a transcription-based amplification  
 CC system without thermalcycling. The method generates oligonucleotides for  
 CC diagnostic or environmental testing, for use e.g. as probes and in  
 CC cloning. Typical applications are the detection of genetic or infectious  
 CC diseases, the monitoring of responses to therapy, the quantitation or  
 CC detection of microorganisms in foods, forensic studies and the  
 CC establishment of paternity. Kits containing the products of the invention  
 CC provide many copies of selected RNA targets under conditions of constant  
 CC temperature, ionic strength and pH. Specific amplification of RNA targets  
 CC increases sensitivity, convenience, accuracy and the reliability of  
 CC assays  
 XX  
 SQ Sequence 24 BP; 7 A; 7 C; 5 G; 5 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 24; DB 2; Length 24;  
 Best Local Similarity 100.0%; Pred. No. 0.00042;  
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGGAGTTTCACACACGAGTTGGTC 24  
 |||||  
 Db 24 TGGAGTTTCACACACGAGTTGGTC 1

RESULT 4  
 AAX83985/c  
 ID AAX83985 standard; DNA; 24 BP.  
 XX  
 AC AAX83985;  
 XX  
 XX  
 DT 08-SEP-1999 (first entry)  
 XX  
 DE bcr-abl sense primer.  
 XX  
 KW Reverse transcription PCR; oligonucleotide-immobilised microplate;  
 KW polypropylene; thermal cycle; solid phase; cell lysate; research;  
 KW gene expression analysis; diagnostic; drug screening; primer; ss.  
 XX  
 OS Synthetic.



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XX PN WO9932654-A1.
XX PD
XX PF 01-JUL-1999.
XX PR 22-DEC-1998; 98WO-US027293.
XX PR 22-DEC-1997; 97US-0068394P.
XX PR 16-JAN-1998; 98US-0071627P.
XX PA (HITB ) HITACHI CHEM CO LTD.
XX PA (HITB ) HITACHI CHEM RES CENT INC.
XX PI Mitsuhashi M;
XX DR WPI; 1999-418942/35.
XX PT Using oligonucleotide-immobilized microplates in polymerase chain
XX PT reactions.
XX PS Example; Page 9; 34pp; English.
XX CC The present invention describes the use of oligonucleotide-immobilized
XX CC microplates having heat-stability for thermal cycles of reverse
XX CC transcription-polymerase chain reaction (RT-PCR). The method of RT-PCR
XX CC comprises: (a) preparing cell lysate of a target cell; (b) transferring
XX CC the cell lysate to an oligonucleotide-immobilized microplate having wells
XX CC to which oligonucleotides are securely immobilized, the microplate having
XX CC heat-stability for thermal cycles of PCR, the oligonucleotides having
XX CC nucleic acid sequences specifically complementary to mRNA of interest
XX CC present in the cell lysate; (c) capturing mRNA by the oligonucleotides of
XX CC the microplate; (d) conducting RT-PCR on the same microplate, using an
XX CC appropriate buffer; and (e) detecting PCR products of interest. The
XX CC method is used for gene expression analysis. The multiple PCR system is
XX CC useful in basic research, diagnostics and drug screening, with potential
XX CC application to future automation. The method simplifies the process of RT
XX CC -PCR. cDNA synthesized from mRNA captured by immobilized oligonucleotide
XX CC on the PCR microplates can be used more than once, thus amplifying
XX CC several times different or same portions of the cDNA by using appropriate
XX CC primers. The method also drastically simplifies the preparation of cell
XX CC lysate and significantly stabilizes the yield of recovered cytosolic RNA.
XX CC The present sequence represents a primer used in an example from the
XX CC present invention
XX SQ Sequence 24 BP; 7 A; 7 C; 5 G; 5 T; 0 U; 0 Other;
      Query Match 100.0%; Score 24; DB 2; Length 24;
      Best Local Similarity 100.0%; Pred. No. 0.00042; Mismatches 0; Gaps 0;
      Matches 24; Conservative 0; Indels 0;

QY 1 TGGAGTTTTCACACGAGTTGGTC 24
Db 24 TGGAGTTTTCACACGAGTTGGTC 1

RESULT 5
AAZ60844/c
ID AAZ60844 standard; DNA; 24 BP.
XX AC AAZ60844;
XX KW Fusion transcript; translocation; bcr b3 region; abl gene;
XX KW amplification assay; detection assay; medical diagnosis;
XX KW clinical monitoring; chimeric RNA; fusion RNA; condition marker;
XX KW disease marker; cancer; leukemia; ss.
XX OS Synthetic.
XX PN WO200005418-A1.

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XX PD 03-FEB-2000.
XX PF 23-JUL-1999; 99WO-US016832.
XX PR 23-JUL-1998; 98US-00121239.
XX PA (GENP-) GEN-PROBE INC.
XX PI Harvey RC, Eastman PS;
XX DR WPI; 2000-182730/16.
XX PT Novel methods for preparing RNA from biological samples, used for the
XX PT detection and measurement of nucleic acids and fusion nucleic acids.
XX PS Claim 19; Page 40; 49pp; English.
XX CC Oligonucleotides AAZ60840-62 and AAZ60855-66 are used in the method of
XX CC the invention to detect fusion transcripts produced from a translocation
XX CC between the bcr b3 region and the abl gene. The specification describes a
XX CC method for detecting a fusion nucleic acid (particularly chimeric mRNA
XX CC species), in a biological sample. The method comprises contacting a
XX CC sample of fusion nucleic acid with primers, amplifying the hybridized
XX CC fusion nucleic acid, and detecting the target hybrid. The method is used
XX CC for the simple and rapid preparation of RNA from a biological sample,
XX CC particularly from the cytoplasm of eukaryotic cells, which is suitable
XX CC for use in an amplification and detection assay. The methods are used for
XX CC the analysis and detection of nucleic acids in biological samples. The
XX CC methods are useful in the human medical and veterinary fields, for
XX CC medical diagnoses and clinical monitoring of a patient's response to
XX CC therapy where a disease or medical condition is associated with a
XX CC particular type and/or level of mRNA present in the sample. The methods
XX CC are also useful for detecting or quantifying fusion or chimeric RNA
XX CC species, and for detecting a translocation as a marker for a given
XX CC condition or disease, e.g. translocations associate with cancers,
XX CC particularly forms of leukemia
XX SQ Sequence 24 BP; 7 A; 7 C; 5 G; 5 T; 0 U; 0 Other;
      Query Match 100.0%; Score 24; DB 3; Length 24;
      Best Local Similarity 100.0%; Pred. No. 0.00042; Mismatches 0; Gaps 0;
      Matches 24; Conservative 0; Indels 0;

QY 1 TGGAGTTTTCACACGAGTTGGTC 24
Db 24 TGGAGTTTTCACACGAGTTGGTC 1

RESULT 6
AAZ60845/c
ID AAZ60845 standard; RNA; 24 BP.
XX AC AAZ60845;
XX DT 16-MAY-2000 (first entry)
XX DE Oligonucleotide used to detect bcr b3-abl fusion transcripts.
XX KW Fusion transcript; translocation; bcr b3 region; abl gene;
XX KW amplification assay; detection assay; medical diagnosis;
XX KW clinical monitoring; chimeric RNA; fusion RNA; condition marker;
XX KW disease marker; cancer; leukemia; ss.
XX OS Synthetic.
XX PN WO200005418-A1.
XX PD 03-FEB-2000.
XX PF 23-JUL-1999; 99WO-US016832.
XX PR 23-JUL-1998; 98US-00121239.

```



CC Oligonucleotides AAZ60840-62 and AAZ60865-66 are used in the method of  
CC the invention to detect fusion transcripts produced from a translocation  
CC between the bcr b3 region and the abl gene. The specification describes a  
CC method for detecting a fusion nucleic acid (particularly chimeric mRNA  
CC species), in a biological sample. The method comprises contacting a  
CC sample of fusion nucleic acid with primers, amplifying the hybridized  
CC fusion nucleic acid, and detecting the target hybrid. The method is used  
CC for the simple and rapid preparation of RNA from a biological sample,  
CC particularly from the cytoplasm of eukaryotic cells, which is suitable  
CC for use in an amplification and detection assay. The methods are used for  
CC the analysis and detection of nucleic acids in biological samples. The  
CC methods are useful in the human medical and veterinary fields, for  
CC medical diagnoses and clinical monitoring of a patient's response to  
CC therapy where a disease or medical condition is associated with a  
CC particular type and/or level of mRNA present in the sample. The methods  
CC are also useful for detecting or quantifying fusion or chimeric RNA  
CC species, and for detecting a translocation as a marker for a given  
CC condition or disease, e.g. translocations associate with cancers,  
CC particularly forms of leukemia

XX SQ Sequence 24 BP; 5 A; 5 C; 7 G; 0 T; 0 U; 0 Other;  
Query Match 100.0%; Score 24; DB 3; Length 24;  
Best Local Similarity 70.8%; Pred. No. 0.00042;  
Matches 17; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGGAGTTTCACACACGAGTTGGTC 24  
:||||:|||||:|||||:|||||:  
Db 1 UGGAGUUUCACACACGAGUUGGUC 24

RESULT 9  
AAD62592/c  
ID AAD62592 standard; DNA; 24 BP.  
XX  
AC AAD62592;  
XX  
DT 15-JAN-2004 (first entry)  
XX  
DE CML chromosomal translocation t(9;22) PCR primer #1.  
XX  
KW Amplification; human immunodeficiency virus; environmental testing; HIV;  
KW detection; diagnostic testing; PCR; primer; ss.  
XX  
OS Unidentified.  
XX  
PN US6589734-B1.  
XX  
PD 08-JUL-2003.  
XX  
PF 08-OCT-1998; 98US-00168947.  
XX  
PR 11-JUL-1989; 89US-00379501.  
PR 10-JUL-1990; 90US-00550837.  
PR 06-JUN-1995; 95US-00469067.  
XX  
PA (GENP-) GEN-PROBE INC.  
XX  
PI Kacian DL, Fultz TJ, McDonough SH;  
XX  
DR WPI; 2003-810379/76.  
XX  
PT New oligonucleotide probe, useful in detecting HIV nucleic acid in a  
PT sample and for environmental and diagnostic testing.  
XX  
PS Example 18; Col 43; 62pp; English.  
XX  
CC The invention relates to oligonucleotides useful in amplifying and  
CC detecting human immunodeficiency virus (HIV) nucleic acid in a sample.  
CC The invention is used for environmental testing, diagnostic testing,  
CC research studies and for the preparation of reagents or materials for  
CC cloning or other purposes. The present sequence is CML chromosomal  
CC translocation t(9;22) PCR primer. This sequence is used in the invention

XX SQ Sequence 24 BP; 7 A; 7 C; 5 G; 5 T; 0 U; 0 Other;  
Query Match 100.0%; Score 24; DB 9; Length 24;  
Best Local Similarity 100.0%; Pred. No. 0.00042;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGGAGTTTCACACACGAGTTGGTC 24  
:||||:|||||:|||||:|||||:  
Db 24 TGGAGTTTCACACACGAGTTGGTC 1

RESULT 10  
AAT88785/c  
ID AAT88785 standard; DNA; 200 BP.  
XX  
AC AAT88785;  
XX  
DT 23-MAR-1998 (first entry)  
XX  
DE Leukaemic cell BCR-ABL mRNA PCR product target sequence.  
XX  
KW Leukaemia; BCR-ABL; cell line K562; target; immunoassay; probe;  
KW hybridisation; diagnostic; luciferase; genetic disease; ss.  
XX  
OS Unidentified.  
XX  
PN CA2186998-A.  
XX  
PD 31-MAY-1997.  
XX  
PF 02-OCT-1996; 96CA-02186998.  
XX  
PR 30-NOV-1995; 95US-00565055.  
XX  
PA (UYWI-) UNIV WINDSOR.  
XX  
PI Christopoulos TK;  
XX  
DR WPI; 1997-415964/39.  
XX  
PT Immunoassays and nucleic acid hybridisation assays - using protein-  
PT encoding nucleic acid fragments as labels.  
XX  
PS Disclosure; Page 26; 39pp; English.  
XX  
CC A novel assay has been developed for determining an analyte. The assay  
CC comprises labelling the analyte with a nucleic acid fragment that encodes  
CC a protein, expressing the nucleic acid, and detecting the protein. The  
CC present sequence represents a target sequence from a leukaemic cell (cell  
CC line K562), used in an example of the present assay. The assay is used  
CC for the determination of antigens or nucleic acids for diagnostic or  
CC research purposes, e.g. detecting low levels of tumour markers, analysing  
CC nucleic acid mutations associated with genetic diseases, diagnosing and  
CC monitoring pathogen infections, or searching for new disease markers. The  
CC immunoassay when using a luciferase for detection is more sensitive than  
CC an enzyme-amplified, time-resolved fluorometric immunoassay and does not  
CC require preparation of a luciferase-antibody conjugate

XX SQ Sequence 200 BP; 49 A; 52 C; 51 G; 48 T; 0 U; 0 Other;  
Query Match 100.0%; Score 24; DB 2; Length 200;  
Best Local Similarity 100.0%; Pred. No. 0.0004;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGGAGTTTCACACACGAGTTGGTC 24  
:||||:|||||:|||||:|||||:  
Db 39 TGGAGTTTCACACACGAGTTGGTC 16

RESULT 11  
ABS73175/c  
ID ABS73175 standard; DNA; 250 BP.

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XX AC ABS73175;
XX XX
XX DT 04-DEC-2002 (first entry)
XX DE
XX DE Human translocation (9: 22) (q34: q11) #3.
XX XX
XX KW Chromosome aberration; oncogenic fusion protein; cancer;
XX KW proliferative disease; cellular protein isoform; heat shock protein 90;
XX KW HSP-90; rheumatoid arthritis; cancer; haematopoietic disorder;
XX KW T cell lymphoma; B cell lymphoma; chronic myeloid leukaemia; CML;
XX KW acute myeloid leukaemia; AML; chronic myelomonocytic leukaemia; CMML;
XX KW acute lymphoblastic leukaemia; ALL; APL; NHL; solid tumour;
XX KW papillary thyroid carcinoma; Ewing's sarcoma; melanoma; liposarcoma;
XX KW rhabdomyosarcoma; synovial sarcoma; viral infection; gene; ds.
XX OS
XX OS Homo sapiens.
XX PN WO200269900-A2.
XX PN
XX PD 12-SEP-2002.
XX XX
XX PF 01-MAR-2002; 2002WO-US006518.
XX PR 01-MAR-2001; 2001US-0272751P.
XX XX
XX PA (CONF-) CONFORMA THERAPEUTICS CORP.
XX XX
XX PI Fritz LC, Burrows FU;
XX DR WPI; 2002-698710/75.
XX XX
XX PT Treating genetically-defined disease associated with chromosomal
XX PT aberrations yielding oncogenic fusion proteins, e.g. cell proliferative
XX PT diseases, involves administering an inhibitor of heat shock protein 90.
XX PS
XX PS Disclosure; Page 97; 389pp; English.
XX XX
XX CC The invention describes a method of treating genetically-defined disease
XX CC associated with chromosomal aberrations yielding oncogenic fusion
XX CC proteins (I), treating cancerous cells containing (I) in a heterogeneous
XX CC cell population, treating proliferative diseases associated with mutant
XX CC protein or cellular protein isoforms (II) dependent on heat shock protein
XX CC (HSP)-90, or selectively treating cells expressing (II) involving
XX CC administering HSP90-inhibitor. The method is useful for treating
XX CC genetically-defined disease with chromosomal aberration yielding
XX CC oncogenic fusion protein, treating cancerous cells containing fusion
XX CC protein in heterogeneous cell population, treating proliferative disease
XX CC (e.g. rheumatoid arthritis or cancer) associated with mutant protein or
XX CC cellular protein isoform dependent on heat shock protein (HSP)-90 (e.g.
XX CC p53), or selectively treating cells expressing mutant protein or cellular
XX CC protein isoform in a patient heterozygous for (II). The method is useful
XX CC for treating a disease e.g. haematopoietic disorder such as T or B cell
XX CC lymphoma, chronic myeloid leukaemia (CML), APL, ALL, NHL and CMML,
XX CC or a disease characterised by a solid tumour such as papillary thyroid
XX CC carcinoma, Ewing's sarcoma, melanoma, liposarcoma, rhabdomyosarcoma and
XX CC synovial sarcoma. The method is also useful for treating viral
XX CC infections. This represents the DNA sequence of a chromosome aberration
XX SQ Sequence 250 BP; 65 A; 62 C; 63 G; 60 T; 0 U; 0 Other;

Query Match 100.0%; Score 24; DB 6; Length 250;
Best Local Similarity 100.0%; Pred. No. 0.00039;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGGAGTTTCACACGAGTTGGTC 24
Db 40 TGGAGTTTCACACGAGTTGGTC 17

RESULT 12
ABS73174/c
ID ABS73174 standard; DNA; 305 BP.

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XX AC ABS73174;
XX XX
XX DT 04-DEC-2002 (first entry)
XX DE
XX DE DNA encoding human translocation (9: 22) (q34: q11) protein #5.
XX XX
XX KW Chromosome aberration; oncogenic fusion protein; cancer;
XX KW proliferative disease; cellular protein isoform; heat shock protein 90;
XX KW HSP-90; rheumatoid arthritis; cancer; haematopoietic disorder;
XX KW T cell lymphoma; B cell lymphoma; chronic myeloid leukaemia; CML;
XX KW acute myeloid leukaemia; AML; chronic myelomonocytic leukaemia; CMML;
XX KW acute lymphoblastic leukaemia; ALL; APL; NHL; solid tumour;
XX KW papillary thyroid carcinoma; Ewing's sarcoma; melanoma; liposarcoma;
XX KW rhabdomyosarcoma; synovial sarcoma; viral infection; gene; ds.
XX OS
XX OS Homo sapiens.
XX PN WO200269900-A2.
XX PN
XX PD 12-SEP-2002.
XX XX
XX PF 01-MAR-2002; 2002WO-US006518.
XX PR 01-MAR-2001; 2001US-0272751P.
XX XX
XX PA (CONF-) CONFORMA THERAPEUTICS CORP.
XX XX
XX PI Fritz LC, Burrows FU;
XX DR WPI; 2002-698710/75.
XX DR P-PSDB; ABG95013.
XX XX
XX PT Treating genetically-defined disease associated with chromosomal
XX PT aberrations yielding oncogenic fusion proteins, e.g. cell proliferative
XX PT diseases, involves administering an inhibitor of heat shock protein 90.
XX PS
XX PS Disclosure; Page 97; 389pp; English.
XX XX
XX CC The invention describes a method of treating genetically-defined disease
XX CC associated with chromosomal aberrations yielding oncogenic fusion
XX CC proteins (I), treating cancerous cells containing (I) in a heterogeneous
XX CC cell population, treating proliferative diseases associated with mutant
XX CC protein or cellular protein isoforms (II) dependent on heat shock protein
XX CC (HSP)-90, or selectively treating cells expressing (II) involving
XX CC administering HSP90-inhibitor. The method is useful for treating
XX CC genetically-defined disease with chromosomal aberration yielding
XX CC oncogenic fusion protein, treating cancerous cells containing fusion
XX CC protein in heterogeneous cell population, treating proliferative disease
XX CC (e.g. rheumatoid arthritis or cancer) associated with mutant protein or
XX CC cellular protein isoform dependent on heat shock protein (HSP)-90 (e.g.
XX CC p53), or selectively treating cells expressing mutant protein or cellular
XX CC protein isoform in a patient heterozygous for (II). The method is useful
XX CC for treating a disease e.g. haematopoietic disorder such as T or B cell
XX CC lymphoma, chronic myeloid leukaemia (CML), APL, ALL, NHL and CMML,
XX CC or a disease characterised by a solid tumour such as papillary thyroid
XX CC carcinoma, Ewing's sarcoma, melanoma, liposarcoma, rhabdomyosarcoma and
XX CC synovial sarcoma. The method is also useful for treating viral
XX CC infections. This represents the DNA sequence of a chromosome aberration
XX SQ Sequence 305 BP; 77 A; 79 C; 77 G; 72 T; 0 U; 0 Other;

Query Match 100.0%; Score 24; DB 6; Length 305;
Best Local Similarity 100.0%; Pred. No. 0.00039;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGGAGTTTCACACGAGTTGGTC 24
Db 87 TGGAGTTTCACACGAGTTGGTC 64

RESULT 13
AA260863/c

```

ID AAZ60863 standard; DNA; 350 BP.  
 AC AAZ60863;  
 XX  
 DT 16-MAY-2000 (first entry)  
 XX  
 DE Region surrounding a bcr-able splice junction.  
 XX  
 KW Fusion transcript; translocation; bcr b3 region; abl gene;  
 KW amplification assay; detection assay; medical diagnosis;  
 KW clinical monitoring; chimeric RNA; fusion RNA; condition marker;  
 KW disease marker; cancer; leukemia; ss.  
 XX  
 OS Unidentified.  
 XX  
 PN WO200005418-A1.  
 XX  
 PD 03-FEB-2000.  
 XX  
 PF 23-JUL-1999; 99WO-US016832.  
 XX  
 PR 23-JUL-1998; 98US-00121239.  
 XX  
 PA (GENP-) GEN-PROBE INC.  
 XX  
 PI Harvey RC, Eastman PS;  
 XX  
 DR WPI; 2000-182730/16.  
 XX  
 PT Novel methods for preparing RNA from biological samples, used for the  
 PT detection and measurement of nucleic acids and fusion nucleic acids.  
 XX  
 PS Disclosure; Fig 2; 49pp; English.  
 XX  
 CC The present sequence represents a region surrounding a bcr-able splice  
 CC junction. The specification describes oligonucleotides which are used to  
 CC detect fusion transcripts produced from a translocation between the bcr  
 CC b3 region and the abl gene. The specification also describes a method for  
 CC detecting a fusion nucleic acid (particularly chimeric mRNA species), in  
 CC a biological sample. The method comprises contacting a sample of fusion  
 CC nucleic acid with primers, amplifying the hybridized fusion nucleic acid,  
 CC and detecting the target hybrid. The method is used for the simple and  
 CC rapid preparation of RNA from a biological sample, particularly from the  
 CC cytoplasm of eukaryotic cells, which is suitable for use in an  
 CC amplification and detection assay. The methods are used for the analysis  
 CC and detection of nucleic acids in biological samples. The methods are  
 CC useful in the human medical and veterinary fields, for medical diagnoses  
 CC and clinical monitoring of a patient's response to therapy where a disease  
 CC or medical condition is associated with a particular type and/or level of  
 CC mRNA present in the sample. The methods are also useful for detecting or  
 CC quantifying fusion or chimeric RNA species, and for detecting a  
 CC translocation as a marker for a given condition or disease, e.g.  
 CC translocations associate with cancers, particularly forms of leukemia  
 XX  
 SQ Sequence 350 BP; 85 A; 92 C; 89 G; 84 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 24; DB 3; Length 350;  
 Best Local Similarity 100.0%; Pred. No. 0.00039;  
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 TGGAGTTTCACACACGAGTTGGTC 24  
 DB 88 TGGAGTTTCACACACGAGTTGGTC 65  
 RESULT 14  
 AAS85023/c  
 ID AAS85023 standard; cDNA; 504 BP.  
 XX  
 AC AAS85023;  
 XX  
 DT 13-FEB-2002 (first entry)  
 XX  
 DE Human endothelial cell cDNA #6375.  
 XX  
 DE DNA encoding novel human diagnostic protein #20827.  
 XX  
 KW Human; chromosome mapping; gene mapping; gene therapy; forensic;  
 KW food supplement; medical imaging; diagnostic; genetic disorder; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200175067-A2.  
 XX  
 PD 11-OCT-2001.  
 XX  
 PF 30-MAR-2001; 2001WO-US008631.  
 XX  
 PR 31-MAR-2000; 2000US-00540217.  
 PR 23-AUG-2000; 2000US-00649167.  
 XX  
 PA (HYSE-) HYSEQ INC.  
 XX  
 PI Drmanac RT, Liu C, Tang YT;  
 XX  
 DR WPI; 2001-639362/73.  
 DR P-PSDB; ABG20836.  
 XX  
 PT New isolated polynucleotide and encoded polypeptides, useful in  
 PT diagnostics, forensics, gene mapping, identification of mutations  
 PT responsible for genetic disorders or other traits and to assess  
 PT biodiversity.  
 XX  
 PS Claim 1; SEQ ID NO 20827; 103pp; English.  
 XX  
 CC The invention relates to isolated polynucleotide (I) and polypeptide (II)  
 CC sequences. (I) is useful as hybridisation probes, polymerase chain  
 CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,  
 CC and in recombinant production of (II). The polynucleotides are also used  
 CC in diagnostics as expressed sequence tags for identifying expressed  
 CC genes. (I) is useful in gene therapy techniques to restore normal  
 CC activity of (II) or to treat disease states involving (II). (II) is  
 CC useful for generating antibodies against it, detecting or quantitating a  
 CC polypeptide in tissue, as molecular weight markers and as a food  
 CC supplement. (II) and its binding partners are useful in medical imaging  
 CC of sites expressing (II). (I) and (II) are useful for treating disorders  
 CC involving aberrant protein expression or biological activity. The  
 CC polypeptide and polynucleotide sequences have applications in  
 CC diagnostics, forensics, gene mapping, identification of mutations  
 CC responsible for genetic disorders or other traits to assess biodiversity  
 CC and to produce other types of data and products dependent on DNA and  
 CC amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic  
 CC coding sequences of the invention. Note: The sequence data for this  
 CC patent did not appear in the printed specification, but was obtained in  
 CC electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 504 BP; 119 A; 122 C; 144 G; 117 T; 0 U; 2 Other;  
 Query Match 100.0%; Score 24; DB 5; Length 504;  
 Best Local Similarity 100.0%; Pred. No. 0.00039;  
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 TGGAGTTTCACACACGAGTTGGTC 24  
 DB 238 TGGAGTTTCACACACGAGTTGGTC 215  
 RESULT 15  
 ACH38242/c  
 ID ACH38242 standard; cDNA; 504 BP.  
 XX  
 AC ACH38242;  
 XX  
 DT 13-OCT-2003 (first entry)  
 XX  
 DE Human endothelial cell cDNA #6375.  
 XX

KW Human; ss; sequencing by hybridisation; SBH; expressed sequence tag; EST;  
 KW genome mapping; biodiversity; genetic disorder.

OS Homo sapiens.

XX US2003073623-A1.

XX 17-APR-2003.

XX 30-JUL-2001; 2001US-00918995.

XX 30-JUL-2001; 2001US-00918995.

XX (DRMA/) DRMANAC R T.

PA (LABA/) LABAT I.

PA (STAC/) STACHE-CRAIN B.

PA (DICK/) DICKSON M C.

XX (JONE/) JONES L W.

XX Drmanac RT, Labat I, Stache-Crain B, Dickson MC, Jones LW;

DR WPI; 2003-615964/58.

XX New polynucleotide sequences obtained from various cDNA libraries, useful  
 PT as hybridization probes, as oligomers for PCR, for chromosome and gene  
 PT mapping, in the recombinant production of protein, or in generating  
 PT antisense DNA or RNA.

PS Claim 1; SEQ ID NO 25454; 44pp; English.

XX The invention relates to an isolated polynucleotide comprising any one of  
 CC 38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence was  
 CC determined by the technique of SBH (sequencing by hybridisation). Also  
 CC included is a purified polypeptide comprising a sequence corresponding to  
 CC a reading frame of the novel polynucleotide. The nucleic acid sequences  
 CC are useful in diagnostics as expressed sequence tags (EST) for  
 CC identifying expressed genes or for physical mapping of the human genome,  
 CC in forensics, in assessing biodiversity, or in identifying mutations  
 CC responsible for genetic disorders and other traits. The nucleotide  
 CC sequences are also useful as hybridisation probes, as oligomers for PCR,  
 CC for chromosome and gene mapping, in the recombinant production of  
 CC protein, or in generating antisense DNA or RNA. The purified polypeptide  
 CC is useful for generating antibodies specific for it. The present sequence  
 CC is one of the 38043 isolated cDNA/EST sequences. Note: The sequence data  
 CC for this patent did not form part of the printed specification, but was  
 CC obtained in electronic format directly from USPTO at  
 CC seqdata.uspto.gov/sequence.html?docID=20030073623

XX Sequence 504 BP; 119 A; 122 C; 144 G; 117 T; 0 U; 2 Other;

Query Match 100.0%; Score 24; DB 8; Length 504;

Best Local Similarity 100.0%; Pred. No. 0.00039; Mismatches 0; Gaps 0;

Matches 24; Conservative 0; Indels 0; Gaps 0;

QY 1 TGGAGTTTCACACGAGTTGGTC 24

Db 238 TGGAGTTTCACACGAGTTGGTC 215

Search completed: May 26, 2004, 16:52:16

Job time : 107.037 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: May 26, 2004, 16:02:51 ; Search time 20.2274 Seconds  
(without alignments)  
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Title: US-09-121-239-7  
Perfect score: 24  
Sequence: 1 TGGAGTTTCACACGAGTTGGTC 24

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 682709 seqs, 277475446 residues

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Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

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6: /cgn2\_6/prodata/2/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	24	100.0	24	US-09-168-947-37	Sequence 37, Appl
C 2	24	100.0	1078	US-09-310-842-1	Sequence 1, Appl
C 3	21	87.5	40	US-08-448-4468-16	Sequence 16, Appl
C 4	20	83.3	20	US-08-363-233B-5	Sequence 5, Appl
C 5	15	62.5	486	US-09-621-976-19145	Sequence 19145, A
C 6	14	58.3	264	US-09-313-294A-3357	Sequence 3357, Appl
C 7	14	58.3	1821	US-09-149-476-90	Sequence 90, Appl
C 8	13	54.2	1638	US-08-253-158A-1	Sequence 1, Appl
C 9	13	54.2	1689	US-08-851-567B-29	Sequence 29, Appl
C 10	13	54.2	2234	US-08-993-088A-8	Sequence 8, Appl
C 11	13	54.2	2234	US-08-993-424B-8	Sequence 8, Appl
C 12	13	54.2	2234	US-09-603-680-8	Sequence 8, Appl
C 13	13	54.2	2692	US-08-036-210-14	Sequence 14, Appl
C 14	13	54.2	2692	US-08-449-609-14	Sequence 14, Appl
C 15	13	54.2	2692	US-09-361-096A-14	Sequence 14, Appl
C 16	13	54.2	3825	5310678-2	Patent No. 5310678
C 17	13	54.2	3900	US-09-976-594-569	Sequence 569, Appl
C 18	13	54.2	6055	US-08-851-567B-25	Sequence 25, Appl
C 19	13	54.2	6527	US-09-492-308A-3	Sequence 3, Appl
C 20	13	54.2	8931	US-09-051-019-1	Sequence 1, Appl
C 21	13	54.2	10878	US-09-911-842A-1	Sequence 1, Appl
C 22	12	50.0	20	US-09-513-729B-81	Sequence 81, Appl
C 23	12	50.0	36	US-08-403-762A-155	Sequence 155, Appl
C 24	12	50.0	207	US-09-511-625B-42	Sequence 42, Appl
C 25	12	50.0	349	US-09-621-976-15221	Sequence 15221, A
C 26	12	50.0	418	US-09-257-179-36	Sequence 36, Appl
C 27	12	50.0	444	US-09-621-976-12314	Sequence 12314, A

C 28	12	50.0	445	4	US-09-621-976-12560	Sequence 12560, A
C 29	12	50.0	502	4	US-09-621-976-1301	Sequence 1301, Ap
C 30	12	50.0	544	4	US-09-621-976-15220	Sequence 15220, A
C 31	12	50.0	611	4	US-09-451-651-12	Sequence 12, Appl
C 32	12	50.0	617	3	US-09-328-111-158	Sequence 158, Appl
C 33	12	50.0	633	4	US-09-242-999-19	Sequence 19, Appl
C 34	12	50.0	693	2	US-08-690-849-1	Sequence 1, Appl
C 35	12	50.0	693	2	US-08-690-849-3	Sequence 3, Appl
C 36	12	50.0	693	3	US-09-004-053-1	Sequence 1, Appl
C 37	12	50.0	693	3	US-09-004-053-3	Sequence 3, Appl
C 38	12	50.0	834	3	US-08-998-416-529	Sequence 529, Appl
C 39	12	50.0	885	3	US-08-545-196B-20	Sequence 20, Appl
C 40	12	50.0	1050	4	US-09-655-270A-16	Sequence 16, Appl
C 41	12	50.0	1050	4	US-09-651-941-20	Sequence 20, Appl
C 42	12	50.0	1050	4	US-09-955-597-20	Sequence 20, Appl
C 43	12	50.0	1092	4	US-09-673-395A-131	Sequence 131, Appl
C 44	12	50.0	1160	4	US-09-153-310-41	Sequence 41, Appl
C 45	12	50.0	1180	3	US-08-897-236-10	Sequence 10, Appl

ALIGNMENTS

RESULT 1

US-09-168-947-37/c  
; Sequence 37, Application US/09168947  
; Patent No. 6589734  
; GENERAL INFORMATION:  
; APPLICANT: KACIAN, DANIEL L.  
; APPLICANT: FULTZ, TIMOTHY J.  
; APPLICANT: MCDONOUGH, SHERROL H.  
; TITLE OF INVENTION: DETECTION OF HIV  
; FILE REFERENCE: 218/130  
; CURRENT APPLICATION NUMBER: US/09/168,947  
; EARLIER FILING DATE: 1998-10-08  
; EARLIER APPLICATION NUMBER: 08/469,067  
; EARLIER FILING DATE: 1995-06-06  
; EARLIER APPLICATION NUMBER: 07/550,837  
; EARLIER FILING DATE: 1990-07-10  
; NUMBER OF SEQ ID NOS: 46  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 37  
; LENGTH: 24  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthesized nucleic acid molecule  
US-09-168-947-37

Query Match 100.0%; Score 24; DB 4; Length 24;  
Best Local Similarity 100.0%; Pred. No. 1.7e-05;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGGAGTTTCACACGAGTTGGTC 24  
DB 24 TGGAGTTTCACACGAGTTGGTC 1

RESULT 2

US-09-310-842-1/c  
; Sequence 1, Application US/09310842A  
; Patent No. 6451593  
; GENERAL INFORMATION:  
; APPLICANT: Wittig, Prof. Burghardt  
; APPLICANT: Jungmans, Claas  
; TITLE OF INVENTION: Design Principle for Constructing Expression Constructs for Gene  
; FILE REFERENCE: XI 597/99  
; CURRENT APPLICATION NUMBER: US/09/310,842A  
; EARLIER FILING DATE: 1999-05-12  
; EARLIER APPLICATION NUMBER: DE 196 48 625.4  
; EARLIER FILING DATE: 1996-11-13  
; NUMBER OF SEQ ID NOS: 13

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; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1078
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: gene
; LOCATION: (1)..(1078)
; OTHER INFORMATION: bcr3=abl2; Oligo DNA Dumbbell
; FEATURE:
; NAME/KEY: misc_binding
; LOCATION: (1)..(2)
; OTHER INFORMATION: intramolecular binding site; the T-nucleotides at position 1 to
; OTHER INFORMATION: 2 can be modified with amino or caroxy features
; FEATURE:
; NAME/KEY: misc_binding
; LOCATION: (1077)..(1078)
; OTHER INFORMATION: intramolecular binding site; the T-nucleotides at position 1077
; OTHER INFORMATION: to 1078 can be modified with amino or caroxy features
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Strandness: both; nucleic
; OTHER INFORMATION: acid (linear), hypothetical: No. 6451593 anti-sense: No
US-09-310-842-1

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Query Match 100.0%; Score 24; DB 4; Length 1078;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-05;  
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGGAGTTTCACACAGAGTTGGTTC 24  
 DB 661 TGGAGTTTCACACAGAGTTGGTTC 638

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RESULT 3
US-08-448-446B-16/c
; Sequence 16, Application US/08448446B
; Patent No. 6080851
; GENERAL INFORMATION:
; APPLICANT: Pachuk et al.
; TITLE OF INVENTION: Compounds and Methods for the Treatment
; TITLE OF INVENTION: of Leukemias
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn
; ADDRESSEE: Kurtz Mackiewicz & No. 6080851ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/448,446B
; FILING DATE: July 10, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/989,852
; FILING DATE: December 4, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Doreen Yanko Trujillo
; REGISTRATION NUMBER: 35,719
; REFERENCE/DOCKET NUMBER: APOL-0020
; TELECOMMUNICATION INFORMATION: C
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 40
; TYPE: Nucleic Acid

```

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; STRANDEDNESS: Single
; TOPOLOGY: Linear
; ANTI-SENSE:
US-08-448-446B-16
Query Match 87.5%; Score 21; DB 3; Length 40;
Best Local Similarity 100.0%; Pred. No. 0.001;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TGGAGTTTCACACAGAGTTG 21
DB 40 TGGAGTTTCACACAGAGTTG 20

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RESULT 4
US-08-363-233B-5/c
; Sequence 5, Application US/08363233B
; Patent No. 5714383
; GENERAL INFORMATION:
; APPLICANT: Thompson, James D.
; TITLE OF INVENTION: METHOD AND REAGENT FOR TREATING CHRONIC
; TITLE OF INVENTION: MYELOGENOUS LEUKEMIA
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; SUITE: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/363,233B
; FILING DATE: December 23, 1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA: including application
; PRIOR APPLICATION DATA: described below: 2
; APPLICATION NUMBER: 07/882,822
; FILING DATE: May 14, 1992
; APPLICATION NUMBER: 08/193,922
; FILING DATE: February 7, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 209/165
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-363-233B-5

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Query Match 83.3%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 0.0039;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGAGTTTCACACAGAGTTG 21  
 DB 20 GGAGTTTCACACAGAGTTG 1



## RESULT 5

US-09-621-976-19145  
; Sequence 19145, Application US/09621976  
; Patent No. 6639063  
; GENERAL INFORMATION:  
; APPLICANT: Dumas Milne Edwards, J.B.  
; APPLICANT: Jobert, S., J.Y.  
; APPLICANT: Giordano, J.Y.  
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.  
; FILE REFERENCE: GENSET.054PR2  
; CURRENT APPLICATION NUMBER: US/09/621,976  
; CURRENT FILING DATE: 2000-07-21  
; NUMBER OF SEQ ID NOS: 19335  
; SOFTWARE: Patent.pm  
; SEQ ID NO 19145  
; LENGTH: 486  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-621-976-19145

Query Match 62.5%; Score 15; DB 4; Length 486;  
Best Local Similarity 100.0%; Pred. No. 3.7;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 CACACACGAGTTGGT 23

Db 2 CACACACGAGTTGGT 16

## RESULT 6

US-09-313-294A-3357/C  
; Sequence 3357, Application US/09313294A  
; Patent No. 6476212  
; GENERAL INFORMATION:  
; APPLICANT: Lalgudi, Raghunath V.  
; APPLICANT: Ito, Laura Y.  
; APPLICANT: Sherman, Bradley K.  
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR  
; FILE REFERENCE: PL-0017 US  
; CURRENT APPLICATION NUMBER: US/09/313,294A  
; CURRENT FILING DATE: 1999-05-14  
; NUMBER OF SEQ ID NOS: 7600  
; SOFTWARE: PERL Program  
; SEQ ID NO 3357  
; LENGTH: 264  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; NAME/KEY: misc\_feature  
; OTHER INFORMATION: Incyte ID No. 6476212 700611411H1  
US-09-313-294A-3357

Query Match 58.3%; Score 14; DB 4; Length 264;  
Best Local Similarity 100.0%; Pred. No. 14;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGGAGTTTCACACA 14

Db 48 TGGAGTTTCACACA 35

## RESULT 7

US-09-149-476-90  
; Sequence 90, Application US/09149476  
; Patent No. 6420526  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: 186 Human Secreted proteins  
; FILE REFERENCE: P2002P1  
; CURRENT APPLICATION NUMBER: US/09/149,476  
; CURRENT FILING DATE: 1998-09-08  
; EARLIER APPLICATION NUMBER: PCT/US98/04493  
; EARLIER FILING DATE: 1998-03-06

; EARLIER APPLICATION NUMBER: 60/040,162  
; EARLIER FILING DATE: 1997-03-07  
; EARLIER APPLICATION NUMBER: 60/040,333  
; EARLIER FILING DATE: 1997-03-07  
; EARLIER APPLICATION NUMBER: 60/038,621  
; EARLIER FILING DATE: 1997-03-07  
; EARLIER APPLICATION NUMBER: 60/040,626  
; EARLIER FILING DATE: 1997-03-07  
; EARLIER APPLICATION NUMBER: 60/040,334  
; EARLIER FILING DATE: 1997-03-07  
; EARLIER APPLICATION NUMBER: 60/040,336  
; EARLIER FILING DATE: 1997-03-07  
; EARLIER APPLICATION NUMBER: 60/040,163  
; EARLIER FILING DATE: 1997-03-07  
; EARLIER APPLICATION NUMBER: 60/047,600  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,615  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,597  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,502  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,633  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,583  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,617  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,618  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,503  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,592  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,581  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,584  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,500  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,587  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,492  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,598  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,613  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,582  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,596  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,612  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,632  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,601  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/043,580  
; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/043,568  
; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/043,314  
; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/043,569  
; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/043,311  
; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/043,671  
; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/043,674  
; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/043,669

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; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,312
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,313
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; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,315
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/048,974
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/056,886
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,877
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; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,630
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,878
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,662
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; EARLIER APPLICATION NUMBER: 60/056,872
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,882
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,637
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,903
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,888
; EARLIER FILING DATE: 1997-08-22
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; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,894
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,911
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,636
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,874
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,910
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,864
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,631
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,845
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,892
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/057,761
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/047,595
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,599
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,588
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,585
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,586
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,590
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,594
; EARLIER FILING DATE: 1997-05-23

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; EARLIER APPLICATION NUMBER: 60/047,589
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,593
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,614
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,578
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,576
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/047,501
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,670
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/056,632
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,664
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,876
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,881
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,909
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,875
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,862
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,887
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,908
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/057,650
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/056,884
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/057,669
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/049,610
; EARLIER FILING DATE: 1997-06-13
; EARLIER APPLICATION NUMBER: 60/061,060
; EARLIER FILING DATE: 1997-10-02

Query Match      58.3%; Score 14; DB 4; Length 1821;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 GGAGTTTCACAC 15
Db      181 GGAGTTTCACAC 194

RESULT 8
US-08-253-155A-1/c
; Sequence 1, Application US/08253155A
; Patent No. 5691147
; GENERAL INFORMATION:
; APPLICANT: Gyuris, Jenö
; APPLICANT: Draetta, Giulio
; TITLE OF INVENTION: CDK4 Binding Proteins
; NUMBER OF SEQUENCES: 95
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM: disk
; MEDIUM TYPE: Floppy
; COMPUTER: IBM PC compatible

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/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: ASCII(text)
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/253,155A
/ FILING DATE: 02-JUN-1994
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Vincent, Matthew P.
/ REGISTRATION NUMBER: 36,709
/ REFERENCE/DOCKET NUMBER: M11-028
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (617) 227-7400
/ TELEFAX: (617) 227-5941
/ INFORMATION FOR SEQ ID NO: 1:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1638 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: cDNA
/ US-08-253-155A-1

Query Match 54.2%; Score 13; DB 1; Length 1638;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCGAGTTTCACAC 13
Db 464 TGGAGTTTCACAC 452

RESULT 9
US-08-851-567B-29
/ Sequence 29, Application US/08851567B
/ Patent No. 6528484
/ GENERAL INFORMATION:
/ APPLICANT: Ensign, Jerald C
/ APPLICANT: Bowen, David J
/ APPLICANT: Petell, James
/ APPLICANT: Fatig, Raymond
/ APPLICANT: Schoonover, Sue
/ APPLICANT: French-Constant, Richard
/ APPLICANT: Rocheleau, Thomas A.
/ APPLICANT: Blackburn, Michael B.
/ APPLICANT: Hey, Timothy D.
/ APPLICANT: Merlo, Donald J.
/ APPLICANT: Orr, Gregory L.
/ APPLICANT: Roberts, Jean L.
/ APPLICANT: Strickland, James A.
/ APPLICANT: Guo, Lining
/ APPLICANT: Ciche, Todd A.
/ APPLICANT: Sukhapinda, Kitisri
/ TITLE OF INVENTION: Insecticidal Protein Toxins From Photorhabdus
/ NUMBER OF SEQUENCES: 88
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Dow Agrosciences Patent Department
/ STREET: 9330 Zionsville Road
/ CITY: Indianapolis
/ STATE: IN
/ COUNTRY: US
/ ZIP: 46268
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/851,567B
/ FILING DATE: 05-MAY-1997
/ CLASSIFICATION: 514
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/063,615
/ FILING DATE: 18-MAY-1993
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/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/395,497
/ FILING DATE: 28-FEB-1995
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 60/007,255
/ FILING DATE: 06-NOV-1995
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/608,423
/ FILING DATE: 28-FEB-1996
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/705,484
/ FILING DATE: 28-AUG-1996
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Seay, Nicholas J
/ REGISTRATION NUMBER: 27386
/ REFERENCE/DOCKET NUMBER: 960296.93804
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 608-251-5000
/ TELEFAX: 608-251-9166
/ INFORMATION FOR SEQ ID NO: 29:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1689 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: double
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA (genomic)
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 1..1689
/ US-08-851-567B-29

Query Match 54.2%; Score 13; DB 4; Length 1689;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 ACACGAGTTGGTC 24
Db 1623 ACACGAGTTGGTC 1635

RESULT 10
US-08-993-088A-8/c
/ Sequence 8, Application US/08993088A
/ Patent No. 6287855
/ GENERAL INFORMATION:
/ APPLICANT: Tan, Carina
/ APPLICANT: Sullivan, Kathleen
/ TITLE OF INVENTION: GALANIN RECEPTOR GALR2 AND
/ NUCLEOTIDES ENCODING SAME
/ NUMBER OF SEQUENCES: 20
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Metck & Co., Inc.
/ STREET: P.O. Box 2000, 126 E. Lincoln Ave.
/ CITY: Rahway
/ STATE: NJ
/ COUNTRY: USA
/ ZIP: 07065-0900
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: Windows
/ SOFTWARE: FastSeq for Windows Version 2.0b
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/993,088A
/ FILING DATE: 18-DEC-1997
/ CLASSIFICATION: 530
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 60/033,851
/ FILING DATE: 27-DEC-1996
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Heber, Sheldon O.
/ REGISTRATION NUMBER: 38,179
/ REFERENCE/DOCKET NUMBER: 19846
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TELECOMMUNICATION INFORMATION:  
TELEPHONE: 732-594-1958  
TELEFAX: 732-594-4720  
TELEX:  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2234 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cdna  
US-08-993-088A-8

Query Match 54.2%; Score 13; DB 3; Length 2234;  
Best Local Similarity 100.0%; Pred. No. 57;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 ACACACGAGTTGG 22  
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DB 1940 ACACACGAGTTGG 1928

RESULT 11  
US-08-993-424B-8/c  
Sequence 8, Application US/08993424B  
Patent No. 6337206  
GENERAL INFORMATION:  
APPLICANT: Tan, Carina  
APPLICANT: Kolakowski, Lee F., Jr.  
TITLE OF INVENTION: MOUSE GALANIN RECEPTOR GALAR2 AND  
TITLE OF INVENTION: NUCLEOTIDES ENCODING SAME  
NUMBER OF SEQUENCES: 18  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Merck & Co., Inc.  
STREET: P.O. Box 2000, 126 E. Lincoln Ave.  
CITY: Rahway  
STATE: NJ  
COUNTRY: USA  
ZIP: 07065-0900  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows  
SOFTWARE: FastSeq for Windows Version 2.0b  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/993,424B  
FILING DATE: 18-DEC-1997  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/033,851  
FILING DATE: 27-DEC-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Heber, Sheldon O.  
REGISTRATION NUMBER: 38,179  
REFERENCE/DOCKET NUMBER: 19846NP2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 732-594-1958  
TELEFAX: 732-594-4720  
TELEX:  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2234 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cdna  
US-08-993-424B-8

Query Match 54.2%; Score 13; DB 4; Length 2234;  
Best Local Similarity 100.0%; Pred. No. 57;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 ACACACGAGTTGG 22

DB 1940 ACACACGAGTTGG 1928  
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RESULT 12  
US-09-603-680-8/c  
Sequence 8, Application US/09603680  
Patent No. 6544753  
GENERAL INFORMATION:  
APPLICANT: Tan, Carina  
APPLICANT: Sullivan, Kathleen  
TITLE OF INVENTION: GALANIN RECEPTOR GALAR2 AND  
NUCLEOTIDES ENCODING SAME  
NUMBER OF SEQUENCES: 20  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Merck & Co., Inc.  
STREET: P.O. Box 2000, 126 E. Lincoln Ave.  
CITY: Rahway  
STATE: NJ  
COUNTRY: USA  
ZIP: 07065-0900  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows  
SOFTWARE: FastSeq for Windows Version 2.0b  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/603,680  
FILING DATE: 26-Jun-2000  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/033,851  
FILING DATE: 27-DEC-1996  
APPLICATION NUMBER: 08/993,088  
FILING DATE: 18-DEC-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Heber, Sheldon O.  
REGISTRATION NUMBER: 38,179  
REFERENCE/DOCKET NUMBER: 19846 CA  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 732-594-1958  
TELEFAX: 732-594-4720  
TELEX: <Unknown>  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2234 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cdna  
SEQUENCE DESCRIPTION: SEQ ID NO: 8:  
US-09-603-680-8

Query Match 54.2%; Score 13; DB 4; Length 2234;  
Best Local Similarity 100.0%; Pred. No. 57;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 ACACACGAGTTGG 22  
|||||

DB 1940 ACACACGAGTTGG 1928

RESULT 13  
US-08-036-210-14/c  
Sequence 14, Application US/08036210  
Patent No. 5585233  
GENERAL INFORMATION:  
APPLICANT: Moller, Niels P.H.  
APPLICANT: Moller, Karin B.  
APPLICANT: Ullrich, Axel  
TITLE OF INVENTION: PTP-S31: A NOVEL PROTEIN TYROSINE  
PHOSPHATASE  
TITLE OF INVENTION: PHOSPHATASE  
NUMBER OF SEQUENCES: 45

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CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/036,210
FILING DATE: 23-MAR-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mierock, S. Leslie
REGISTRATION NUMBER: 18,972
REFERENCE/DOCKET NUMBER: 7683-025
TELEPHONE: 212-790-9090
TELEFAX: 212-869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 2692 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: misc feature
LOCATION: 2149
OTHER INFORMATION: /note= "N=x=unknown nucleotide"
US-08-036-210-14

Query Match 54.2%; Score 13; DB 1; Length 2692;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGAGTTTCACACA 14
Db 228 GGAGTTTCACACA 216

RESULT 14
US-08-449-609-14/c
Sequence 14, Application US/08449609
Patent No. 5952212
GENERAL INFORMATION:
APPLICANT: Moller, Niels P.H.
APPLICANT: Moller, Karin B.
APPLICANT: Ullrich, Axel
TITLE OF INVENTION: PTP-S31: A NOVEL PROTEIN TYROSINE
PHOSPHATASE
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESSES:
ADDRESSEE: PENNIE & EDMONDS
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/449,609
FILING DATE: 24-MAY-1995
CLASSIFICATION: 435

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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/036,210
FILING DATE: 23-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Mierock, S. Leslie
REGISTRATION NUMBER: 18,972
REFERENCE/DOCKET NUMBER: 7683-025
TELEPHONE: 212-790-9090
TELEFAX: 212-869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 2692 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: misc feature
LOCATION: 2149
OTHER INFORMATION: /note= "N=x=unknown nucleotide"
US-08-449-609-14

Query Match 54.2%; Score 13; DB 2; Length 2692;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGAGTTTCACACA 14
Db 228 GGAGTTTCACACA 216

RESULT 15
US-09-361-096A-14/c
Sequence 14, Application US/09361096A
Patent No. 6492495
GENERAL INFORMATION:
APPLICANT: MOLLER, NIELS P.H.
APPLICANT: MOLLER, KARIN B.
APPLICANT: ULLRICH, AXEL
TITLE OF INVENTION: PTP-S31: A NOVEL PROTEIN TYROSINE PHOSPHATASE
FILE REFERENCE: 038602/0886
CURRENT APPLICATION NUMBER: US/09/361,096A
CURRENT FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: 08/449,609
PRIOR FILING DATE: 1995-05-24
PRIOR APPLICATION NUMBER: 08/036,210
PRIOR FILING DATE: 1995-03-23
NUMBER OF SEQ ID NOS: 53
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 14
LENGTH: 2692
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: modified base
LOCATION: (1)..(2692)
OTHER INFORMATION: n = unknown nucleotide
NAME/KEY: CDS
LOCATION: (92..139, 259..1414)
US-09-361-096A-14

Query Match 54.2%; Score 13; DB 4; Length 2692;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGAGTTTCACACA 14
Db 228 GGAGTTTCACACA 216

Search completed: May 27, 2004, 02:25:09

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Job time : 20.2274 secs

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OM nucleic - nucleic search, using sw model

Run on: May 27, 2004, 11:30:47 ; Search time 126.301 Seconds  
(without alignments)  
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Title: US-09-121-239-7  
Perfect score: 24  
Sequence: 1 TGGAGTTTCACACGAGTTGGTC 24

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Gapop 60.0 , Gapext 60.0

Searched: 2960401 seqs, 2274450654 residues

Word size : 0

Total number of hits satisfying chosen parameters: 5920802

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published Applications NA.\*

- 1: /cgn2\_6/ptodata/2/pubpna/US07\_PUBCOMB.seq.\*
- 2: /cgn2\_6/ptodata/2/pubpna/US07\_PUBCOMB.seq.\*
- 3: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq.\*
- 4: /cgn2\_6/ptodata/2/pubpna/US06\_PUBCOMB.seq.\*
- 5: /cgn2\_6/ptodata/2/pubpna/US07\_NEW\_PUB.seq.\*
- 6: /cgn2\_6/ptodata/2/pubpna/US07\_PUBCOMB.seq.\*
- 7: /cgn2\_6/ptodata/2/pubpna/US08\_NEW\_PUB.seq.\*
- 8: /cgn2\_6/ptodata/2/pubpna/US08\_PUBCOMB.seq.\*
- 9: /cgn2\_6/ptodata/2/pubpna/US09A\_PUBCOMB.seq.\*
- 10: /cgn2\_6/ptodata/2/pubpna/US09B\_PUBCOMB.seq.\*
- 11: /cgn2\_6/ptodata/2/pubpna/US09C\_PUBCOMB.seq.\*
- 12: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq.\*
- 13: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq.\*
- 14: /cgn2\_6/ptodata/2/pubpna/US10A\_PUBCOMB.seq.\*
- 15: /cgn2\_6/ptodata/2/pubpna/US10B\_PUBCOMB.seq.\*
- 16: /cgn2\_6/ptodata/2/pubpna/US10C\_PUBCOMB.seq.\*
- 17: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq.\*
- 18: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq.\*
- 19: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	24	100.0	24	15	US-10-244-490-37
C 2	24	100.0	24	15	US-10-404-033-5
C 3	24	100.0	24	15	US-10-404-988-5
C 4	24	100.0	504	10	US-09-918-995-25454
C 5	24	100.0	542	9	US-09-796-692-8117
C 6	24	100.0	542	15	US-10-040-862-8117
C 7	24	100.0	542	16	US-10-057-475B-8117
C 8	24	100.0	542	16	US-10-154-884B-8117
C 9	24	100.0	596	9	US-09-796-692-8967
C 10	24	100.0	596	15	US-10-040-862-8967
C 11	24	100.0	596	16	US-10-057-475B-8967
C 12	24	100.0	596	16	US-10-154-884B-8967
C 13	24	100.0	1078	15	US-10-228-811-1
C 14	24	100.0	4739	9	US-09-954-531-586

C 15	24	100.0	4739	13	US-10-193-651-22	Sequence 22, Appl
C 16	15	62.5	280	13	US-10-424-599-88397	Sequence 88397, A
C 17	15	62.5	572	13	US-10-027-632-22240	Sequence 22240,
C 18	15	62.5	572	16	US-10-027-632-22240	Sequence 22240,
C 19	15	62.5	3125	16	US-10-320-797-93	Sequence 93, Appl
C 20	15	62.5	7727	10	US-09-764-891-7685	Sequence 7685, Ap
C 21	15	62.5	17324	10	US-09-764-891-7727	Sequence 7727, Ap
C 22	14	58.3	28	9	US-09-747-165-7	Sequence 7, Appl
C 23	14	58.3	249	9	US-09-864-761-22645	Sequence 22645, A
C 24	14	58.3	442	9	US-09-864-761-5884	Sequence 5884, A
C 25	14	58.3	627	13	US-10-027-632-84494	Sequence 84494, A
C 26	14	58.3	627	16	US-10-027-632-84494	Sequence 84494, A
C 27	14	58.3	891	13	US-10-027-632-159524	Sequence 159524,
C 28	14	58.3	891	16	US-10-027-632-159524	Sequence 159524,
C 29	14	58.3	1731	16	US-10-369-493-26178	Sequence 26178, A
C 30	14	58.3	1821	10	US-09-809-391-90	Sequence 90, Appl
C 31	14	58.3	1821	10	US-09-882-171-90	Sequence 90, Appl
C 32	14	58.3	1821	13	US-10-164-861-90	Sequence 90, Appl
C 33	14	58.3	1837	13	US-10-425-114-33609	Sequence 33609, A
C 34	14	58.3	2375	16	US-10-094-749-492	Sequence 492, App
C 35	14	58.3	2379	9	US-09-938-842A-2348	Sequence 2348, Ap
C 36	14	58.3	2379	11	US-09-938-842A-2348	Sequence 2348, Ap
C 37	14	58.3	2465	13	US-10-425-114-26663	Sequence 26663, A
C 38	14	58.3	2797	16	US-10-104-047-1557	Sequence 1557, Ap
C 39	14	58.3	7920	14	US-10-044-090-781	Sequence 781, App
C 40	14	58.3	41874	13	US-10-087-192-319	Sequence 319, App
C 41	14	58.3	51198	13	US-10-087-192-1729	Sequence 1729, Ap
C 42	13	54.2	20	9	US-09-895-382-17	Sequence 17, Appl
C 43	13	54.2	25	15	US-10-098-263B-38799	Sequence 38799, A
C 44	13	54.2	104	9	US-09-864-761-25827	Sequence 25827, A
C 45	13	54.2	133	13	US-10-085-783A-32550	Sequence 32550, A

## ALIGNMENTS

### RESULT 1

US-10-244-490-37/c  
; Sequence 37, Application US/10244490  
; Publication NO. US20030152916A1  
; GENERAL INFORMATION:  
; APPLICANT: KACIAN, DANIEL L.  
; APPLICANT: FULTZ, TIMOTHY J.  
; TITLE OF INVENTION: DETECTION OF HIV  
; FILE REFERENCE: 218/130  
; CURRENT APPLICATION NUMBER: US/10/244,490  
; PRIOR FILING DATE: 2002-09-16  
; PRIOR APPLICATION NUMBER: US/09/168,947  
; PRIOR FILING DATE: 1998-10-08  
; PRIOR APPLICATION NUMBER: 08/469,067  
; PRIOR FILING DATE: 1995-06-06  
; PRIOR APPLICATION NUMBER: 07/550,837  
; PRIOR FILING DATE: 1990-07-10  
; NUMBER OF SEQ ID NOS: 46  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 37  
; LENGTH: 24  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthesized nucleic acid molecule  
US-10-244-490-37

Query Match 100.0%; Score 24; DB 15; Length 24;  
Best Local Similarity 100.0%; Pred. No. 6.5e-05;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGGAGTTTCACACGAGTTGGTC 24  
|||||  
DB 24 TGGAGTTTCACACGAGTTGGTC 1  
|||||

RESULT 2  
 US-10-404-033-5/c  
 ; Sequence 5, Application US/10404033  
 ; Publication No. US20030152998A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Mitsuhashi, M.  
 ; TITLE OF INVENTION: DIRECT RT-PCR ON  
 ; FILE REFERENCE: HITACHI.031A  
 ; CURRENT APPLICATION NUMBER: US/10/404,033  
 ; CURRENT FILING DATE: 2003-03-31  
 ; PRIOR APPLICATION NUMBER: US/10/048,800  
 ; PRIOR FILING DATE: 2002-01-31  
 ; PRIOR APPLICATION NUMBER: PCT/US98/27293  
 ; PRIOR FILING DATE: 1998-12-22  
 ; PRIOR APPLICATION NUMBER: 60/068,394  
 ; PRIOR FILING DATE: 1997-12-22  
 ; PRIOR APPLICATION NUMBER: 60/071,627  
 ; PRIOR FILING DATE: 1998-01-16  
 ; NUMBER OF SEQ ID NOS: 6  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 5  
 ; LENGTH: 24  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Primer for bcr-able sense.  
 US-10-404-033-5

Query Match 100.0%; Score 24; DB 15; Length 24;  
 Best Local Similarity 100.0%; Pred. No. 6.5e-05;  
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGGAGTTTCACACGAGTTGGTC 24  
 |||||  
 Db 24 TGGAGTTTCACACGAGTTGGTC 1

RESULT 3  
 US-10-404-988-5/c  
 ; Sequence 5, Application US/10404988  
 ; Publication No. US20030157550A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Mitsuhashi, M.  
 ; TITLE OF INVENTION: DIRECT RT-PCR ON  
 ; FILE REFERENCE: HITACHI.031A  
 ; CURRENT APPLICATION NUMBER: US/10/404,988  
 ; CURRENT FILING DATE: 2003-03-31  
 ; PRIOR APPLICATION NUMBER: US/10/048,800  
 ; PRIOR FILING DATE: 2002-01-31  
 ; PRIOR APPLICATION NUMBER: PCT/US98/27293  
 ; PRIOR FILING DATE: 1998-12-22  
 ; PRIOR APPLICATION NUMBER: 60/068,394  
 ; PRIOR FILING DATE: 1997-12-22  
 ; PRIOR APPLICATION NUMBER: 60/071,627  
 ; PRIOR FILING DATE: 1998-01-16  
 ; NUMBER OF SEQ ID NOS: 6  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 5  
 ; LENGTH: 24  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Primer for bcr-able sense.  
 US-10-404-988-5

Query Match 100.0%; Score 24; DB 15; Length 24;  
 Best Local Similarity 100.0%; Pred. No. 6.5e-05;  
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGGAGTTTCACACGAGTTGGTC 24  
 |||||

Db 24 TGGAGTTTCACACGAGTTGGTC 1

RESULT 4  
 US-09-918-995-25454/c  
 ; Sequence 25454, Application US/09918995  
 ; Publication No. US20030073623A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Hyseq, Inc.  
 ; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED  
 ; FILE REFERENCE: 20411-756  
 ; CURRENT APPLICATION NUMBER: US/09/918,995  
 ; CURRENT FILING DATE: 2001-07-30  
 ; PRIOR APPLICATION NUMBER: US/09/235,076  
 ; PRIOR FILING DATE: 1993-01-20  
 ; NUMBER OF SEQ ID NOS: 38054  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 25454  
 ; LENGTH: 504  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: misc.feature  
 ; LOCATION: (1)...(504)  
 ; OTHER INFORMATION: n = A,T,C or G  
 US-09-918-995-25454

Query Match 100.0%; Score 24; DB 10; Length 504;  
 Best Local Similarity 100.0%; Pred. No. 6.2e-05;  
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGGAGTTTCACACGAGTTGGTC 24  
 |||||  
 Db 238 TGGAGTTTCACACGAGTTGGTC 215

RESULT 5  
 US-09-796-692-8117/c  
 ; Sequence 8117, Application US/09796692  
 ; Publication No. US20020198362A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Gaiger, Alexander  
 ; APPLICANT: Algate, Paul A.  
 ; APPLICANT: Mannion, Jane  
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY  
 ; FILE REFERENCE: 2077.001200  
 ; CURRENT APPLICATION NUMBER: US/09/796,692  
 ; CURRENT FILING DATE: 2001-03-01  
 ; PRIOR APPLICATION NUMBER: 60/186,126  
 ; PRIOR FILING DATE: 2000-03-01  
 ; PRIOR APPLICATION NUMBER: 60/190,479  
 ; PRIOR FILING DATE: 2000-03-17  
 ; PRIOR APPLICATION NUMBER: 60/200,545  
 ; PRIOR FILING DATE: 2000-04-27  
 ; PRIOR APPLICATION NUMBER: 60/200,303  
 ; PRIOR FILING DATE: 2000-04-28  
 ; PRIOR APPLICATION NUMBER: 60/200,779  
 ; PRIOR FILING DATE: 2000-04-28  
 ; PRIOR APPLICATION NUMBER: 60/200,999  
 ; PRIOR FILING DATE: 2000-05-01  
 ; PRIOR APPLICATION NUMBER: 60/202,084  
 ; PRIOR FILING DATE: 2000-05-04  
 ; PRIOR APPLICATION NUMBER: 60/206,201  
 ; PRIOR FILING DATE: 2000-05-22  
 ; PRIOR APPLICATION NUMBER: 60/218,950  
 ; PRIOR FILING DATE: 2000-07-14  
 ; PRIOR APPLICATION NUMBER: 60/222,903  
 ; PRIOR FILING DATE: 2000-08-03  
 ; PRIOR APPLICATION NUMBER: 60/223,416  
 ; PRIOR FILING DATE: 2000-08-04  
 ; PRIOR APPLICATION NUMBER: 60/223,378



;; PRIOR FILING DATE: 2000-08-07  
;; NUMBER OF SEQ ID NOS: 9597  
;; SOFTWARE: FastSeq for Windows Version 3.0  
;; SEQ ID NO 8117  
;; LENGTH: 542  
;; TYPE: DNA  
;; ORGANISM: Homo sapiens  
US-09-796-692-8117

Query Match 100.0%; Score 24; DB 9; Length 542;  
Best Local Similarity 100.0%; Pred. No. 6.2e-05;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGGAGTTTCACACGAGTTGGTC 24  
|||||  
Db 432 TGGAGTTTCACACGAGTTGGTC 409

RESULT 6  
US-10-040-862-8117/c  
; Sequence 8117, Application US/10040862  
; Publication No. US20030078396A1  
; GENERAL INFORMATION:  
; APPLICANT: Gaiger, Alexander  
; APPLICANT: Algate, Paul A.  
; APPLICANT: Mannion, Jane  
; APPLICANT: Retter, Marc  
; APPLICANT: Corixa Corporation  
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy  
; FILE OF INVENTION: Hematological Malignancies  
; FILE REFERENCE: 014058-013520US  
; CURRENT APPLICATION NUMBER: US/10/040,862  
; CURRENT FILING DATE: 2001-11-06  
; PRIOR APPLICATION NUMBER: US 60/186,126  
; PRIOR FILING DATE: 2000-03-01  
; PRIOR APPLICATION NUMBER: US 60/190,479  
; PRIOR FILING DATE: 2000-03-17  
; PRIOR APPLICATION NUMBER: US 60/200,545  
; PRIOR FILING DATE: 2000-04-27  
; PRIOR APPLICATION NUMBER: US 60/200,303  
; PRIOR FILING DATE: 2000-04-28  
; PRIOR APPLICATION NUMBER: US 60/200,779  
; PRIOR FILING DATE: 2000-04-28  
; PRIOR APPLICATION NUMBER: US 60/200,999  
; PRIOR FILING DATE: 2000-05-01  
; PRIOR APPLICATION NUMBER: US 60/202,084  
; PRIOR FILING DATE: 2000-05-04  
; PRIOR APPLICATION NUMBER: US 60/206,201  
; PRIOR FILING DATE: 2000-05-22  
; PRIOR APPLICATION NUMBER: US 60/218,950  
; PRIOR FILING DATE: 2000-07-14  
; PRIOR APPLICATION NUMBER: US 60/222,903  
; PRIOR FILING DATE: 2000-08-03  
; PRIOR APPLICATION NUMBER: US 60/223,378  
; PRIOR FILING DATE: 2000-08-07  
; PRIOR APPLICATION NUMBER: US 09/796,692  
; PRIOR FILING DATE: 2001-03-01  
; NUMBER OF SEQ ID NOS: 10467  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 8117  
; LENGTH: 542  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-040-862-8117

Query Match 100.0%; Score 24; DB 15; Length 542;  
Best Local Similarity 100.0%; Pred. No. 6.2e-05;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGGAGTTTCACACGAGTTGGTC 24  
|||||

Db 432 TGGAGTTTCACACGAGTTGGTC 409  
RESULT 7  
US-10-057-475B-8117/c  
; Sequence 8117, Application US/10057475B  
; Publication No. US20040002068A1  
; GENERAL INFORMATION:  
; APPLICANT: Gaiger, Alexander  
; APPLICANT: Algate, Paul A.  
; APPLICANT: Mannion, Jane  
; APPLICANT: Clapper, Jonathan David  
; APPLICANT: Wang, Aijun  
; APPLICANT: Ordonez, Nadia  
; APPLICANT: Carter, Lauren  
; APPLICANT: McNeill, Patricia Dianne  
; APPLICANT: Corixa Corporation  
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy  
; FILE OF INVENTION: Hematological Malignancies  
; FILE REFERENCE: 014058-014402US  
; CURRENT APPLICATION NUMBER: US/10/057,475B  
; CURRENT FILING DATE: 2002-01-22  
; PRIOR APPLICATION NUMBER: US 60/186,126  
; PRIOR FILING DATE: 2000-03-01  
; PRIOR APPLICATION NUMBER: US 60/190,479  
; PRIOR FILING DATE: 2000-03-17  
; PRIOR APPLICATION NUMBER: US 60/200,545  
; PRIOR FILING DATE: 2000-04-27  
; PRIOR APPLICATION NUMBER: US 60/200,303  
; PRIOR FILING DATE: 2000-04-28  
; PRIOR APPLICATION NUMBER: US 60/200,779  
; PRIOR FILING DATE: 2000-04-28  
; PRIOR APPLICATION NUMBER: US 60/200,999  
; PRIOR FILING DATE: 2000-05-01  
; PRIOR APPLICATION NUMBER: US 60/202,084  
; PRIOR FILING DATE: 2000-05-04  
; PRIOR APPLICATION NUMBER: US 60/206,201  
; PRIOR FILING DATE: 2000-05-22  
; PRIOR APPLICATION NUMBER: US 60/218,950  
; PRIOR FILING DATE: 2000-07-14  
; PRIOR APPLICATION NUMBER: US 60/222,903  
; PRIOR FILING DATE: 2000-08-03  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 10979  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 8117  
; LENGTH: 542  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-057-475B-8117

Query Match 100.0%; Score 24; DB 16; Length 542;  
Best Local Similarity 100.0%; Pred. No. 6.2e-05;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGGAGTTTCACACGAGTTGGTC 24  
|||||  
Db 432 TGGAGTTTCACACGAGTTGGTC 409

RESULT 8  
US-10-154-884B-8117/c  
; Sequence 8117, Application US/10154884B  
; Publication No. US20040005561A1  
; GENERAL INFORMATION:  
; APPLICANT: Gaiger, Alexander  
; APPLICANT: Algate, Paul A.  
; APPLICANT: Mannion, Jane  
; APPLICANT: Retter, Marc W.  
; APPLICANT: Corixa Corporation  
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy  
; FILE OF INVENTION: Hematological Malignancies  
; FILE REFERENCE: 014058-013521US

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; CURRENT APPLICATION NUMBER: US/10/154,884B
; CURRENT FILING DATE: 2002-05-23
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 11290
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8117
; LENGTH: 542
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-154-884B-8117

Query Match      100.0%; Score 24; DB 16; Length 542;
Best Local Similarity 100.0%; Pred. No. 6.2e-05;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TGGAGTTTCACACACGAGTTGGTC 24
        |||||
Db      432 TGGAGTTTCACACACGAGTTGGTC 409

RESULT 9
US-09-796-692-8967/c
; Sequence 8967, Application US/09796692
; Publication No. US20020198362A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY
; TITLE OF INVENTION: HEMATOLOGICAL MALIGNANCIES
; FILE REFERENCE: 2077.001200
; CURRENT APPLICATION NUMBER: US/09/796,692
; CURRENT FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/200,779
; PRIOR FILING DATE: 2000-04-28
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; PRIOR APPLICATION NUMBER: 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/222,903
; PRIOR FILING DATE: 2000-08-03
;
; PRIOR APPLICATION NUMBER: 60/223,416
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: 60/223,378
; PRIOR FILING DATE: 2000-08-07
; NUMBER OF SEQ ID NOS: 9597
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8967
; LENGTH: 596
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (13)
; OTHER INFORMATION: n=A,T,C or G
; NAME/KEY: unsure
; LOCATION: (47)
; OTHER INFORMATION: n=A,T,C or G
; NAME/KEY: unsure
; LOCATION: (49)
; OTHER INFORMATION: n=A,T,C or G
; NAME/KEY: unsure
; LOCATION: (58)
; OTHER INFORMATION: n=A,T,C or G
; NAME/KEY: unsure
; LOCATION: (63)
; OTHER INFORMATION: n=A,T,C or G
; NAME/KEY: unsure
; LOCATION: (81)
; OTHER INFORMATION: n=A,T,C or G
; NAME/KEY: unsure
; LOCATION: (155)
; OTHER INFORMATION: n=A,T,C or G
; NAME/KEY: unsure
; LOCATION: (196)
; OTHER INFORMATION: n=A,T,C or G
; NAME/KEY: unsure
; LOCATION: (211)
; OTHER INFORMATION: n=A,T,C or G
; NAME/KEY: unsure
; LOCATION: (267)
; OTHER INFORMATION: n=A,T,C or G
; NAME/KEY: unsure
; LOCATION: (281)
; OTHER INFORMATION: n=A,T,C or G
; NAME/KEY: unsure
; LOCATION: (282)
; OTHER INFORMATION: n=A,T,C or G
; NAME/KEY: unsure
; LOCATION: (332)
; OTHER INFORMATION: n=A,T,C or G
; NAME/KEY: unsure
; LOCATION: (372)
; OTHER INFORMATION: n=A,T,C or G
; NAME/KEY: unsure
; LOCATION: (520)
; OTHER INFORMATION: n=A,T,C or G
; NAME/KEY: unsure
; LOCATION: (521)
; OTHER INFORMATION: n=A,T,C or G
; NAME/KEY: unsure
; LOCATION: (551)
; OTHER INFORMATION: n=A,T,C or G
; NAME/KEY: unsure
; LOCATION: (579)
; OTHER INFORMATION: n=A,T,C or G
; NAME/KEY: unsure
; LOCATION: (585)
; OTHER INFORMATION: n=A,T,C or G
; NAME/KEY: unsure
; LOCATION: (586)
; OTHER INFORMATION: n=A,T,C or G
; US-09-796-692-8967
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Query Match 100.0%; Score 24; DB 9; Length 596;  
Best Local Similarity 100.0%; Pred. No. 6.2e-05;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGGAGTTTCACACGAGTTGGTC 24  
|||||  
DB 432 TGGAGTTTCACACGAGTTGGTC 409

RESULT 10  
US-10-040-862-8967/c  
; Sequence 8967, Application US/10040862  
; Publication No. US20030078396A1  
; GENERAL INFORMATION:  
; APPLICANT: Gaiger, Alexander  
; APPLICANT: Algate, Paul A.  
; APPLICANT: Mannion, Jane  
; APPLICANT: Retter, Marc  
; APPLICANT: Corixa Corporation  
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy  
; TITLE OF INVENTION: Hematological Malignancies  
; FILE REFERENCE: 014058-013520US  
; CURRENT APPLICATION NUMBER: US/10/040,862  
; CURRENT FILING DATE: 2001-11-06  
; PRIOR APPLICATION NUMBER: US 60/186,126  
; PRIOR FILING DATE: 2000-03-01  
; PRIOR APPLICATION NUMBER: US 60/190,479  
; PRIOR FILING DATE: 2000-03-17  
; PRIOR APPLICATION NUMBER: US 60/200,545  
; PRIOR FILING DATE: 2000-04-27  
; PRIOR APPLICATION NUMBER: US 60/200,303  
; PRIOR FILING DATE: 2000-04-28  
; PRIOR APPLICATION NUMBER: US 60/200,779  
; PRIOR FILING DATE: 2000-04-28  
; PRIOR APPLICATION NUMBER: US 60/200,999  
; PRIOR FILING DATE: 2000-05-01  
; PRIOR APPLICATION NUMBER: US 60/202,084  
; PRIOR FILING DATE: 2000-05-04  
; PRIOR APPLICATION NUMBER: US 60/206,201  
; PRIOR FILING DATE: 2000-05-22  
; PRIOR APPLICATION NUMBER: US 60/218,950  
; PRIOR FILING DATE: 2000-07-14  
; PRIOR APPLICATION NUMBER: US 60/222,903  
; PRIOR FILING DATE: 2000-08-03  
; PRIOR APPLICATION NUMBER: US 60/223,416  
; PRIOR FILING DATE: 2000-08-04  
; PRIOR APPLICATION NUMBER: US 60/223,378  
; PRIOR FILING DATE: 2000-08-07  
; PRIOR APPLICATION NUMBER: US 09/796,692  
; PRIOR FILING DATE: 2001-03-01  
; NUMBER OF SEQ ID NOS: 10467  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 8967  
; LENGTH: 596  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (13)  
; OTHER INFORMATION: n=A,T,C or G  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (47)  
; OTHER INFORMATION: n=A,T,C or G  
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; NAME/KEY: unsure  
; LOCATION: (49)  
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; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (58)  
; OTHER INFORMATION: n=A,T,C or G  
; FEATURE:

; NAME/KEY: unsure  
; LOCATION: (63)  
; OTHER INFORMATION: n=A,T,C or G  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (81)  
; OTHER INFORMATION: n=A,T,C or G  
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; LOCATION: (586)  
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US-10-040-862-8967

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Best Local Similarity 100.0%; Pred. No. 6.2e-05;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGGAGTTTCACACGAGTTGGTC 24  
|||||  
DB 432 TGGAGTTTCACACGAGTTGGTC 409

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; TITLE OF INVENTION: Hematological Malignancies
; FILE REFERENCE: 014058-013521US
; CURRENT APPLICATION NUMBER: US/10/154,884B
; CURRENT FILING DATE: 2002-05-23
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; Remaining Prior Application data removed - See File Wrapper or PALM
; NUMBER OF SEQ ID NOS: 11290
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8967
; LENGTH: 596
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1) -(596)
; OTHER INFORMATION: n = g, a, c or t
; US-154-884B-8967

Query Match 100.0%; Score 24; DB 16; Length 596;
Best Local Similarity 100.0%; Pred. No. 6.2e-05;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGGAGTTTCACACGAGTTGGTC 24
|||||
Db 432 TGGAGTTTCACACGAGTTGGTC 409

RESULT 13
US-10-228-811-1/c
; Sequence 1, Application US/1022811
; Publication No. US20030054392A1
; GENERAL INFORMATION:
; APPLICANT: Wittig, Prof. Burghardt
; TITLE OF INVENTION: Design Principle for Constructing Expression Co
; TITLE OF INVENTION: Therapy
; FILE REFERENCE: XI 597/99
; CURRENT APPLICATION NUMBER: US/10/228,811
; CURRENT FILING DATE: 2002-08-27
; PRIOR APPLICATION NUMBER: DE 196 48 625.4
; PRIOR FILING DATE: 1996-11-13
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1078
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: gene
; LOCATION: (1) -(1078)
; OTHER INFORMATION: bcrl3-abl2; Oligo DNA Dumbbell
; FEATURE:
; NAME/KEY: misc binding
; LOCATION: (1) -(2)

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; OTHER INFORMATION: intramolecular binding site; the T-nucleotides at position 1 to  
; OTHER INFORMATION: 2 can be modified with amino or caroxy features  
; FEATURE:  
; NAME/KEY: misc.binding  
; LOCATION: (1077)..(1078)  
; OTHER INFORMATION: intramolecular binding site; the T-nucleotides at position 1077  
; OTHER INFORMATION: to 1078 can be modified with amino or caroxy features  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Strandness: both; nucleic  
; OTHER INFORMATION: acid (linear), hypothetical: No. US20030054392A1 anti-sense: No  
US-10-228-811-1

Query Match 100.0%; Score 24; DB 15; Length 1078;  
Best Local Similarity 100.0%; Pred. No. 6.1e-05;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGGAGTTTCACACACGAGTTGGTC 24  
|||||  
Db 661 TGGAGTTTCACACACGAGTTGGTC 638

## RESULT 14

US-09-954-531-586/c  
; Sequence 586, Application US/09954531  
; Patent No. US20020165180A1  
; GENERAL INFORMATION:  
; APPLICANT: Weaver, Zoe  
; TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Cand  
; FILE REFERENCE: 689290-77  
; CURRENT APPLICATION NUMBER: US/09/954,531  
; CURRENT FILING DATE: 2002-05-02  
; PRIOR APPLICATION NUMBER: US/60/233,133  
; PRIOR FILING DATE: 2000-09-18  
; PRIOR APPLICATION NUMBER: US/60/234,009  
; PRIOR FILING DATE: 2000-09-20  
; PRIOR APPLICATION NUMBER: US/60/234,034  
; PRIOR FILING DATE: 2000-09-20  
; PRIOR APPLICATION NUMBER: US/60/234,509  
; PRIOR FILING DATE: 2000-09-22  
; PRIOR APPLICATION NUMBER: US/60/234,567  
; PRIOR FILING DATE: 2000-09-22  
; NUMBER OF SEQ ID NOS: 1392  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 586  
; LENGTH: 4739  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-954-531-586

Query Match 100.0%; Score 24; DB 9; Length 4739;  
Best Local Similarity 100.0%; Pred. No. 5.9e-05;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGGAGTTTCACACACGAGTTGGTC 24  
|||||  
Db 3157 TGGAGTTTCACACACGAGTTGGTC 3134

## RESULT 15

US-10-193-651-22/c  
; Sequence 22, Application US/10193651  
; Publication No. US20030064061A1  
; GENERAL INFORMATION:  
; APPLICANT: Zhao, Xun  
; APPLICANT: Chaffari, Saghi  
; APPLICANT: Lodish, Harvey F.  
; APPLICANT: Malashkevich, Vladimir N.  
; APPLICANT: Kim, Peter S.  
; TITLE OF INVENTION: Bcr-Abl Oligomerization Domain  
; TITLE OF INVENTION: Polypeptides and Uses Therefor  
; FILE REFERENCE: 0399.2031-001  
; CURRENT APPLICATION NUMBER: US/10/193,651

; CURRENT FILING DATE: 2002-11-19  
; PRIOR APPLICATION NUMBER: US 60/303,857  
; PRIOR FILING DATE: 2001-07-09  
; NUMBER OF SEQ ID NOS: 22  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 22  
; LENGTH: 4739  
; TYPE: DNA  
; ORGANISM: Homo Sapiens  
; FEATURE:  
; OTHER INFORMATION: Bcr nucleic acid  
US-10-193-651-22

Query Match 100.0%; Score 24; DB 13; Length 4739;  
Best Local Similarity 100.0%; Pred. No. 5.9e-05;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGGAGTTTCACACACGAGTTGGTC 24  
|||||  
Db 3157 TGGAGTTTCACACACGAGTTGGTC 3134

Search completed: May 27, 2004, 14:58:26  
Job time : 126.301 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 26, 2004, 15:22:41 ; Search time 847.385 Seconds  
(without alignments)  
845.770 Million cell updates/sec

Title: US-09-121-239-7

Perfect score: 24

Sequence: 1 TGGAGTTTCACACACGAGTTGGTC 24

Scoring table: OLIGO\_NUC  
Gapop\_60.0 , Gapext 60.0

Searched: 27513289 seqs, 14931090276 residues

Word size : 0

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Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : EST:\*

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10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pin:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_pbg:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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C 1	24	100.0	181	14	H55545
C 2	24	100.0	314	14	D79153
C 3	24	100.0	377	10	BF800308
C 4	24	100.0	401	14	R54267

C	5	24	100.0	417	9	AA126116
6	6	24	100.0	437	10	BF873838
7	7	24	100.0	438	10	BE938059
C	8	24	100.0	443	10	AW452440
C	9	24	100.0	531	12	BG927169
C	10	24	100.0	588	10	BF380221
C	11	24	100.0	588	10	BF094682
C	12	24	100.0	597	10	BE396942
C	13	24	100.0	599	9	AU132798
C	14	24	100.0	605	10	AW961897
C	15	24	100.0	621	10	BE267891
C	16	24	100.0	637	14	CB267185
C	17	24	100.0	642	10	BE019411
C	18	24	100.0	653	12	BG829045
C	19	24	100.0	665	10	BE514596
C	20	24	100.0	684	10	BF530440
C	21	24	100.0	686	10	BE397010
C	22	24	100.0	712	10	BE397695
C	23	24	100.0	734	10	BE513555
C	24	24	100.0	741	10	BE265121
C	25	24	100.0	750	10	BE513994
C	26	24	100.0	770	12	BI226004
C	27	24	100.0	785	12	BG393462
C	28	24	100.0	813	12	BM050194
C	29	24	100.0	819	14	CF242964
C	30	24	100.0	844	14	CD652568
C	31	24	100.0	853	13	BQ227532
C	32	24	100.0	875	10	BF241073
C	33	24	100.0	878	10	BF338795
C	34	24	100.0	880	13	BQ422888
C	35	24	100.0	880	13	BQ539742
C	36	24	100.0	893	13	BU540933
C	37	24	100.0	895	13	EX368536
C	38	24	100.0	903	13	BQ441890
C	39	24	100.0	918	13	BQ212925
C	40	24	100.0	936	13	EX350695
C	41	24	100.0	955	13	BQ945725
C	42	24	100.0	975	12	BG392048
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C	44	19	79.2	544	10	BF901573
C	45	19	79.2	725	29	AG178980

#### ALIGNMENTS

RESULT 1  
H55545/c  
LOCUS  
DEFINITION  
H55545  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
MEDLINE  
PUBMED  
COMMENT

H55545  
CHR220484 Chromosome 22 exon Homo sapiens cDNA clone C22\_652 5', mRNA linear EST 07-DEC-1995  
mRNA sequence.  
H55545  
H55545.1 GI:1108411  
EST.  
Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 181)  
Trafletter, J.A., Long, K.R., Murrell, J.R., Stotler, C.J., Gusella, J.F. and Buckler, A.J.  
An expression-independent catalog of genes from human chromosome 22  
Genome Res. 5 (3), 214-224 (1995)  
96159527  
8593609  
Contact: Buckler AJ  
Molecular Neurogenetics Unit  
Massachusetts General Hospital  
Building 149, 13th St., Charlestown MA 02129  
Tel: 6177249616  
Fax: 6177265736  
Email: buckler@helix.mgh.harvard.edu  
Seq primer: T3.

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FEATURES
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      /mol_type="mRNA"
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      /clone="C22_652"
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      /clone_lib="Chromosome 22 exon"
      /note="Vector: pBluescriptIIKS+; Site_1: Sal I; Site_2:
      Bam HI (destroyed); Exons were isolated from human
      chromosome 22 specific cosmids using a modification of
      the method of exon amplification (Proc. Natl. Acad. Sci.
      USA 88:4005-4009, 1991). Amplified exons were digested
      with Sal I and Bgl II and subsequently cloned into
      pBluescriptIIKS+ at the Sal I and Bam HI sites."

ORIGIN
Query Match      100.0%; Score 24; DB 14; Length 181;
Best Local Similarity 100.0%; Pred. No. 0.0007;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGGAGTTTCACACGAGTTGGTC 24
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Db 143 TGGAGTTTCACACGAGTTGGTC 120

RESULT 2
D79153/c
LOCUS
DEFINITION
HUM532H1B Human placenta polyA+ (TFujiwara) Homo sapiens cDNA
clone GEN-532H11 5', mRNA sequence.
ACCESSION
D79153
VERSION
D79153.1 GI:1181026
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 314)
AUTHORS
Fujiwara, T., Hirano, H., Katagiri, T., Kawai, A., Kuga, Y., Nagata, M.,
Okuno, S., Ozaki, K., Shimizu, F., Shimada, Y., Shinomiya, H.,
Takaichi, A., Takeda, S., Watanabe, T., Takahashi, E., Hirai, Y.,
Maekawa, H., Shin, S. and Nakamura, Y.
TITLE
Fujiwara et al. (1995)
JOURNAL
Unpublished (1995)
COMMENT
Contact: Tsutomu Fujiwara
Otsuka GEN Research Institute
Otsuka Pharmaceutical Co., Ltd
463-10 Kagasuno Kawauchi-cho, Tokushima, Tokushima, 771-01 Japan
Tel: 0886-65-2888
Fax: 0886-37-1035.

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RESULT 3
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LOCUS
DEFINITION
CM4-CI0062-181000-370-b10 CI0062 Homo sapiens cDNA, mRNA sequence.
ACCESSION
BF800308
VERSION
BF800308.1 GI:12129297
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 377)
AUTHORS
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,
Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V.,
O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.J.
TITLE
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
JOURNAL
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE
20202663
PUBMED
10737800
COMMENT
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CM4&t2=CM4-CI0062-
181000-370-b10&t3=2000-10-18&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 18
High quality sequence stop: 377.

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      Site_2: SmaI; A mini-library was made by cloning products
      derived from ORESTES PCR (U.S. Letters Patent application
      No. 196,716 - Ludwig Institute for Cancer Research)
      profiles into the pUC 18 vector. Reverse transcription of
      tissue mRNA and cDNA amplification were performed under
      low stringency conditions."

ORIGIN
Query Match      100.0%; Score 24; DB 10; Length 377;
Best Local Similarity 100.0%; Pred. No. 0.00083;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 249 TGGAGTTTCACACGAGTTGGTC 226

RESULT 4
R54267/c
LOCUS
DEFINITION
Y974h05.r1 Soares infant brain IN1B Homo sapiens cDNA clone
IMAGE:39270 5', similar to gb:U01147 BREAKPOINT CLUSTER REGION
PROTEIN (HUMAN) ;, mRNA sequence.
ACCESSION
R54267
VERSION
R54267.1 GI:816169
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

```



REFERENCE  
AUTHORS

1 (bases 1 to 401)  
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,  
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,  
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,  
Trevisakis,E., Waterston,R., Williamson,A., Wohlmann,P. and  
Wilson,R.  
The WashU-Merck EST Project  
Unpublished (1995)  
Contact: Wilson RK  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu  
Insert Size: 1872  
High quality sequence stops: 342 Source: IMAGE Consortium, LLNL  
This clone is available royalty-free through LLNL; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.  
Insert Length: 1872 Std Error: 0.00  
Seq primer: M13RP1  
High quality sequence stop: 342.  
Location/Qualifiers  
1. .401  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="GDB:411811"  
/db\_xref="taxon:9606"  
/clone="IMAGE:39270"  
/sex="female"  
/dev stage="73 days post natal"  
/lab\_host="DH10B (ampicillin resistant)"  
/clone\_lib="Soares infant brain INIB"  
/note="Organ: whole brain; Vector: Lafmid BA; Site 1: Not  
I; Site 2: Hind III; 1st strand cDNA was primed with a Not  
I - oligo(dT) primer [5',  
AACTGGAGAATTCGGCGCCGAGGAATTTTTTTTTTTT 3'];  
double-stranded cDNA was ligated to Hind III adaptors  
(Pharmacia), digested with Not I and directionally cloned  
into the Not I and Hind III sites of the Lafmid BA vector.  
Library went through one round of normalization. Library  
constructed by Bento Soares and M.Fatima Bonaldo."

ORIGIN

Query Match 100.0%; Score 24; DB 14; Length 401;  
Best Local Similarity 100.0%; Pred. NO. 0.00084;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGGAGTTTCACACGAGTTGGTC 24  
|||||

Db 225 TGGAGTTTCACACGAGTTGGTC 202  
|||||

RESULT 5  
LOCUS A126116/c 417 bp mRNA linear EST 19-MAY-1997  
DEFINITION Z185904.r1 Stratagene colon (#937204) Homo sapiens cDNA clone  
IMAGE:511446 5' similar to TR:G1185071 G1185071 BCR/ABL FUSION  
PROTEIN i, mRNA sequence.  
ACCESSION A126116  
VERSION A126116.1 GI:1685791  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 417)  
Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B.,  
Chisoe,S., Dietrich,N., Dubuque,T., Pavello,A., Gish,W.,  
Hawkins,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le.N.,  
Mardis,E., Moore,B., Morris,M., Parsons,J., Prange,C., Rifkin,L.,  
Rohlfing,T., Schellenberg,K., Soares,M.B., Tan,F., Thierry-Mieg,J.,  
Trevisakis,E., Underwood,K., Wohlmann,P., Waterston,R., Wilson,R.  
and Marra,M.

TITLE  
JOURNAL  
MEDLINE  
PUBMED  
COMMENT

Generation and analysis of 280,000 human expressed sequence tags  
Genome Res. 6 (9), 807-828 (1996)  
97044478  
8889549  
Contact: Wilson RK  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu  
This clone is available royalty-free through LLNL; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.  
Insert Length: 2180 Std Error: 0.00  
Seq primer: -28M13 rev2 from Amersham  
High quality sequence stop: 294.  
Location/Qualifiers  
1. .417  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="GDB:3843941"  
/db\_xref="taxon:9606"  
/clone="IMAGE:511446"  
/tissue type="tumor"  
/cell\_line="T84 carcinoma cell line"  
/lab\_host="SOUL cells (kanamycin resistant)"  
/clone\_lib="Stratagene colon (#937204)"  
/note="Organ: colon; Vector: phuescript SK-; Site 1:  
EcoRI; Site 2: XhoI; Cloned unidirectionally. Primer:  
Oligo dT. T-84 colonic epithelial cell line. Average  
insert size: 1.0 kb; Uni-ZAP XR Vector; -5' adaptor  
insert size: 5' GAATTCGCGAG 3' -3' adaptor sequence: 5'  
CTCGAGTTTTTTTTTTTTTTT 3'"

FEATURES  
source

Query Match 100.0%; Score 24; DB 9; Length 417;  
Best Local Similarity 100.0%; Pred. NO. 0.00085;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGGAGTTTCACACGAGTTGGTC 24  
|||||

Db 362 TGGAGTTTCACACGAGTTGGTC 339  
|||||

RESULT 6  
LOCUS BF873838 437 bp mRNA linear EST 17-JAN-2001  
DEFINITION IL3-ET0114-071100-338-C02 ET0114 Homo sapiens cDNA, mRNA sequence.  
ACCESSION BF873838  
VERSION BF873838.1 GI:12264007  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 437)  
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,  
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,  
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,  
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,  
O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and  
Simpson,A.J.  
Shotgun sequencing of the human transcriptome with ORF expressed  
sequence tags  
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
20202663  
10737800  
Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001

TITLE  
JOURNAL  
MEDLINE  
PUBMED  
COMMENT

Email: asimpson@ludwig.org.br  
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL  
(http://www.ludwig.org.br/scripts/gethtml2.pl?ti=il3&t2=il3-ET0114-071100-338-C02&t3=2000-11-07&t4=1)  
Seq primer: puc 18 forward  
High quality sequence stop: 390.

# FEATURES

source  
1. 437  
Location/Qualifiers

/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/dev\_stage="Adult"  
/clone\_lib="ET0114"  
/note="Organ: lung tumor; Vector: puc18; Site\_1: SmaI; Site\_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

# ORIGIN

Query Match 100.0%; Score 24; DB 10; Length 437;  
Best Local Similarity 100.0%; Pred. No. 0.00085;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGGAGTTTCACACGAGTTGGTC 24

Db 319 TGGAGTTTCACACGAGTTGGTC 342

# RESULT 7

BE938059  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

BE938059  
MR1-TN0045-290800-003-e03 TN0045 Homo sapiens cDNA, mRNA sequence.  
BE938059  
BE938059.1 GI:10464948  
EST.  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 438)  
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.  
Shotgun sequencing of the human transcriptome with ORF expressed sequence tags  
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
20202663  
10737800  
Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL  
(http://www.ludwig.org.br/scripts/gethtml2.pl?ti=il3&t2=MR1-TN0045-290800-003-e03&t3=2000-08-29&t4=1)  
Seq primer: puc 18 forward  
High quality sequence stop: 297.

# FEATURES

source  
1. 438  
Location/Qualifiers

/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone\_lib="ET0114"  
/note="Organ: lung tumor; Vector: puc18; Site\_1: SmaI; Site\_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

/db\_xref="taxon:9606"  
/dev\_stage="Adult"  
/clone\_lib="TN0045"  
/note="Organ: testis normal; Vector: puc18; Site\_1: SmaI; Site\_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

# ORIGIN

Query Match 100.0%; Score 24; DB 10; Length 438;  
Best Local Similarity 100.0%; Pred. No. 0.00086;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGGAGTTTCACACGAGTTGGTC 24

Db 145 TGGAGTTTCACACGAGTTGGTC 168

# RESULT 8

AW452440/c  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

AW452440  
UI-H-B13-als-c-04-0-UI.s1 NCI\_CGAP\_Sub5 Homo sapiens cDNA clone IMAGE:3068526 3', mRNA sequence.  
AW452440  
AW452440.1 GI:6993216  
EST.  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 443)  
NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index  
Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapps@mail.nih.gov

Oligo-dT track not found, Not I site shown in beginning of sequence is likely internal to the message. cDNA Library Preparation: M.B. Soares Lab Clone distribution: NCI-CCAP clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: www.bio.llnl.gov/bbrp/image/image.html The following repetitive elements were found in this cDNA sequence: 147-207, >HSR1T  
Seq primer: M13 Forward  
POLYA=No.

# FEATURES

source

1. 443  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:3068526"  
/lab\_host="DH10B (Life Technologies)"  
/clone\_lib="NCI CGAP Subs"  
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site\_1: Not I; Site\_2: Eco RI; NCI CGAP Subs is a subtracted library derived from NCI\_CGAP\_Sub4. The NCI CGAP Subs library had 3 million recombinants. A single-stranded DNA preparation of NCI CGAP Sub4 was used as a tracer in a subtractive hybridization with a driver comprising: the IMAGE pool (NCI CGAP Kid3 pool 1 LLAM 3334-3337, 3682-3683, 3798-3803 (IMAGE CloneIDs 132376-132391), 1456008-1456775, 1500552-1502855); NCI CGAP Kid5 pool 1 LLAM 3338-3342, 3722-3725, 3776-3778 (IMAGE CloneIDs 1323912-1325831, 1471368-1472903, 1492104-1493255); NCI CGAP Lu5 pool 1 LLAM 3575-3582, 3851-3854 (IMAGE CloneIDs 1414920-1417991, 1520904-1522439); NCI CGAP GC4 pool 1 LLAM 3164-3167, 3716-3720, 3733-3735 (IMAGE CloneIDs 1257096-1258631, 1469064-1470983, 1475592-1476743); NCI CGAP\_Pr22 pool 1 LLAM 2457-2459, 2758-2759, 3062-3068

(IMAGE Clonoids 985608-986759,1101192-1101959, 1217928-1220615); NCI CGAP\_Co10 pool 1 LLAM 2644-2653, 2871-2872 (IMAGE Clonoids 1057416-1061255,1144584-1145351). (10% of the driver population), plus a pool of 3,840 arrayed clones from NCI CGAP Sub1 (IMAGE Clonoids 2708616-2710535) and NCI CGAP Sub2 (IMAGE Clonoids 2710536-2712453) (10% of the driver population), plus a pool of 11,136 clones from NCI CGAP Sub3 (IMAGE Clonoids 2712456-2723591) (10% of the driver population), plus a pool of 5,472 clones from NCI CGAP Sub4 (IMAGE Clonoids 2723592-2728969) (70% of the driver population). Subtraction was performed as previously described [Bonaldi, Lennon & Soares (1996): Normalization and Subtraction: Two Approaches To Facilitate Gene Discovery. Genome Research 6, 791-806. TAG\_TISSUE=germ cell TAG\_LIB=NCI CGAP\_GC4 TAG\_SEQ=AAATC"

## ORIGIN

Query Match 100.0%; Score 24; DB 10; Length 443;  
Best Local Similarity 100.0%; Pred. No. 0.00086;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGGAGTTTCACACGAGTTGGTC 24  
|||||  
DB 355 TGGAGTTTCACACGAGTTGGTC 332

## RESULT 9

LOCUS BG927169/c  
DEFINITION HNC18-1-D3.R HNC (Human Normal Cartilage) Homo sapiens cDNA, mRNA  
ACCESSION BG927169  
VERSION BG927169.1 GI:143221692  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE 1 (bases 1 to 531)  
AUTHORS Kumar,S., Connor,J.R., Dodds,R.A., Halsey,W., Van Horn,M., Mao,J., Sathe,G., Mui,P., Agarwal,P., Badger,A.M., Lee,J.C., Gowen,M. and Lark,M.W.

TITLE Identification and initial characterization of 5000 expressed sequenced tags (ESTs) each from adult human normal and osteoarthritic cartilage cDNA libraries  
JOURNAL Osteoarthr. Cartil. 9 (7), 641-653 (2001)  
MEDLINE 21482651  
PUBMED 11597177

## COMMENT

Contact: Sanjay Kumar  
UN2109  
GlaxoSmithKline  
709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA  
Tel: 610-270-7245  
Fax: 610-270-5598  
Email: sanjay.kumar-l@gsk.com  
Seq primer: T7:  
Location/Qualifiers

## FEATURES

source  
1..531  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/tissue\_type="cartilage"  
/lab\_host="E.coli DH10 B"  
/clone\_lib="HNC (Human Normal Cartilage)"  
/note="Vector: pSPORT 1; Site 1: SalI; Site 2: NotI; Directional"

## ORIGIN

Query Match 100.0%; Score 24; DB 12; Length 531;  
Best Local Similarity 100.0%; Pred. No. 0.00089;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TGGAGTTTCACACGAGTTGGTC 24  
|||||  
DB 438 TGGAGTTTCACACGAGTTGGTC 415

## RESULT 10

LOCUS BF380221/c  
DEFINITION MR3-UT0050-250900-003-g03 UT0050 Homo sapiens cDNA, mRNA sequence.  
ACCESSION BF380221  
VERSION BF380221.1 GI:11369346  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 588)  
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.

TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags  
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
MEDLINE 20202663  
PUBMED 10737800

COMMENT Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001

Email: asimpson@ludwig.org.br  
This sequence was derived from the FAPESP/LICR Human Cancer Genome project. This entry can be seen in the following URL  
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=MR3&t2=MR3-UT0050-250900-003-g03&t3=2000-09-25&t4=1)  
Seq primer: puc 18 forward  
High quality sequence stop: 586.  
Location/Qualifiers  
1..588  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/dev\_stages="Adult"  
/clone\_lib="UT0050"  
/note="Organ: uterus tumor; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

## FEATURES

source  
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/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/dev\_stages="Adult"  
/clone\_lib="UT0050"  
/note="Organ: uterus tumor; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

## ORIGIN

Query Match 100.0%; Score 24; DB 10; Length 588;  
Best Local Similarity 100.0%; Pred. No. 0.00092;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGGAGTTTCACACGAGTTGGTC 24  
|||||  
DB 452 TGGAGTTTCACACGAGTTGGTC 429

## RESULT 11

LOCUS BF094682/c  
DEFINITION MR3-UT0050-130900-003-g03 UT0050 Homo sapiens cDNA, mRNA sequence.  
Query Match 100.0%; Score 24; DB 12; Length 531;  
Best Local Similarity 100.0%; Pred. No. 0.00089;

```

ACCESSION      BF094682
VERSION        BF094682.1  GI:10900392
KEYWORDS
SOURCE         Homo sapiens (human)
ORGANISM       Homo sapiens
REFERENCE      1 (bases 1 to 588)
AUTHORS        Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
               Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
               Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
               O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
               Simpson,A.J.
TITLE          Shotgun sequencing of the human transcriptome with ORF expressed
               sequence tags
JOURNAL        Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE        20202663
PUBMED        10737800
COMMENT        Contact: Simpson A.J.G.
               Laboratory of Cancer Genetics
               Ludwig Institute for Cancer Research
               Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
               Brazil
               Tel: +55-11-2704922
               Fax: +55-11-2707001
               Email: asimpson@ludwig.org.br
               This sequence was derived from the FAPESP/LICR Human Cancer Genome
               Project. This entry can be seen in the following URL
               (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=MR3-UT0050-130
               900-003-g03&t3=2000-09-13&t4=1)
               Seq primer: puc 18 forward
               High quality sequence stop: 586.
FEATURES       source
               1..588
               /organism="Homo sapiens"
               /mol_type="mRNA"
               /db_xref="taxon:9606"
               /clone_lib="UT0050"
               /note="Organ: uterus tumor; Vector: puc18; Site 1: SmaI;
               Site 2: SmaI; A mini-library was made by cloning products
               derived from ORESTES PCR (U.S. Letters Patent application
               No. 196,716 - Ludwig Institute for Cancer Research)
               profiles into the pUC 18 vector. Reverse transcription of
               tissue mRNA and cDNA amplification were performed under
               low stringency conditions."
ORIGIN
Query Match      100.0%; Score 24; DB 10; Length 588;
Best Local Similarity 100.0%; Pred. No. 0.00092;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGGAGTTTCACACGAGTTGGTC 24
    |||||||||||||||||||
Db 452 TGGAGTTTCACACGAGTTGGTC 429

RESULT 12
LOCUS      BE396942/c
DEFINITION 601290652F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3621156 5',
mRNA sequence.
ACCESSION  BE396942
VERSION     BE396942.1  GI:9342307
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
REFERENCE   1 (bases 1 to 597)
AUTHORS      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE       NIH-MGC http://mgc.nci.nih.gov/.
            National Institutes of Health, Mammalian Gene Collection (MGC)

ACCESSION      BF094682
VERSION        BF094682.1  GI:10900392
KEYWORDS
SOURCE         Homo sapiens (human)
ORGANISM       Homo sapiens
REFERENCE      1 (bases 1 to 588)
AUTHORS        Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
               Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
               Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
               O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
               Simpson,A.J.
TITLE          Shotgun sequencing of the human transcriptome with ORF expressed
               sequence tags
JOURNAL        Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE        20202663
PUBMED        10737800
COMMENT        Contact: Simpson A.J.G.
               Laboratory of Cancer Genetics
               Ludwig Institute for Cancer Research
               Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
               Brazil
               Tel: +55-11-2704922
               Fax: +55-11-2707001
               Email: asimpson@ludwig.org.br
               This sequence was derived from the FAPESP/LICR Human Cancer Genome
               Project. This entry can be seen in the following URL
               (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=MR3-UT0050-130
               900-003-g03&t3=2000-09-13&t4=1)
               Seq primer: puc 18 forward
               High quality sequence stop: 586.
FEATURES       source
               1..588
               /organism="Homo sapiens"
               /mol_type="mRNA"
               /db_xref="taxon:9606"
               /dev_stage="Adult"
               /clone_lib="UT0050"
               /note="Organ: uterus tumor; Vector: puc18; Site 1: SmaI;
               Site 2: SmaI; A mini-library was made by cloning products
               derived from ORESTES PCR (U.S. Letters Patent application
               No. 196,716 - Ludwig Institute for Cancer Research)
               profiles into the pUC 18 vector. Reverse transcription of
               tissue mRNA and cDNA amplification were performed under
               low stringency conditions."
ORIGIN
Query Match      100.0%; Score 24; DB 10; Length 588;
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RESULT 13
LOCUS      AU132798/c
DEFINITION AU132798 NT2RP4 Homo sapiens cDNA clone NT2RP4000561 5', mRNA
sequence.
ACCESSION  AU132798
VERSION     AU132798.1  GI:10993337
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
REFERENCE   1 (bases 1 to 599)
AUTHORS      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE       Ota,T., Sugiyama,T., Ishii,S., Suzuki,Y., Saito,K., Yamamoto,J.,
             Nishikawa,T., Nakamura,Y., Nagai,T., Sugano,S., Masuho,Y. and
             Isogai,T.
             HRI human cDNA project (Ota,T., Sugiyama,T., Ishii,S., Suzuki,Y.,
             Saito,K., Yamamoto,J., Nishikawa,T., Nakamura,Y., Nagai,T.,
             Sugano,S., Masuho,Y., Isogai,T.)
             Unpublished (2000)
JOURNAL      Genomics Laboratory
COMMENT      Contact: Takao Isogai
             Helix Research Institute
             1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
             Tel: 81-438-52-3975
             Fax: 81-438-52-3986
             Email: genomics@hri.co.jp
             HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
             Research Institute; cDNA library construction: Department of
             Virology, Institute of Medical Science, University of Tokyo, and
             Helix Research Institute.
             Location/Qualifiers
               1..599
               /organism="Homo sapiens"

JOURNAL        Unpublished (1999)
COMMENT        Contact: Robert Strausberg, Ph.D.
               Email: cga@bbs-r@mail.nih.gov
               Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
               cDNA library Preparation: Ling Hong/Rubin Laboratory
               cDNA library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
               DNA Sequencing by: Incyte Genomics, Inc.
               Clone distribution: MGC clone distribution information can be
               found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
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               insert size 1.8kb. Library constructed by Ling Hong in
               the laboratory of Gerald M. Rubin (University of
               California, Berkeley) using ZAP-cDNA synthesis kit
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Best Local Similarity 100.0%; Pred. No. 0.00092;
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Db 568 TGGAGTTTCACACGAGTTGGTC 545

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DEFINITION AU132798 NT2RP4 Homo sapiens cDNA clone NT2RP4000561 5', mRNA
sequence.
ACCESSION  AU132798
VERSION     AU132798.1  GI:10993337
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
REFERENCE   1 (bases 1 to 599)
AUTHORS      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE       Ota,T., Sugiyama,T., Ishii,S., Suzuki,Y., Saito,K., Yamamoto,J.,
             Nishikawa,T., Nakamura,Y., Nagai,T., Sugano,S., Masuho,Y. and
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             HRI human cDNA project (Ota,T., Sugiyama,T., Ishii,S., Suzuki,Y.,
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             Sugano,S., Masuho,Y., Isogai,T.)
             Unpublished (2000)
JOURNAL      Genomics Laboratory
COMMENT      Contact: Takao Isogai
             Helix Research Institute
             1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
             Tel: 81-438-52-3975
             Fax: 81-438-52-3986
             Email: genomics@hri.co.jp
             HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
             Research Institute; cDNA library construction: Department of
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LOCUS      605 bp mRNA linear EST 01-JUN-2000
DEFINITION EST373970 MAGE resequences, MAGG Homo sapiens cDNA, mRNA sequence.
ACCESSION  AW961897
VERSION     AW961897.1 GI:8151583
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 605)
AUTHORS   Hegde,P., Qi,R., Abernathy,K., Dharap,S., Gaspard,R., Gay,C.,
            Holt,I.E., Saeed,A.I., Sharov,V., Lee,N.H., Yeatman,T.J. and
            Quackenbush,J.
TITLE     Assessment of gene expression patterns in a model of colon tumor
            metastasis using a 19,200 element cDNA microarray
JOURNAL    Unpublished (2000)
COMMENT    Contact: John Quackenbush
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850, USA
            Tel: 301 838 3528
            Fax: 301 838 0208
            Email: johnq@tigr.org
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Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DEFINITION 601125452F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3345084 5',
            mRNA sequence.
ACCESSION  BE267891
VERSION     BE267891.1 GI:9141488
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
            NIH-MGC http://mgc.mci.nih.gov/.
            National Institutes of Health, Mammalian Gene Collection (MGC)
            Unpublished (1999)
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-remail.nih.gov
            Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
            cDNA Library Preparation: Ling Hong/Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
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            insert size 1.8kb. Library constructed by Ling Hong in
            the laboratory of Gerald M. Rubin (University of
            California, Berkeley) using ZAP-cDNA synthesis kit
            (Stratagene) and Superscript II RT (Life Technologies)."
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NIH-MGC http://mgc.mci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM132 row: h column: 13
High quality sequence stop: 619.
Location/Qualifiers
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/lab_host="DH10B (phage-resistant)"
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EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5',
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
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## ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0.00093;
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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 26, 2004, 16:00:31 ; Search time 510.783 Seconds  
(without alignments)  
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Title: US-09-121-239-8

Perfect score: 24

Sequence: 1 UGAGUUUACACACAGUUGUC 24

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 3470272 seqs, 21671516995 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

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Post-processing: Listing first 45 summaries

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6: gb\_pat.\*

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11: gb\_sts.\*

12: gb\_sy.\*

13: gb\_un.\*

14: gb\_vi.\*

15: em\_ba.\*

16: em\_fun.\*

17: em\_hum.\*

18: em\_in.\*

19: em\_mu.\*

20: em\_om.\*

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23: em\_pat.\*

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34: em\_hg\_pln.\*

35: em\_hg\_rod.\*

36: em\_hg\_man.\*

37: em\_hg\_vrt.\*

38: em\_sy.\*

39: em\_hgo\_hum.\*

40: em\_hgo\_mus.\*

41: em\_hgo\_other.\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

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C 2	24	100.0	24	6	AR352049	AR352049 Sequence
C 3	24	100.0	24	6	BD140611	BD140611 Direct RT
C 4	24	100.0	24	6	BD222527	BD222527 Methods f
C 5	24	100.0	24	6	BD222528	BD222528 Methods f
C 6	24	100.0	24	6	BD222529	BD222529 Methods f
C 7	24	100.0	24	6	BD222530	BD222530 Methods f
C 8	24	100.0	210	9	AY043457	AY043457 Homo sapi
C 9	24	100.0	250	9	AF321981	AF321981 Homo sapi
C 10	24	100.0	305	9	AF192533	AF192533 Homo sapi
C 11	24	100.0	350	6	BD222546	BD222546 Methods f
C 12	24	100.0	561	9	HUMMK562B	M19695 Human myelo
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C 14	24	100.0	854	9	HUMABLD	M30829 Human bcr/a
C 15	24	100.0	922	9	HSA131467	AJ131467 Homo sapi
C 16	24	100.0	997	9	HSA131466	AJ131466 Homo sapi
C 17	24	100.0	1078	6	A92081	A92081 Sequence 5
C 18	24	100.0	1078	6	AR230688	AR230688 Sequence
C 19	24	100.0	1157	6	BD177069	BD177069 Standard
C 20	24	100.0	2255	6	E00984	E00984 Probe detec
C 21	24	100.0	2255	6	I04527	I04527 Sequence 1
C 22	24	100.0	2541	9	HUMBCRX	M55395 Human break
C 23	24	100.0	2811	6	AX780333	AX780333 Sequence
C 24	24	100.0	3481	9	AK128501	AK128501 Homo sapi
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C 35	18	75.0	209030	2	AC122318	AC122318 Mus muscu
C 36	17	70.8	201752	2	AC113044	AC113044 Mus muscu
C 37	17	70.8	232458	2	AC099334	AC099334 Mus muscu
C 38	16	66.7	22	6	BD133933	BD133933 Method of
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C 40	16	66.7	40	6	E16986	E16986 Sense prime
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ALIGNMENTS

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LOCUS	E61323		
DEFINITION	Probe for detecting oligonucleotide.		
ACCESSION	E61323		
VERSION	E61323.1 GI:13025885		
KEYWORDS	JP 1999046778-A/37.		
SOURCE	synthetic construct		
ORGANISM	artificial sequences.		
REFERENCE	1 (bases 1 to 24)		
AUTHORS	Daniel L.K. and Timothy J.F.		
TITLE	Probe for detecting oligonucleotide		
JOURNAL	Patent: JP 1999046778-A 37 23-FEB-1999;		
	GEN-PROBE INC		

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COMMENT      OS Artificial Sequence
PN JP 1999046778-A/37
PD 23-FEB-1999
PF 14-JAN-1998 JP 1998005607
PR 11-JUL-1989 US 379501
PI DANIEL LOUIS KASHIAN,TIMOTHY J FURUTSU
PC C12N15/09,C12Q1/68,C12N15/00
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Best Local Similarity 70.8%; Pred. No. 0.049;
Matches 17; Conservative 7; Mismatches 0; Indels 0; Gaps 0;
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DEFINITION Sequence 37 from patent US 6589734.
ACCESSION AR352049
VERSION AR352049.1 GI:33757012
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 24)
AUTHORS Kacian,D.L., Fultz,T.J. and McDonough,S.H.
TITLE Detection of HIV
JOURNAL Patent: US 6589734-A 37 08-JUL-2003;
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Matches 17; Conservative 7; Mismatches 0; Indels 0; Gaps 0;
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LOCUS BD140611/c 24 bp DNA linear PAT 18-SEP-2002
DEFINITION Direct RT-PCR on oligonucleotide-immobilized PCR microplate.
ACCESSION BD140611
VERSION BD140611.1 GI:23235556
KEYWORDS JP 2002505080-A/5.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 24)
AUTHORS Mitsuhashi,M.
TITLE Direct RT-PCR on oligonucleotide-immobilized PCR microplate
JOURNAL Patent: JP 2002505080-A 5 19-FEB-2002;
COMMENT HITACHI CHEMICAL CO LTD
OS Artificial Sequence
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PN JP 2002505080-A/5
PD 19-FEB-2002
PF 22-DEC-1998 JP 2000525571
PR 22-DEC-1997 US 60/068394,16-JAN-1998 US 60/071627 PI
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LOCUS BD222527/c 24 bp DNA linear PAT 17-JUL-2003
DEFINITION Methods for detecting and measuring spliced nucleic acids.
ACCESSION BD222527
VERSION BD222527.1 GI:33032297
KEYWORDS JP 2002521037-A/5.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 24)
AUTHORS Harvey,R.C. and Eastman,P.S.
TITLE Methods for detecting and measuring spliced nucleic acids
JOURNAL Patent: JP 2002521037-A 5 16-JUL-2002;
COMMENT GEN PROBE INC
OS Artificial Sequence
PN JP 2002521037-A/5
PD 16-JUL-2002
PF 23-JUL-1999 JP 2000561364
PR 23-JUL-1998 US 09/121239
PI RICHARD C HARVEY,PAUL S EASTMAN
PC C12Q1/68,C12N15/09,C12N15/00
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Best Local Similarity 70.8%; Pred. No. 0.049;
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DEFINITION Methods for detecting and measuring spliced nucleic acids.
ACCESSION BD222528
VERSION BD222528.1 GI:33032298

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KEYWORDS JP 2002521037-A/6.  
SOURCE synthetic construct  
ORGANISM artificial sequences.  
REFERENCE 1 (bases 1 to 24)  
AUTHORS Harvey,R.C. and Eastman,P.S.  
TITLE Methods for detecting and measuring spliced nucleic acids  
JOURNAL Patent: JP 2002521037-A 6 16-JUL-2002;  
GEN PROBE INC  
OS Artificial Sequence  
PN JP 2002521037-A/6  
PD 16-JUL-2002  
PF 23-JUL-1999 JP 2000561364  
PR 23-JUL-1998 US 09/121239  
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DB 24 TGGAGTTTCACACGAGTTGGTC 1  
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LOCUS 24 bp DNA linear PAT 17-JUL-2003  
DEFINITION Methods for detecting and measuring spliced nucleic acids.  
ACCESSION BD222529  
VERSION BD222529.1 GI:33032299  
KEYWORDS JP 2002521037-A/7.  
SOURCE synthetic construct  
ORGANISM artificial sequences.  
REFERENCE 1 (bases 1 to 24)  
AUTHORS Harvey,R.C. and Eastman,P.S.  
TITLE Methods for detecting and measuring spliced nucleic acids  
JOURNAL Patent: JP 2002521037-A 7 16-JUL-2002;  
GEN PROBE INC  
OS Artificial Sequence  
PN JP 2002521037-A/7  
PD 16-JUL-2002  
PF 23-JUL-1999 JP 2000561364  
PR 23-JUL-1998 US 09/121239  
PI RICHARD C HARVEY, PAUL S EASTMAN  
PC C12Q1/68,C12N15/09,C12N15/00  
CC Description of Artificial Sequence: Reverse complement of SEQ ID NO:5  
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Matches 17; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 UGGAGUUUCACACGAGUUGGUC 24  
DB 1 TGGAGTTTCACACGAGTTGGTC 24  
RESULT 7  
BD222530  
LOCUS 24 bp RNA linear PAT 17-JUL-2003  
DEFINITION Methods for detecting and measuring spliced nucleic acids.  
ACCESSION BD222530  
VERSION BD222530.1 GI:33032300  
KEYWORDS JP 2002521037-A/8.  
SOURCE synthetic construct  
ORGANISM artificial sequences.  
REFERENCE 1 (bases 1 to 24)  
AUTHORS Harvey,R.C. and Eastman,P.S.  
TITLE Methods for detecting and measuring spliced nucleic acids  
JOURNAL Patent: JP 2002521037-A 8 16-JUL-2002;  
GEN PROBE INC  
OS Artificial Sequence  
PN JP 2002521037-A/8  
PD 16-JUL-2002  
PF 23-JUL-1999 JP 2000561364  
PR 23-JUL-1998 US 09/121239  
PI RICHARD C HARVEY, PAUL S EASTMAN  
PC C12Q1/68,C12N15/09,C12N15/00  
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Best Local Similarity 70.8%; Pred. No. 0.049;  
Matches 17; Conservative 7; Mismatches 0; Indels 0; Gaps 0;  
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DB 1 TGGAGTTTCACACGAGTTGGTC 24  
RESULT 8  
AY043457/c  
LOCUS 210 bp mRNA linear PRI 27-JUN-2003  
DEFINITION Homo sapiens BCR-ABL fusion protein (BCR-ABL fusion) mRNA, partial cds.  
ACCESSION AY043457  
VERSION AY043457.1 GI:22073966  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 210)  
AUTHORS Otazu,I.B., Helen Rivero,M., Olicio,R., Pinto,A., Zalberg,I. and Seunarez,H.N.  
TITLE A rare, in-frame BCR-ABL fusion (e13a3) in a patient with an aggressive chronic myeloid leukaemia  
JOURNAL Acta Haematol. 108 (3), 150-153 (2002)  
MEDLINE 2259050  
PUBMED 12373087  
REFERENCE 2 (bases 1 to 210)  
AUTHORS Otazu,I.B., Rivero,M.B. and Olicio,R.  
TITLE Direct Submission  
JOURNAL Submitted (03-JUL-2001) Genetics Division, Instituto Nacional de Cancer, Praca da Cruz Vermelha, 23, sexto andar, Rio de Janeiro, RJ



```

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 350)
REFERENCE
AUTHORS Harvey,R.C. and Eastman,P.S.
TITLE Methods for detecting and measuring spliced nucleic acids
JOURNAL Patent: JP 2002521037-A 24 16-JUL-2002;
COMMENT
GEN PROBE INC
OS Homo sapiens (human)
PN JP 2002521037-A/24
PD 16-JUL-2002
PF 23-JUL-1999 JP 2000561364
PR 23-JUL-1998 US 09/121239
PI RICHARD C HARVEY, PAUL S EASTMAN
PC C12Q1/68,C12N15/09,C12N15/00
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Db 88 TGGAGTTTCACACACGAGTTGGTC 65

RESULT 12
LOCUS HUMK562B/c 561 bp mRNA linear PRI 27-APR-1993
DEFINITION Human myelocytic chimeric bcr and chromosome 9 fusion gene, exons 1-4.
ACCESSION M19695
VERSION M19695.1 GI:188567
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 561)
REFERENCE
AUTHORS Grosveld,G., Verwoerd,T., van Agthoven,T., de Klein,A.,
Ramachandran,K.L., Heisterkamp,N., Stam,K. and Groffen,J.
TITLE The chimeric myelocytic cell line K562 contains a breakpoint in bcr
and produces a chimeric bcr/c-abl transcript
Mol. Cell. Biol. 6 (2), 607-616 (1986)
JOURNAL
MEDLINE 87064346
PUBMED 3023859
COMMENT Original source text: Human myelocytic Ph(1)-positive CML K562 cell
line, cDNA to mRNA, clone 8E.
The bcr region of the fusion protein is located on chromosome
22q11; the abl region was translocated from chromosome 9q34.
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Query Match 100.0%; Score 24; DB 9; Length 561;
Best Local Similarity 70.8%; Pred. No. 0.016;
Matches 17; Conservative 7; Mismatches 0; Indels 0; Gaps 0;
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Db 93 TGGAGTTTCACACACGAGTTGGTC 60

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 350)
REFERENCE
AUTHORS Harvey,R.C. and Eastman,P.S.
TITLE Methods for detecting and measuring spliced nucleic acids
JOURNAL Patent: JP 2002521037-A 24 16-JUL-2002;
COMMENT
GEN PROBE INC
OS Homo sapiens (human)
PN JP 2002521037-A/24
PD 16-JUL-2002
PF 23-JUL-1999 JP 2000561364
PR 23-JUL-1998 US 09/121239
PI RICHARD C HARVEY, PAUL S EASTMAN
PC C12Q1/68,C12N15/09,C12N15/00
CC Methods for detecting and measuring spliced nucleic acids FH
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Db 88 TGGAGTTTCACACACGAGTTGGTC 65

RESULT 13
LOCUS HUMBLB/c 679 bp mRNA linear PRI 13-FEB-1996
DEFINITION Human bcr/abl fusion protein, partial cds, clone E3.
ACCESSION M30832
VERSION M30832.1 GI:177944
KEYWORDS Philadelphia chromosome; abl proto-oncogene; translocation.
SOURCE Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 679)
REFERENCE
AUTHORS Shivelman,E., Lifshitz,B., Gale,R.P. and Canaani,E.
TITLE Fused transcript of abl and bcr genes in chronic myelogenous
leukaemia
Nature 315 (6020), 550-554 (1985)
JOURNAL
MEDLINE 85240529
PUBMED 2989692
COMMENT source text: Homo sapiens (clone: E3.) cDNA to mRNA.
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Query Match 100.0%; Score 24; DB 9; Length 679;
Best Local Similarity 70.8%; Pred. No. 0.015;
Matches 17; Conservative 7; Mismatches 0; Indels 0; Gaps 0;
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Db 301 TGGAGTTTCACACACGAGTTGGTC 278

RESULT 14
LOCUS HUMBLD/c 854 bp mRNA linear PRI 14-FEB-1996
DEFINITION Human bcr/abl fusion protein mRNA, partial cds, clone K28.
ACCESSION M30829
VERSION M30829.1 GI:177953
KEYWORDS Philadelphia chromosome; abl proto-oncogene; translocation.
SOURCE Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 854)
REFERENCE
AUTHORS Shivelman,E., Lifshitz,B., Gale,R.P. and Canaani,E.
TITLE Fused transcript of abl and bcr genes in chronic myelogenous
leukaemia
Nature 315 (6020), 550-554 (1985)
JOURNAL
MEDLINE 85240529
PUBMED 2989692
COMMENT source text: Homo sapiens (clone: K28.) cDNA to mRNA.
Location/Qualifiers
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Db 476 TGGAGTTTCACACACGAGTTGGTC 453  
  
RESULT 15  
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LOCUS HSA131467 922 bp mRNA linear PRI 11-OCT-2000  
DEFINITION Homo sapiens mRNA for BCR/ABL chimeric fusion peptide, partial.  
ACCESSION AJ131467  
VERSION AJ131467.1 GI:4033556  
KEYWORDS BCR/ABL chimeric fusion peptide; bcr/abl gene.  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
  
REFERENCE 1  
AUTHORS Burneister T., Maurer J., Aivado M., Elmaagacli A.H., Grunebach F.,  
Held K.R., Hese G., Hochhaus A., Hoppner W., Lentes K.U.,  
Lubbert M., Schafer K.L., Schathausen P., Schmidt C.A., Schuler F.,  
Seeger K., Seelig R., Thiede C., Viethmann S., Weber C., Wilhelm S.,  
Christmann A., Clement J.H., Ebener U., Enczmann J., Leo R.,  
Schleuning M., Schoch R. and Thiel E.  
TITLE Quality assurance in RT-PCR-based BCR/ABL diagnostics--results of  
an interlaboratory test and a standardization approach  
JOURNAL Leukemia 14 (10), 1850-1856 (2000)  
MEDLINE 20471781  
PubMed 11021760  
REFERENCE 2 (bases 1 to 922)  
AUTHORS Burneister T.  
TITLE Direct Submission  
JOURNAL Submitted (04-DEC-1998) Burneister T., Medizinische Klinik III, FU  
Berlin, Hindenburgdamm 30, Berlin, Germany 12200, Germany  
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Search completed: May 27, 2004, 02:16:38  
Job time : 511.783 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: May 26, 2004, 14:55:11 ; Search time 107.037 Seconds  
(without alignments)  
952.539 Million cell updates/sec

Title: US-09-121-239-8

Perfect score: 24  
Sequence: 1 UGAGUUUACACACGAGUUGUC 24

Scoring table: OLIGO NUC  
Gapop 60.0 , Gapext 60.0

Searched: 3373863 seqs, 2124099041 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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2: Geneseqn1990s:\*

3: Geneseqn2000s:\*

4: Geneseqn2001as:\*

5: Geneseqn2001bs:\*

6: Geneseqn2002s:\*

7: Geneseqn2003as:\*

8: Geneseqn2003bs:\*

9: Geneseqn2003cs:\*

10: Geneseqn2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 1	24	100.0	24	2 Aaq86635	Aaq86635 Modified
C 2	24	100.0	24	2 Aav66353	Aav66353 CML-2 chr
C 3	24	100.0	24	2 Aax23204	Aax23204 CML t(14;
C 4	24	100.0	24	2 Aax83385	Aax83385 bcr-abl s
C 5	24	100.0	24	3 Aaz60844	Aaz60844 Oligonuc1
C 6	24	100.0	24	3 Aaz60845	Aaz60845 Oligonuc1
C 7	24	100.0	24	3 Aaz60846	Aaz60846 Oligonuc1
C 8	24	100.0	24	3 Aaz60847	Aaz60847 Oligonuc1
C 9	24	100.0	24	9 Aad62592	Aad62592 CML chrom
C 10	24	100.0	200	2 Aat88785	Aat88785 Leukaemic
C 11	24	100.0	250	6 Abs73175	Abs73175 Human tra
C 12	24	100.0	305	6 Abs73174	Abs73174 DNA encod
C 13	24	100.0	350	3 Aaz60863	Aaz60863 Region su
C 14	24	100.0	504	5 Aas85023	Aas85023 DNA encod
C 15	24	100.0	504	8 Ach38242	Ach38242 Human end
C 16	24	100.0	561	6 Abs73169	Abs73169 Human tra
C 17	24	100.0	679	6 Abs73172	Abs73172 DNA encod
C 18	24	100.0	766	5 Abv29306	Abv29306 Human pro
C 19	24	100.0	766	5 Abv23449	Abv23449 Human pro
C 20	24	100.0	854	6 Abs73170	Abs73170 DNA encod
C 21	24	100.0	921	5 Aas85025	Aas85025 DNA encod
C 22	24	100.0	922	6 Abs73180	Abs73180 DNA encod
C 23	24	100.0	997	6 Abs73173	Abs73173 DNA encod

C 24	24	100.0	1097	2 AAT91764	Aat91764 Chimeric
C 25	24	100.0	1157	9 ADC64640	Adc64640 Hepatitis
C 26	24	100.0	1212	5 Aas85028	Aas85028 DNA encod
C 27	24	100.0	2255	1 AAN60228	Aan60228 Sequence
C 28	24	100.0	4725	5 Aas76375	Aas76375 DNA encod
C 29	24	100.0	4739	6 ABL63316	Ab163316 Breat ca
C 30	24	100.0	4739	7 ACC00031	Acc00031 Human Bcr
C 31	24	100.0	4756	5 Aas85030	Aas85030 DNA encod
C 32	24	100.0	4775	5 Aas76377	Aas76377 DNA encod
C 33	24	100.0	5795	5 Aas85031	Aas85031 DNA encod
C 34	24	100.0	152141	7 ACA64961	Ac64961 Human BCR
C 35	21	87.5	40	2 Aaq66789	Aaq66789 L6 bcr ex
C 36	20	83.3	20	2 Aaq51829	Aaq51829 bcr mRNA
C 37	19	79.2	47	2 AAT91751	Aat91751 Primer BB
C 38	17	70.8	47	2 AAT91749	Aat91749 Primer BB
C 39	16	66.7	22	6 ABQ92608	Abq92608 Human leu
C 40	16	66.7	40	2 Aav58775	Aav58775 Forward p
C 41	15	62.5	47	2 AAT03636	Aat03636 3SR prime
C 42	15	62.5	47	2 AAT91753	Aat91753 Primer BB
C 43	15	62.5	2097	7 ADA70851	Ada70851 Rice gene
C 44	15	62.5	2674	4 ABL18554	Ab118554 Drosophil
C 45	15	62.5	3125	9 ADB68966	Adb68966 C. neofor

ALIGNMENTS

RESULT 1  
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ID AAQ86635 standard; DNA; 24 BP.  
XX  
AC AAQ86635;  
XX  
DT 25-MAR-2003 (revised)  
DT 16-NOV-1995 (first entry)  
XX  
DE Modified non-promoter primer for the CML major breakpoint region.  
XX  
KW Primer; autocatalytic; PCR; target; sequence; ss.  
XX  
OS Synthetic.  
XX  
PN US5399491-A.  
XX  
PD 21-MAR-1995.  
XX  
PF 19-MAR-1992; 92US-00855732.  
XX  
PR 11-JUL-1989; 89US-00379501.  
PR 10-JUL-1990; 90US-00550837.  
XX  
(GENP-) GEN-PROBE INC.  
XX  
PI Fultz TJ, Kacian DL;  
XX  
DR WPI; 1995-130686/17.  
XX  
PT Amplification of nucleic acid targets - using a reverse transcriptase  
PT with RNase H activity and a RNA polymerase at constant temp.  
XX  
PS Example 18; Col 47; 58pp; English.  
XX  
CC The oligonucleotide AAQ86635 is a non-promoter primer for the CML major  
CC breakpoint amplification region. It is used to illustrate that small  
CC changes in the NA sequence result in large changes in the amplification  
CC efficiency. AAQ86635 is capable of serving as a primer for the synthesis  
CC of autocatalytic oligonucleotides which require no change in the PCR  
CC conditions i.e.constant temperature, pH and ionic strength. This sequence  
CC is useful in generating multiple copies of specific nucleic acid target  
CC sequences. (Updated on 25-MAR-2003 to correct PF field.)  
XX  
SQ Sequence 24 BP; 7 A; 7 C; 5 G; 5 T; 0 U; 0 Other;

Query Match 100.0%; Score 24; DB 2; Length 24;  
 Best Local Similarity 70.8%; Pred. No. 0.00042;  
 Matches 17; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

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 Db 24 TGGAGTTTTCACACGAGTTGGTC 1

RESULT 2  
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 ID AAV66353 standard; DNA; 24 BP.  
 AC AAV66353;  
 XX  
 DT 06-JAN-1999 (first entry)  
 DE  
 DE CML-2 chromosomal translocation major breakpoint non-promoter primer.  
 XX  
 KW CML-2 chromosomal translocation t(14; 18) major breakpoint;  
 KW block splice template; autocatalytic RNA amplification; primer; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN US5824518-A.  
 XX  
 PD 20-OCT-1998.  
 XX  
 PF 06-JUN-1995; 95US-00469067.  
 XX  
 PR 11-JUL-1989; 89US-00379501.  
 PR 10-JUL-1990; 90US-00550837.  
 XX  
 PA (GENP-) GEN-PROBE INC.  
 XX  
 PI Fultz TJ, Kacian DL;  
 PI WPI; 1998-582557/49.  
 DR  
 XX Block splice template useful for amplification of nucleic acids -  
 PT comprises two nucleic acid regions, the first region located 3' of the  
 PT second region and blocked at its 3' terminus to inhibit primer extension  
 PT by a DNA polymerase.  
 XX  
 PS Example 18; Col 43; 5lpp; English.  
 XX

AAV66352-55 represent CML-2 chromosomal translocation t(14;18) major  
 breakpoint amplification region non-promoter primers. The primers are  
 used to amplify the invention. The specification describes methods of  
 synthesising multiple copies of a target nucleic acid sequence  
 autocatalytically under conditions of substantially constant temperature,  
 ionic strength and pH are provided in which multiple RNA copies of the  
 target sequence autocatalytically generate additional copies. The target  
 sequence is a block splice template which comprises two nucleic acid  
 regions. The first region is located 3' of the second region and is  
 blocked at its 3' terminus to inhibit primer extension by a DNA  
 polymerase, and the second region comprises a promoter sequence  
 recognised by an RNA polymerase. The methods are used to amplify nucleic  
 acid, especially RNA, for analysis, cloning or probe production

QY 1 UGGAGUUUACACACGAGUUGGUC 24  
 Db 24 TGGAGTTTTCACACGAGTTGGTC 1

RESULT 3  
 AAX23204/c

ID AAX23204 standard; DNA; 24 BP.  
 AC AAX23204;  
 XX  
 DT 11-JUN-1999 (first entry)  
 DE  
 DE CML t(14; 18) non-promoter primer #2.  
 XX  
 KW Autocatalytic amplification; transcription-based amplification; CML;  
 KW thermalcycling; diagnostic; environmental testing; probe; detection;  
 KW genetic disease; infectious disease; microorganism; food; forensic;  
 KW paternity; primer; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN US5888779-A.  
 XX  
 PD 30-MAR-1999.  
 XX  
 PF 05-JUN-1995; 95US-00461654.  
 XX  
 PR 11-JUL-1989; 89US-00379501.  
 PR 10-JUL-1990; 90US-00550837.  
 XX  
 PA (GENP-) GEN-PROBE INC.  
 XX  
 PI Fultz TJ, Kacian DL;  
 PI WPI; 1999-253231/21.  
 DR  
 XX Kit for autocatalytic amplification of RNA targets.  
 XX  
 PS Example 18; Col 43; 5lpp; English.  
 XX

This invention describes a novel method for the autocatalytic  
 amplification of an RNA target in a transcription-based amplification  
 system without thermalcycling. The method generates oligonucleotides for  
 diagnostic or environmental testing, for use e.g. as probes and in  
 cloning. Typical applications are the detection of genetic or infectious  
 diseases, the monitoring of responses to therapy, the quantitation or  
 detection of microorganisms in foods, forensic studies and the  
 establishment of paternity. Kits containing the products of the invention  
 provide many copies of selected RNA targets under conditions of constant  
 temperature, ionic strength and pH. Specific amplification of RNA targets  
 increases sensitivity, convenience, accuracy and the reliability of  
 assays

QY 1 UGGAGUUUACACACGAGUUGGUC 24  
 Db 24 TGGAGTTTTCACACGAGTTGGTC 1

RESULT 4  
 AAX83985/c  
 ID AAX83985 standard; DNA; 24 BP.  
 AC AAX83985;  
 XX  
 DT 08-SEP-1999 (first entry)  
 DE  
 DE bcr-abl sense primer.  
 XX  
 KW Reverse transcription PCR; oligonucleotide-immobilised microplate;  
 KW polypropylene; thermal cycle; solid phase; cell lysate; research;  
 KW gene expression analysis; diagnostic; drug screening; primer; ss.  
 XX  
 OS Synthetic.

Query Match 100.0%; Score 24; DB 2; Length 24;  
 Best Local Similarity 70.8%; Pred. No. 0.00042;  
 Matches 17; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 UGGAGUUUACACACGAGUUGGUC 24  
 Db 24 TGGAGTTTTCACACGAGTTGGTC 1

RESULT 4  
 AAX83985/c  
 ID AAX83985 standard; DNA; 24 BP.  
 AC AAX83985;  
 XX  
 DT 08-SEP-1999 (first entry)  
 DE  
 DE bcr-abl sense primer.  
 XX  
 KW Reverse transcription PCR; oligonucleotide-immobilised microplate;  
 KW polypropylene; thermal cycle; solid phase; cell lysate; research;  
 KW gene expression analysis; diagnostic; drug screening; primer; ss.  
 XX  
 OS Synthetic.

```

XX PN WO9932854-A1.
XX PD
XX PF 01-JUL-1999.
XX PP 22-DEC-1998; 98WO-US027293.
XX PR 22-DEC-1997; 97US-0068394P.
XX PR 16-JAN-1998; 98US-0071627P.
XX XX
XX PA (HITB ) HITACHI CHEM CO LTD.
XX PA (HITB ) HITACHI CHEM RES CENT INC.
XX PI Mitsuhashi M;
XX PT
XX DR WPI; 1999-418942/35.
XX DR
XX PT Using oligonucleotide-immobilized microplates in polymerase chain
XX PT reactions.
XX PS
XX PS Example; Page 9; 34pp; English.
XX CC The present invention describes the use of oligonucleotide-immobilized
XX CC microplates having heat-stability for thermal cycles of reverse
XX CC transcription-polymerase chain reaction (RT-PCR). The method of RT-PCR
XX CC comprises: (a) preparing cell lysate of a target cell; (b) transferring
XX CC the cell lysate to an oligonucleotide-immobilized microplate having wells
XX CC to which oligonucleotides are securely immobilized, the microplate having
XX CC heat-stability for thermal cycles of PCR, the oligonucleotides having
XX CC nucleic acid sequences specifically complementary to mRNA of interest
XX CC present in the cell lysate; (c) capturing mRNA by the oligonucleotides of
XX CC the microplate; (d) conducting RT-PCR on the same microplate, using an
XX CC appropriate buffer; and (e) detecting PCR products of interest. The
XX CC method is used for gene expression analysis. The multiple PCR system is
XX CC useful in basic research, diagnostics and drug screening, with potential
XX CC application to future automation. The method simplifies the process of RT
XX CC -PCR. cDNA synthesized from mRNA captured by immobilized oligonucleotide
XX CC on the PCR microplates can be used more than once, thus amplifying
XX CC several times different or same portions of the cDNA by using appropriate
XX CC primers. The method also drastically simplifies the preparation of cell
XX CC lysate and significantly stabilizes the yield of recovered cytosolic RNA.
XX CC The present sequence represents a primer used in an example from the
XX CC present invention
XX SQ Sequence 24 BP; 7 A; 7 C; 5 G; 5 T; 0 U; 0 Other;
XX Query Match 100.0%; Score 24; DB 2; Length 24;
XX Best Local Similarity 70.8%; Pred. No. 0.00042;
XX Matches 17; Conservative 7; Mismatches 0; Indels 0; Gaps 0;
XX QY 1 UGGAGUUUCACACACGAGUUGGUC 24
XX Db :||||:|||||:|||||:|||||:
XX 24 TGGAGTTTCACACACGAGTTGGTC 1
XX RESULT 5
XX AAZ60844/c
XX ID AAZ60844 standard; DNA; 24 BP.
XX XX
XX AC AAZ60844;
XX XX
XX DT 16-MAY-2000 (first entry)
XX DE Oligonucleotide used to detect bcr b3-abl fusion transcripts.
XX KW Fusion transcript; translocation; bcr b3 region; abl gene;
XX KW amplification assay; detection assay; medical diagnosis;
XX KW clinical monitoring; chimeric RNA; fusion RNA; condition marker;
XX KW disease marker; cancer; leukemia; ss.
XX OS Synthetic.
XX PN WO200005418-A1.
XX PF 23-JUL-1999; 99WO-US016832.
XX PR 23-JUL-1998; 98US-00121239.
XX XX
XX PA (GENP-) GEN-PROBE INC.
XX PI Harvey RC, Eastman PS;
XX DR WPI; 2000-182730/16.
XX PT
XX PT Novel methods for preparing RNA from biological samples, used for the
XX PT detection and measurement of nucleic acids and fusion nucleic acids.
XX PS
XX PS Claim 19; Page 40; 49pp; English.
XX CC Oligonucleotides AAZ60840-62 and AAZ60855-66 are used in the method of
XX CC the invention to detect fusion transcripts produced from a translocation
XX CC between the bcr b3 region and the abl gene. The specification describes a
XX CC method for detecting a fusion nucleic acid (particularly chimeric mRNA
XX CC species), in a biological sample. The method comprises contacting a
XX CC sample of fusion nucleic acid with primers, amplifying the hybridized
XX CC fusion nucleic acid, and detecting the target hybrid. The method is used
XX CC for the simple and rapid preparation of RNA from a biological sample,
XX CC particularly from the cytoplasm of eukaryotic cells, which is suitable
XX CC for use in an amplification and detection assay. The methods are used for
XX CC the analysis and detection of nucleic acids in biological samples. The
XX CC methods are useful in the human medical and veterinary fields, for
XX CC medical diagnoses and clinical monitoring of a patient's response to
XX CC therapy where a disease or medical condition is associated with a
XX CC particular type and/or level of mRNA present in the sample. The methods
XX CC are also useful for detecting or quantifying fusion or chimeric RNA
XX CC species, and for detecting a translocation as a marker for a given
XX CC condition or disease, e.g. translocations associate with cancers,
XX CC particularly forms of leukemia
XX SQ Sequence 24 BP; 7 A; 7 C; 5 G; 5 T; 0 U; 0 Other;
XX Query Match 100.0%; Score 24; DB 3; Length 24;
XX Best Local Similarity 70.8%; Pred. No. 0.00042;
XX Matches 17; Conservative 7; Mismatches 0; Indels 0; Gaps 0;
XX QY 1 UGGAGUUUCACACACGAGUUGGUC 24
XX Db :||||:|||||:|||||:|||||:
XX 24 TGGAGTTTCACACACGAGTTGGTC 1
XX RESULT 6
XX AAZ60845/c
XX ID AAZ60845 standard; RNA; 24 BP.
XX XX
XX AC AAZ60845;
XX XX
XX DT 16-MAY-2000 (first entry)
XX DE Oligonucleotide used to detect bcr b3-abl fusion transcripts.
XX KW Fusion transcript; translocation; bcr b3 region; abl gene;
XX KW amplification assay; detection assay; medical diagnosis;
XX KW clinical monitoring; chimeric RNA; fusion RNA; condition marker;
XX KW disease marker; cancer; leukemia; ss.
XX OS Synthetic.
XX PN WO200005418-A1.
XX PF 23-JUL-1999; 99WO-US016832.
XX PR 23-JUL-1998; 98US-00121239.
XX XX

```

XX (GENP-) GEN-PROBE INC.  
 PA Harvey RC, Eastman PS;  
 XX WPI; 2000-182730/16.  
 XX Novel methods for preparing RNA from biological samples, used for the  
 PT detection and measurement of nucleic acids and fusion nucleic acids.  
 XX Claim 19; Page 40; 49pp; English.  
 XX Oligonucleotides AAZ60840-62 and AAZ60865-66 are used in the method of  
 CC the invention to detect fusion transcripts produced from a translocation  
 CC between the bcr b3 region and the abl gene. The specification describes a  
 CC method for detecting a fusion nucleic acid (particularly chimeric mRNA  
 CC species), in a biological sample. The method comprises contacting a  
 CC sample of fusion nucleic acid with primers, amplifying the hybridized  
 CC fusion nucleic acid, and detecting the target hybrid. The method is used  
 CC for the simple and rapid preparation of RNA from a biological sample,  
 CC particularly from the cytoplasm of eukaryotic cells, which is suitable  
 CC for use in an amplification and detection assay. The methods are used for  
 CC the analysis and detection of nucleic acids in biological samples. The  
 CC methods are useful in the human medical and veterinary fields, for  
 CC medical diagnoses and clinical monitoring of a patient's response to  
 CC therapy where a disease or medical condition is associated with a  
 CC particular type and/or level of mRNA present in the sample. The methods  
 CC are also useful for detecting or quantifying fusion or chimeric RNA  
 CC species, and for detecting a translocation as a marker for a given  
 CC condition or disease, e.g. translocations associate with cancers,  
 CC particularly forms of leukemia  
 XX Sequence 24 BP; 7 A; 7 C; 5 G; 0 T; 5 U; 0 Other;  
 SQ Query Match 100.0%; Score 24; DB 3; Length 24;  
 Best Local Similarity 70.8%; Pred. NO. 0.00042;  
 Matches 17; Conservative 7; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 UGAGUUUCACACACGAGUUGGUC 24  
 DB 24 TGGAGTTTCACACACGAGTTGGTC 1  
 RESULT 7  
 AAZ60846  
 ID AAZ60846 standard; DNA; 24 BP.  
 XX AAZ60846;  
 AC 16-MAY-2000 (first entry)  
 DT Oligonucleotide used to detect bcr b3-abl fusion transcripts.  
 DE Fusion transcript; translocation; bcr b3 region; abl gene;  
 XX amplification assay; detection assay; medical diagnosis;  
 KW clinical monitoring; chimeric RNA; fusion RNA; condition marker;  
 KW disease marker; cancer; leukemia; ss.  
 XX Synthetic.  
 OS WO200005418-A1.  
 PN 03-FEB-2000.  
 PD 23-JUL-1999; 99WO-US016832.  
 PF 23-JUL-1998; 98US-00121239.  
 PR (GENP-) GEN-PROBE INC.  
 XX Harvey RC, Eastman PS;  
 XX WPI; 2000-182730/16.

XX Novel methods for preparing RNA from biological samples, used for the  
 PT detection and measurement of nucleic acids and fusion nucleic acids.  
 XX Claim 19; Page 40; 49pp; English.  
 XX Oligonucleotides AAZ60840-62 and AAZ60865-66 are used in the method of  
 CC the invention to detect fusion transcripts produced from a translocation  
 CC between the bcr b3 region and the abl gene. The specification describes a  
 CC method for detecting a fusion nucleic acid (particularly chimeric mRNA  
 CC species), in a biological sample. The method comprises contacting a  
 CC sample of fusion nucleic acid with primers, amplifying the hybridized  
 CC fusion nucleic acid, and detecting the target hybrid. The method is used  
 CC for the simple and rapid preparation of RNA from a biological sample,  
 CC particularly from the cytoplasm of eukaryotic cells, which is suitable  
 CC for use in an amplification and detection assay. The methods are used for  
 CC the analysis and detection of nucleic acids in biological samples. The  
 CC methods are useful in the human medical and veterinary fields, for  
 CC medical diagnoses and clinical monitoring of a patient's response to  
 CC therapy where a disease or medical condition is associated with a  
 CC particular type and/or level of mRNA present in the sample. The methods  
 CC are also useful for detecting or quantifying fusion or chimeric RNA  
 CC species, and for detecting a translocation as a marker for a given  
 CC condition or disease, e.g. translocations associate with cancers,  
 CC particularly forms of leukemia  
 XX Sequence 24 BP; 5 A; 5 C; 7 G; 7 T; 0 U; 0 Other;  
 SQ Query Match 100.0%; Score 24; DB 3; Length 24;  
 Best Local Similarity 70.8%; Pred. NO. 0.00042;  
 Matches 17; Conservative 7; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 UGAGUUUCACACACGAGUUGGUC 24  
 DB 1 TGGAGTTTCACACACGAGTTGGTC 24  
 RESULT 8  
 AAZ60847  
 ID AAZ60847 standard; RNA; 24 BP.  
 XX AAZ60847;  
 AC 16-MAY-2000 (first entry)  
 DT Oligonucleotide used to detect bcr b3-abl fusion transcripts.  
 DE Fusion transcript; translocation; bcr b3 region; abl gene;  
 XX amplification assay; detection assay; medical diagnosis;  
 KW clinical monitoring; chimeric RNA; fusion RNA; condition marker;  
 KW disease marker; cancer; leukemia; ss.  
 XX Synthetic.  
 OS WO200005418-A1.  
 PN 03-FEB-2000.  
 PD 23-JUL-1999; 99WO-US016832.  
 PF 23-JUL-1998; 98US-00121239.  
 PR (GENP-) GEN-PROBE INC.  
 XX Harvey RC, Eastman PS;  
 XX WPI; 2000-182730/16.  
 XX Novel methods for preparing RNA from biological samples, used for the  
 PT detection and measurement of nucleic acids and fusion nucleic acids.  
 XX Claim 19; Page 41; 49pp; English.



CC Oligonucleotides AAZ60840-62 and AAZ60865-66 are used in the method of  
CC the invention to detect fusion transcripts produced from a translocation  
CC between the bcr b3 region and the abl gene. The specification describes a  
CC method for detecting a fusion nucleic acid (particularly chimeric mRNA  
CC species), in a biological sample. The method comprises contacting a  
CC sample of fusion nucleic acid with primers, amplifying the hybridized  
CC fusion nucleic acid, and detecting the target hybrid. The method is used  
CC for the simple and rapid preparation of RNA from a biological sample,  
CC particularly from the cytoplasm of eukaryotic cells, which is suitable  
CC for use in an amplification and detection assay. The methods are used for  
CC the analysis and detection of nucleic acids in biological samples. The  
CC methods are useful in the human medical and veterinary fields, for  
CC medical diagnoses and clinical monitoring of a patient's response to  
CC therapy where a disease or medical condition is associated with a  
CC particular type and/or level of mRNA present in the sample. The methods  
CC are also useful for detecting or quantifying fusion or chimeric RNA  
CC species, and for detecting a translocation as a marker for a given  
CC condition or disease, e.g. translocations associate with cancers,  
CC particularly forms of leukemia

XX SQ Sequence 24 BP; 5 A; 5 C; 7 G; 0 T; 0 U; 0 Other;  
Query Match 100.0%; Score 24; DB 3; Length 24;  
Best Local Similarity 100.0%; Pred. No. 0.00042; Mismatches 0; Indels 0; Gaps 0;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 UGGAGUUUCACACGAGUUGGUC 24  
|||||  
Db 1 UGGAGUUUCACACGAGUUGGUC 24  
|||||

RESULT 9  
AAD62592/c  
ID AAD62592 standard; DNA; 24 BP.

AC AAD62592;

XX 15-JAN-2004 (first entry)

XX CML chromosomal translocation t(9;22) PCR primer #1.

XX Amplification; human immunodeficiency virus; environmental testing; HIV;  
KW detection; diagnostic testing; PCR; primer; ss.

XX Unidentified.

XX US6589734-B1.

XX 08-JUL-2003.

XX 08-OCT-1998; 98US-00168947.

XX 11-JUL-1989; 89US-00379501.

PR 10-JUL-1990; 90US-00550837.

PR 06-JUN-1995; 95US-00469067.

XX (GENP-) GEN-PROBE INC.

XX Kacian DL, Fultz TJ, McDonough SH;

XX WPI; 2003-810379/76.

XX New oligonucleotide probe, useful in detecting HIV nucleic acid in a

XX sample and for environmental and diagnostic testing.

XX Example 18; Col 43; 62pp; English.

XX The invention relates to oligonucleotides useful in amplifying and  
CC detecting human immunodeficiency virus (HIV) nucleic acid in a sample.  
CC The invention is used for environmental testing, diagnostic testing,  
CC research studies and for the preparation of reagents or materials for  
CC cloning or other purposes. The present sequence is CML chromosomal  
CC translocation t(9;22) PCR primer. This sequence is used in the invention

XX SQ Sequence 24 BP; 7 A; 7 C; 5 G; 5 T; 0 U; 0 Other;  
Query Match 100.0%; Score 24; DB 9; Length 24;  
Best Local Similarity 70.8%; Pred. No. 0.00042; Mismatches 17; Conservative 7; Mismatches 0; Indels 0; Gaps 0;  
QY 1 UGGAGUUUCACACGAGUUGGUC 24  
|||||  
Db 24 TGGAGTTTCACACGAGTTGGTC 1  
|||||

RESULT 10

AAT88785/c

ID AAT88785 standard; DNA; 200 BP.

XX AAT88785;

XX 23-MAR-1998 (first entry)

XX Leukaemic cell BCR-ABL mRNA PCR product target sequence.

XX Leukaemia; BCR-ABL; cell line K562; target; immunoassay; probe;  
KW hybridisation; diagnostic; luciferase; genetic disease; ss.

XX Unidentified.

XX CA2186998-A.

XX 31-MAY-1997.

XX 02-OCT-1996; 96CA-02186998.

XX 30-NOV-1995; 95US-00565055.

XX (UYWI-) UNIV WINDSOR.

XX Christopoulos TK;

XX WPI; 1997-415964/39.

XX Immunoassays and nucleic acid hybridisation assays - using protein-  
PT encoding nucleic acid fragments as labels.

XX Disclosure; Page 26; 39pp; English.

XX A novel assay has been developed for determining an analyte. The assay  
CC comprises labelling the analyte with a nucleic acid fragment that encodes  
CC a protein, expressing the nucleic acid, and detecting the protein. The  
CC present sequence represents a target sequence from a leukaemic cell (cell  
CC line K562), used in an example of the present assay. The assay is used  
CC for the determination of antigens or nucleic acids for diagnostic or  
CC research purposes, e.g. detecting low levels of tumour markers, analysing  
CC nucleic acid mutations associated with genetic diseases, diagnosing and  
CC monitoring pathogen infections, or searching for new disease markers. The  
CC immunoassay when using a luciferase for detection is more sensitive than  
CC an enzyme-amplified, time-resolved fluorometric immunoassay and does not  
CC require preparation of a luciferase-antibody conjugate

XX SQ Sequence 200 BP; 49 A; 52 C; 51 G; 48 T; 0 U; 0 Other;

Query Match 100.0%; Score 24; DB 2; Length 200;  
Best Local Similarity 70.8%; Pred. No. 0.0004; Mismatches 17; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 UGGAGUUUCACACGAGUUGGUC 24

Db 39 TGGAGTTTCACACGAGTTGGTC 16  
|||||

RESULT 11

ABS73175/c

ID ABS73175 standard; DNA; 250 BP.



```
ID AAZ60863 standard; DNA; 350 BP.
XX
AC AAZ60863;
XX
XX
DT 16-MAY-2000 (first entry)
XX
XX Region surrounding a bcr-able splice junction.
DE
XX Fusion transcript; translocation; bcr b3 region; abl gene;
KW amplification assay; detection assay; medical diagnosis;
KW clinical monitoring; chimeric RNA; fusion RNA; condition marker;
KW disease marker; cancer; leukemia; ss.
XX
XX Unidentified.
OS
XX WO200005418-A1.
PN
XX 03-FEB-2000.
PD
XX
XX 23-JUL-1999; 99WO-US016832.
PF
XX
XX 23-JUL-1998; 98US-00121239.
PR
XX (GENP-) GEN-PROBE INC.
PA
XX Harvey RC, Eastman PS;
PI
XX WPI; 2000-182730/16.
DR
XX Novel methods for preparing RNA from biological samples, used for the
PT detection and measurement of nucleic acids and fusion nucleic acids.
PT
XX Disclosure; Fig 2; 49pp; English.
XX
XX The present sequence represents a region surrounding a bcr-able splice
CC junction. The specification describes oligonucleotides which are used to
CC detect fusion transcripts produced from a translocation between the bcr
CC b3 region and the abl gene. The specification also describes a method for
CC detecting a fusion nucleic acid (particularly chimeric mRNA species), in
CC a biological sample. The method comprises contacting a sample of fusion
CC nucleic acid with primers, amplifying the hybridized fusion nucleic acid,
CC and detecting the target hybrid. The method is used for the simple and
CC rapid preparation of RNA from a biological sample, particularly from the
CC cytoplasm of eukaryotic cells, which is suitable for use in an
CC amplification and detection assay. The methods are used for the analysis
CC and detection of nucleic acids in biological samples. The methods are
CC useful in the human medical and veterinary fields, for medical diagnoses
CC and clinical monitoring of a patient's response to therapy where a disease
CC or medical condition is associated with a particular type and/or level of
CC mRNA present in the sample. The methods are also useful for detecting or
CC quantifying fusion or chimeric RNA species, and for detecting a
CC translocation as a marker for a given condition or disease, e.g.
CC translocations associate with cancers, particularly forms of leukemia
XX
XX Sequence 350 BP; 85 A; 92 C; 89 G; 84 T; 0 U; 0 Other;
SQ Query Match 100.0%; Score 24; DB 3; Length 350;
Best Local Similarity 70.8%; Pred. NO. 0.00039;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 UGGAGUUUCACACAGAGUUGGUC 24
:||||:|||||:|||||:|||||:
DB 88 TGGAGTTTTCACACAGAGTTGGTC 65

RESULT 14
AAS85023/c
ID AAS85023 standard; cDNA; 504 BP.
XX
AC AAS85023;
XX
XX 13-FEB-2002 (first entry)
DT
XX
XX Human endothelial cell cDNA #6375.
DE
XX
```

```
DE DNA encoding novel human diagnostic protein #20827.
XX
KW Human; Chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US008631.
XX
PR 31-MAR-2000; 2000US-00540217.
PR 23-AUG-2000; 2000US-00649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
XX WPI; 2001-639362/73.
DR P-PSDB; ABG20836.
XX
XX New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.
XX
PS Claim 1; SEQ ID NO 20827; 103pp; English.
XX
XX The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activity. The
CC polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic
CC coding sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 504 BP; 119 A; 122 C; 144 G; 117 T; 0 U; 2 Other;
Query Match 100.0%; Score 24; DB 5; Length 504;
Best Local Similarity 70.8%; Pred. NO. 0.00039;
Matches 17; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 UGGAGUUUCACACAGAGUUGGUC 24
:||||:|||||:|||||:|||||:
DB 238 TGGAGTTTTCACACAGAGTTGGTC 215

RESULT 15
ACH38242/c
ID ACH38242 standard; cDNA; 504 BP.
XX
AC ACH38242;
XX
XX 13-OCT-2003 (first entry)
DT
XX
XX Human endothelial cell cDNA #6375.
DE
XX
```

KW Human; ss; sequencing by hybridisation; SBH; expressed sequence tag; EST;  
KW genome mapping; biodiversity; genetic disorder.

OS Homo sapiens.

XX US2003073623-A1.

XX 17-APR-2003.

XX 30-JUL-2001; 2001US-00918995.

XX 30-JUL-2001; 2001US-00918995.

XX (DRMA/) DRMANAC R T.

PA (LABA/) LABAT I.

PA (STAC/) STACHE-CRAIN B.

PA (DICK/) DICKSON M C.

PA (JONE/) JONES L W.

XX Drmanac RT, Labat I, Stache-Crain B, Dickson MC, Jones LW;

PI WPI; 2003-615964/58.

XX New polynucleotide sequences obtained from various cDNA libraries, useful  
PT as hybridization probes, as oligomers for PCR, for chromosome and gene  
PT mapping, in the recombinant production of protein, or in generating  
PT antisense DNA or RNA.

PS Claim 1; SEQ ID NO 25454; 44pp; English.

XX The invention relates to an isolated polynucleotide comprising any one of  
CC 38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence was  
CC determined by the technique of SBH (sequencing by hybridisation). Also  
CC included is a purified polypeptide comprising a sequence corresponding to  
CC a reading frame of the novel polynucleotide. The nucleic acid sequences  
CC are useful in diagnostics as expressed sequence tags (EST) for  
CC identifying expressed genes or for physical mapping of the human genome,  
CC in forensics, in assessing biodiversity, or in identifying mutations  
CC responsible for genetic disorders and other traits. The nucleotide  
CC sequences are also useful as hybridisation probes, as oligomers for PCR,  
CC for chromosome and gene mapping, in the recombinant production of  
CC protein, or in generating antisense DNA or RNA. The purified polypeptide  
CC is useful for generating antibodies specific for it. The present sequence  
CC is one of the 38043 isolated cDNA/EST sequences. Note: The sequence data  
CC for this patent did not form part of the printed specification, but was  
CC obtained in electronic format directly from USPTO at  
CC seqdata.uspto.gov/sequence.html?docID=20030073623

XX SQ Sequence 504 BP; 119 A; 122 C; 144 G; 117 T; 0 U; 2 Other;

Query Match 100.0%; Score 24; DB 8; Length 504;

Best Local Similarity 70.8%; Pred.No. 0.00039;

Matches 17; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 UGGAGUUUCACACACGAGUUGGUC 24

DB 238 TGGAGTTTCACACACGAGTTGTC 215

Search completed: May 26, 2004, 16:52:16  
Job time : 107.037 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: May 26, 2004, 16:02:51 ; Search time 20.2274 Seconds  
(without alignments)  
658.454 Million cell updates/sec

Title: US-09-121-239-8  
Perfect score: 24  
Sequence: 1 UGGAGUUCACACGAGUGGUC 24

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 682709 seqs, 277475446 residues

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Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

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Post-processing: Listing first 45 summaries

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2: /cgn2\_6/ptodata/2/ina/5B COMB.seq.\*  
3: /cgn2\_6/ptodata/2/ina/6A COMB.seq.\*  
4: /cgn2\_6/ptodata/2/ina/6B COMB.seq.\*  
5: /cgn2\_6/ptodata/2/ina/PTUS COMB.seq.\*  
6: /cgn2\_6/ptodata/2/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	24	100.0	24	4	US-09-168-947-37
C 2	24	100.0	1078	4	US-09-310-842-1
C 3	21	87.5	40	3	US-08-448-448B-16
C 4	20	83.3	20	1	US-08-363-233B-5
C 5	15	62.5	486	4	US-09-621-976-19145
C 6	14	58.3	264	4	US-09-313-294A-3357
C 7	14	58.3	1821	4	US-09-149-476-90
C 8	13	54.2	1638	1	US-08-253-155A-1
C 9	13	54.2	1689	4	US-08-851-567B-29
C 10	13	54.2	2234	3	US-08-993-088A-8
C 11	13	54.2	2234	4	US-08-993-424B-8
C 12	13	54.2	2234	4	US-09-603-680-8
C 13	13	54.2	2692	1	US-08-036-210-14
C 14	13	54.2	2692	2	US-08-449-609-14
C 15	13	54.2	2692	4	US-09-361-096A-14
C 16	13	54.2	3825	6	5310678-2
C 17	13	54.2	3900	4	US-09-976-594-569
C 18	13	54.2	6055	4	US-08-851-567B-25
C 19	13	54.2	6527	4	US-09-492-308A-3
C 20	13	54.2	8931	3	US-09-051-019-1
C 21	13	54.2	10878	4	US-09-511-842A-1
C 22	12	50.0	20	3	US-09-513-729B-81
C 23	12	50.0	36	1	US-08-403-762A-155
C 24	12	50.0	207	4	US-09-511-625B-42
C 25	12	50.0	349	4	US-09-621-976-15221
C 26	12	50.0	418	4	US-09-257-179-36
C 27	12	50.0	444	4	US-09-621-976-12314

C 28	12	50.0	445	4	US-09-621-976-12560	Sequence 12560, A
C 29	12	50.0	502	4	US-09-621-976-1301	Sequence 1301, Ap
C 30	12	50.0	544	4	US-09-621-976-15220	Sequence 15220, A
C 31	12	50.0	611	4	US-09-451-651-12	Sequence 12, Appl
C 32	12	50.0	617	3	US-09-328-111-158	Sequence 158, App
C 33	12	50.0	633	4	US-09-242-999-19	Sequence 19, Appl
C 34	12	50.0	693	2	US-08-690-849-1	Sequence 1, Appl1
C 35	12	50.0	693	2	US-08-690-849-3	Sequence 3, Appl1
C 36	12	50.0	693	3	US-09-004-053-1	Sequence 3, Appl1
C 37	12	50.0	693	3	US-09-004-053-3	Sequence 3, Appl1
C 38	12	50.0	834	3	US-08-998-416-529	Sequence 529, App
C 39	12	50.0	885	3	US-08-545-196B-20	Sequence 20, Appl
C 40	12	50.0	1050	4	US-09-655-270A-16	Sequence 16, Appl
C 41	12	50.0	1050	4	US-09-651-941-20	Sequence 20, Appl
C 42	12	50.0	1050	4	US-09-955-597-20	Sequence 20, Appl
C 43	12	50.0	1092	4	US-09-673-395A-131	Sequence 131, App
C 44	12	50.0	1160	4	US-09-153-310-41	Sequence 41, Appl
C 45	12	50.0	1180	3	US-08-897-236-10	Sequence 10, Appl

ALIGNMENTS

RESULT 1

US-09-168-947-37/c  
; Sequence 37, Application US/09168947  
; Patent No. 6589734  
; GENERAL INFORMATION:  
; APPLICANT: KACIAN, DANIEL L.  
; APPLICANT: FULTZ, TIMOTHY J.  
; APPLICANT: MCDONOUGH, SHERROL H.  
; TITLE OF INVENTION: DETECTION OF HIV  
; FILE REFERENCE: 218/130  
; CURRENT APPLICATION NUMBER: US/09/168,947  
; CURRENT FILING DATE: 1998-10-08  
; EARLIER APPLICATION NUMBER: 08/469,067  
; EARLIER FILING DATE: 1995-06-06  
; EARLIER APPLICATION NUMBER: 07/550,837  
; EARLIER FILING DATE: 1990-07-10  
; NUMBER OF SEQ ID NOS: 46  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 37  
; LENGTH: 24  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthesized nucleic acid molecule  
US-09-168-947-37

Query Match 100.0%; Score 24; DB 4; Length 24;  
Best Local Similarity 70.8%; Pred. No. 1.7e-05;  
Matches 17; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 UGGAGUUCACACGAGUGGUC 24  
DB 24 TGGAGTTTCACACGAGTTGTC 1

RESULT 2

US-09-310-842-1/c  
; Sequence 1, Application US/09310842A  
; Patent No. 6451593  
; GENERAL INFORMATION:  
; APPLICANT: Wittig, Prof. Burghardt  
; APPLICANT: Junghans, Claas  
; TITLE OF INVENTION: Design Principle for Constructing Expression Constructs for Gene  
; FILE REFERENCE: XI 597/99  
; CURRENT APPLICATION NUMBER: US/09/310,842A  
; CURRENT FILING DATE: 1999-05-12  
; EARLIER APPLICATION NUMBER: DE 196 48 625.4  
; EARLIER FILING DATE: 1996-11-13  
; NUMBER OF SEQ ID NOS: 13

SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 1  
LENGTH: 1078  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
NAME/KEY: gene  
LOCATION: (1)..(1078)  
OTHER INFORMATION: bcr3=abl2; Oligo DNA Dumbbell  
FEATURE:  
NAME/KEY: misc\_binding  
LOCATION: (1)..(2)  
OTHER INFORMATION: intramolecular binding site; the T-nucleotides at position 1 to  
OTHER INFORMATION: 2 can be modified with amino or caroxy features  
FEATURE:  
NAME/KEY: misc\_binding  
LOCATION: (1077)..(1078)  
OTHER INFORMATION: intramolecular binding site; the T-nucleotides at position 1077  
OTHER INFORMATION: to 1078 can be modified with amino or caroxy features  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Strandness: both; nucleic  
OTHER INFORMATION: acid (linear), hypothetical: No. 6451593 anti-sense: No  
US-09-310-842-1

Query Match 100.0%; Score 24; DB 4; Length 1078;  
Best Local Similarity 70.8%; Pred. No. 1.8e-05;  
Matches 17; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 UGGAGUUUCACACAGGUGUC 24  
DB 661 TGGAGTTTCACACAGGTTGTC 638

RESULT 3  
US-08-448-446B-16/c  
Sequence 16, Application US/08448446B  
Patent No. 6080851  
GENERAL INFORMATION:  
APPLICANT: Pachuk et al.  
TITLE OF INVENTION: Compounds and Methods for the Treatment  
TITLE OF INVENTION: of Leukemias  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Woodcock Washburn  
ADDRESSEE: Kurtz Mackiewicz & No. 6080851ris  
STREET: One Liberty Place - 46th Floor  
CITY: Philadelphia  
STATE: PA  
COUNTRY: USA  
ZIP: 19103  
COMPUTER READABLE FORM:  
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE  
COMPUTER: IBM PS/2  
OPERATING SYSTEM: PC-DOS  
SOFTWARE: WORDPERFECT 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/448,446B  
FILING DATE: July 10, 1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/989,852  
FILING DATE: December 4, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Doreen Yanko Trujillo  
REGISTRATION NUMBER: 35,719  
REFERENCE/DOCKET NUMBER: APOL-0020  
TELECOMMUNICATION INFORMATION: C  
TELEPHONE: (215) 568-3100  
TELEFAX: (215) 568-3439  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 40  
TYPE: Nucleic Acid

STRANDEDNESS: Single  
TOPOLOGY: Linear  
ANTI-SENSE:  
US-08-448-446B-16  
Query Match 87.5%; Score 21; DB 3; Length 40;  
Best Local Similarity 71.4%; Pred. No. 0.001;  
Matches 15; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 UGGAGUUUCACACAGGUG 21  
DB 40 TGGAGTTTCACACAGGTTG 20

RESULT 4  
US-08-363-233B-5/c  
Sequence 5, Application US/08363233B  
Patent No. 5714383  
GENERAL INFORMATION:  
APPLICANT: Thompson, James D.  
TITLE OF INVENTION: METHOD AND REAGENT FOR TREATING CHRONIC  
TITLE OF INVENTION: MYELOGENOUS LEUKEMIA  
NUMBER OF SEQUENCES: 39  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
STREET: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: FastSeq for Windows 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/363,233B  
FILING DATE: December 23, 1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
PRIOR APPLICATION DATA: including application  
PRIOR APPLICATION DATA: described below: 2  
APPLICATION NUMBER: 07/882,822  
FILING DATE: May 14, 1992  
APPLICATION NUMBER: 08/193,922  
FILING DATE: February 7, 1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 209/165  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-363-233B-5

Query Match 83.3%; Score 20; DB 1; Length 20;  
Best Local Similarity 75.0%; Pred. No. 0.0039;  
Matches 15; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGAGUUUCACACACAGGUG 21  
DB 20 GGAGTTTCACACAGGTTG 1

## RESULT 5

US-09-621-976-19145  
; Sequence 19145, Application US/09621976  
; Patent No. 6639063  
; GENERAL INFORMATION:  
; APPLICANT: Dumas Milne Edwards, J.B.  
; APPLICANT: Jobert, S.  
; APPLICANT: Giordano, J.Y.  
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.  
; FILE REFERENCE: GENSET.054PR2  
; CURRENT APPLICATION NUMBER: US/09/621,976  
; CURRENT FILING DATE: 2000-07-21  
; NUMBER OF SEQ ID NOS: 19335  
; SOFTWARE: Patent.pm  
; SEQ ID NO 19145  
; LENGTH: 486  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-621-976-19145

Query Match 62.5%; Score 15; DB 4; Length 486;  
Best Local Similarity 80.0%; Pred. No. 3.7;  
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 9 CACACACGAGUUGU 23

|||||

Db 2 CACACACGAGTTGGT 16

## RESULT 6

US-09-313-294A-3357/C  
; Sequence 3357, Application US/09313294A  
; Patent No. 6476212  
; GENERAL INFORMATION:  
; APPLICANT: Ialugudi, Raghunath V.  
; APPLICANT: Ito, Laura Y.  
; APPLICANT: Sherman, Bradley K.  
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR  
; FILE REFERENCE: PL-0017 US  
; CURRENT APPLICATION NUMBER: US/09/313,294A  
; CURRENT FILING DATE: 1999-05-14  
; NUMBER OF SEQ ID NOS: 7600  
; SOFTWARE: PERL Program  
; SEQ ID NO 3357  
; LENGTH: 264  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; NAME/KEY: misc\_feature  
; OTHER INFORMATION: Incyte ID No. 6476212 700611411H1  
US-09-313-294A-3357

Query Match 58.3%; Score 14; DB 4; Length 264;  
Best Local Similarity 71.4%; Pred. No. 14;  
Matches 10; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 UGGAGUUUCACACA 14

:|||||

Db 48 TGGAGTTTCACACA 35

## RESULT 7

US-09-149-476-90  
; Sequence 90, Application US/09149476  
; Patent No. 6420526  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: 186 Human Secreted proteins  
; FILE REFERENCE: PZ002P1  
; CURRENT APPLICATION NUMBER: US/09/149,476  
; CURRENT FILING DATE: 1998-09-08  
; EARLIER APPLICATION NUMBER: PCT/US98/04493  
; EARLIER FILING DATE: 1998-03-06

; EARLIER APPLICATION NUMBER: 60/040,162  
; EARLIER FILING DATE: 1997-03-07  
; EARLIER APPLICATION NUMBER: 60/040,333  
; EARLIER FILING DATE: 1997-03-07  
; EARLIER APPLICATION NUMBER: 60/038,621  
; EARLIER FILING DATE: 1997-03-07  
; EARLIER APPLICATION NUMBER: 60/040,626  
; EARLIER FILING DATE: 1997-03-07  
; EARLIER APPLICATION NUMBER: 60/040,334  
; EARLIER FILING DATE: 1997-03-07  
; EARLIER APPLICATION NUMBER: 60/040,336  
; EARLIER FILING DATE: 1997-03-07  
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; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,615  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,597  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,502  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,633  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,583  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,617  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,618  
; EARLIER FILING DATE: 1997-05-23  
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; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,592  
; EARLIER FILING DATE: 1997-05-23  
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; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,584  
; EARLIER FILING DATE: 1997-05-23  
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; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,613  
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; EARLIER APPLICATION NUMBER: 60/047,582  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,596  
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; EARLIER APPLICATION NUMBER: 60/047,612  
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; EARLIER FILING DATE: 1997-05-23  
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; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/043,580  
; EARLIER FILING DATE: 1997-04-11  
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; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/043,311  
; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/043,671  
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; EARLIER APPLICATION NUMBER: 60/043,674  
; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/043,669

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EARLIER APPLICATION NUMBER: 60/043,315  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/048,974  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/056,886  
EARLIER FILING DATE: 1997-08-22  
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EARLIER FILING DATE: 1997-08-22  
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EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,903  
EARLIER FILING DATE: 1997-08-22  
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EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,879  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,880  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,894  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,911  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,636  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,874  
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EARLIER APPLICATION NUMBER: 60/056,910  
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EARLIER APPLICATION NUMBER: 60/056,631  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,845  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,892  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/057,761  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/047,595  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,599  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,588  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,585  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,586  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,590  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,594  
EARLIER FILING DATE: 1997-05-23

EARLIER APPLICATION NUMBER: 60/047,589  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,593  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,614  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/043,578  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/043,576  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/047,501  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/043,670  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/056,632  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,664  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,876  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,881  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,909  
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EARLIER APPLICATION NUMBER: 60/056,862  
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EARLIER APPLICATION NUMBER: 60/056,887  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,908  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/048,964  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/057,650  
EARLIER FILING DATE: 1997-09-05  
EARLIER APPLICATION NUMBER: 60/056,884  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/057,669  
EARLIER FILING DATE: 1997-09-05  
EARLIER APPLICATION NUMBER: 60/049,610  
EARLIER FILING DATE: 1997-06-13  
EARLIER APPLICATION NUMBER: 60/061,060  
EARLIER FILING DATE: 1997-10-02

Query Match 58.3%; Score 14; DB 4; Length 1821;  
Best Local Similarity 78.6%; Pred. No. 15;  
Matches 11; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGAGUUUCACAC 15  
Db 181 GGAGUUCACAC 194

RESULT 8  
US-08-253-155A-1/c  
Sequence 1, Application US/08253155A  
Patent No. 5691147  
GENERAL INFORMATION:  
APPLICANT: Gyuris, Jenio  
APPLICANT: Draetta, Giulio  
TITLE OF INVENTION: CDK4 Binding Proteins  
NUMBER OF SEQUENCES: 95  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD  
STREET: 60 State Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible



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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII(text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/253,155A
; FILING DATE: 02-JUN-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: M11-028
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1638 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-253-155A-1

Query Match 54.2%; Score 13; DB 1; Length 1638;
Best Local Similarity 69.2%; Pred. No. 56;
Matches 9; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 UGAGGUUUCACAC 13
Db 464 TGGAGTTTCACAC 452

RESULT 9
US-08-851-567B-29
; Sequence 29, Application US/08851567B
; Patent No. 6528484
; GENERAL INFORMATION:
; APPLICANT: Ensign, Jerald C
; APPLICANT: Bowen, David J
; APPLICANT: Petell, James
; APPLICANT: Fatig, Raymond
; APPLICANT: Schoonover, Sue
; APPLICANT: ffrench-Constant, Richard
; APPLICANT: Rocheleau, Thomas A.
; APPLICANT: Blackburn, Michael B.
; APPLICANT: Hey, Timothy D.
; APPLICANT: Merlo, Donald J.
; APPLICANT: Orr, Gregory L.
; APPLICANT: Roberts, Jean L.
; APPLICANT: Strickland, James A.
; APPLICANT: Guo, Lining
; APPLICANT: Ciche, Todd A.
; TITLE OF INVENTION: Insecticidal Protein Toxins From Photorhabdus
; NUMBER OF SEQUENCES: 88
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dow Agrosciences Patent Department
; STREET: 9330 Zionsville Road
; CITY: Indianapolis
; STATE: IN
; COUNTRY: US
; ZIP: 46268
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/851,567B
; FILING DATE: 05-MAY-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/063,615
; FILING DATE: 18-MAY-1993
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/395,497
; FILING DATE: 28-FEB-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/007,255
; FILING DATE: 06-NOV-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/608,423
; FILING DATE: 28-FEB-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/705,484
; FILING DATE: 28-AUG-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Seay, Nicholas J
; REGISTRATION NUMBER: 27386
; REFERENCE/DOCKET NUMBER: 960296.93804
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 608-251-5000
; TELEFAX: 608-251-9166
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1689 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1689
US-08-851-567B-29

Query Match 54.2%; Score 13; DB 4; Length 1689;
Best Local Similarity 76.9%; Pred. No. 56;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 12 ACACGAGUUGGUC 24
Db 1623 ACACGAGTTGGTC 1635

RESULT 10
US-08-993-088A-8/c
; Sequence 8, Application US/08993088A
; Patent No. 6287855
; GENERAL INFORMATION:
; APPLICANT: Tan, Carina
; APPLICANT: Sullivan, Kathleen
; TITLE OF INVENTION: GALANIN RECEPTOR GALR2 AND
; TITLE OF INVENTION: NUCLEOTIDES ENCODING SAME
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: P.O. Box 2000, 126 E. Lincoln Ave.
; CITY: Rahway
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065-0900
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/993,088A
; FILING DATE: 18-DEC-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/033,851
; FILING DATE: 27-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Heber, Sheldon O.
; REGISTRATION NUMBER: 38,179
; REFERENCE/DOCKET NUMBER: 19846
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TELECOMMUNICATION INFORMATION:  
TELEPHONE: 732-594-1958  
TELEFAX: 732-594-4720  
TELEX:  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2234 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cdna  
US-08-993-088A-8

Query Match 54.2%; Score 13; DB 3; Length 2234;  
Best Local Similarity 84.6%; Pred. No. 57;  
Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 10 ACACACGAGUUGG 22  
|||||:|  
Db 1940 ACACACGAGTGG 1928

RESULT 11  
US-08-993-424B-8/c  
Sequence 8, Application US/08993424B  
Patent No. 6337206  
GENERAL INFORMATION:  
APPLICANT: Tan, Carina  
APPLICANT: Kolakowski, Lee F., Jr.  
TITLE OF INVENTION: MOUSE GALANIN RECEPTOR GALR2 AND  
TITLE OF INVENTION: NUCLEOTIDES ENCODING SAME  
NUMBER OF SEQUENCES: 18  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Merck & Co., Inc.  
STREET: P.O. Box 2000, 126 E. Lincoln Ave.  
CITY: Rahway  
STATE: NJ  
COUNTRY: USA  
ZIP: 07065-0900  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows  
SOFTWARE: FastSeq for Windows Version 2.0b  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/993,424B  
FILING DATE: 18-DEC-1997  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/033,851  
FILING DATE: 27-DEC-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Heber, Sheldon O.  
REGISTRATION NUMBER: 38,179  
REFERENCE/DOCKET NUMBER: 19846NP2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 732-594-1958  
TELEFAX: 732-594-4720  
TELEX:

INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2234 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cdna  
US-08-993-424B-8

Query Match 54.2%; Score 13; DB 4; Length 2234;  
Best Local Similarity 84.6%; Pred. No. 57;  
Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 10 ACACACGAGUUGG 22  
|||||:|

Db 1940 ACACACGAGTGG 1928  
|||||:|

RESULT 12  
US-09-603-680-8/c  
Sequence 8, Application US/09603680  
Patent No. 6544753  
GENERAL INFORMATION:  
APPLICANT: Tan, Carina  
APPLICANT: Sullivan, Kathleen  
TITLE OF INVENTION: GALANIN RECEPTOR GALR2 AND  
TITLE OF INVENTION: NUCLEOTIDES ENCODING SAME  
NUMBER OF SEQUENCES: 20  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Merck & Co., Inc.  
STREET: P.O. Box 2000, 126 E. Lincoln Ave.  
CITY: Rahway  
STATE: NJ  
COUNTRY: USA  
ZIP: 07065-0900  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows  
SOFTWARE: FastSeq for Windows Version 2.0b  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/603,680  
FILING DATE: 26-Jun-2000  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/033,851  
FILING DATE: 27-DEC-1996  
APPLICATION NUMBER: 08/993,088  
FILING DATE: 18-DEC-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Heber, Sheldon O.  
REGISTRATION NUMBER: 38,179  
REFERENCE/DOCKET NUMBER: 19846 CA  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 732-594-1958  
TELEFAX: 732-594-4720  
TELEX:

INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2234 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cdna  
US-09-603-680-8

Query Match 54.2%; Score 13; DB 4; Length 2234;  
Best Local Similarity 84.6%; Pred. No. 57;  
Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 10 ACACACGAGUUGG 22  
|||||:|

RESULT 13  
US-08-036-210-14/c  
Sequence 14, Application US/08036210  
Patent No. 5585233  
GENERAL INFORMATION:  
APPLICANT: Moller, Niels P.H.  
APPLICANT: Moller, Karin B.  
APPLICANT: Ullrich, Axel  
TITLE OF INVENTION: PTP-S31: A NOVEL PROTEIN TYROSINE  
TITLE OF INVENTION: PHOSPHATASE  
NUMBER OF SEQUENCES: 45

Query Match 54.2%; Score 13; DB 4; Length 2234;  
Best Local Similarity 84.6%; Pred. No. 57;  
Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 10 ACACACGAGUUGG 22  
|||||:|

RESULT 13  
US-08-036-210-14/c  
Sequence 14, Application US/08036210  
Patent No. 5585233  
GENERAL INFORMATION:  
APPLICANT: Moller, Niels P.H.  
APPLICANT: Moller, Karin B.  
APPLICANT: Ullrich, Axel  
TITLE OF INVENTION: PTP-S31: A NOVEL PROTEIN TYROSINE  
TITLE OF INVENTION: PHOSPHATASE  
NUMBER OF SEQUENCES: 45

Query Match 54.2%; Score 13; DB 4; Length 2234;  
Best Local Similarity 84.6%; Pred. No. 57;  
Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 10 ACACACGAGUUGG 22  
|||||:|

RESULT 13  
US-08-036-210-14/c  
Sequence 14, Application US/08036210  
Patent No. 5585233  
GENERAL INFORMATION:  
APPLICANT: Moller, Niels P.H.  
APPLICANT: Moller, Karin B.  
APPLICANT: Ullrich, Axel  
TITLE OF INVENTION: PTP-S31: A NOVEL PROTEIN TYROSINE  
TITLE OF INVENTION: PHOSPHATASE  
NUMBER OF SEQUENCES: 45

QY 10 ACACACGAGUUGG 22  
|||||:|

```
;
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/036,210
; FILING DATE: 23-MAR-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mirock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7683-025
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2692 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: unknown
; MOLECULE TYPE: CDNA
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 2149
; OTHER INFORMATION: /note= "N=x=unknown nucleotide"
; US-08-036-210-14
;
; Query Match 54.2%; Score 13; DB 1; Length 2692;
; Best Local Similarity 76.9%; Pred. No. 57;
; Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
;
; QY 2 GGAGUUUCACACA 14
; DB 228 GGAGTTTCACACA 216
;
; RESULT 14
; US-08-449-609-14/c
; Sequence 14, Application US/08449609
; Patent No. 5952212
; GENERAL INFORMATION:
; APPLICANT: Moller, Niels P.H.
; APPLICANT: Moller, Karin B.
; APPLICANT: Ullrich, Axel
; TITLE OF INVENTION: PTP-S31: A NOVEL PROTEIN TYROSINE
; PHOSPHATASE
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/449,609
; FILING DATE: 24-MAY-1995
; CLASSIFICATION: 435
;
; Query Match 54.2%; Score 13; DB 1; Length 2692;
; Best Local Similarity 76.9%; Pred. No. 57;
; Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
;
; QY 2 GGAGUUUCACACA 14
; DB 228 GGAGTTTCACACA 216
;
; RESULT 15
; US-09-361-096A-14/c
; Sequence 14, Application US/09361096A
; Patent No. 6492495
; GENERAL INFORMATION:
; APPLICANT: MOLLER, NIELS P.H.
; APPLICANT: MOLLER, KARIN B.
; APPLICANT: ULLRICH, AXEL
; TITLE OF INVENTION: PTP-S31: A NOVEL PROTEIN TYROSINE PHOSPHATASE
; FILE REFERENCE: 038602/0686
; CURRENT APPLICATION NUMBER: US/09/361,096A
; CURRENT FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: 08/449,609
; PRIOR FILING DATE: 1995-05-24
; PRIOR APPLICATION NUMBER: 08/036,210
; PRIOR FILING DATE: 1995-03-23
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 14
; LENGTH: 2692
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified base
; LOCATION: (1)..(2692)
; OTHER INFORMATION: n = unknown nucleotide
; NAME/KEY: CDS
; LOCATION: (92..139, 259..1414)
; US-09-361-096A-14
;
; Query Match 54.2%; Score 13; DB 4; Length 2692;
; Best Local Similarity 76.9%; Pred. No. 57;
; Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
;
; QY 2 GGAGUUUCACACA 14
; DB 228 GGAGTTTCACACA 216
;
; Search completed: May 27, 2004, 02:25:10
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Job time : 21.2274 secs

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; PRIOR FILING DATE: 2000-08-07  
; NUMBER OF SEQ ID NOS: 9597  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 8117  
; LENGTH: 542  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-796-692-8117

Query Match 100.0%; Score 24; DB 9; Length 542;  
Best Local Similarity 70.8%; Pred. No. 6.2e-05;  
Matches 17; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

Qy 1 UGAGUUUCACACAGAGUUGUC 24  
:||||:|||||:|||||:|||||:  
Db 432 TGGAGTTTCACACAGAGTTGGTC 409

RESULT 6  
US-10-040-862-8117/c  
; Sequence 8117, Application US/10040862  
; Publication No. US20030078396A1  
; GENERAL INFORMATION:  
; APPLICANT: Gaiger, Alexander  
; APPLICANT: Algate, Paul A.  
; APPLICANT: Mannion, Jane  
; APPLICANT: Retter, Marc  
; APPLICANT: Corixa Corporation  
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy  
; FILE REFERENCE: 014058-013520US  
; CURRENT APPLICATION NUMBER: US/10/040,862  
; PRIOR FILING DATE: 2001-11-06  
; PRIOR APPLICATION NUMBER: US 60/186,126  
; PRIOR FILING DATE: 2000-03-01  
; PRIOR APPLICATION NUMBER: US 60/190,479  
; PRIOR FILING DATE: 2000-03-17  
; PRIOR APPLICATION NUMBER: US 60/200,545  
; PRIOR FILING DATE: 2000-04-27  
; PRIOR APPLICATION NUMBER: US 60/200,303  
; PRIOR FILING DATE: 2000-04-28  
; PRIOR APPLICATION NUMBER: US 60/200,779  
; PRIOR FILING DATE: 2000-04-28  
; PRIOR APPLICATION NUMBER: US 60/200,999  
; PRIOR FILING DATE: 2000-05-01  
; PRIOR APPLICATION NUMBER: US 60/202,084  
; PRIOR FILING DATE: 2000-05-04  
; PRIOR APPLICATION NUMBER: US 60/206,201  
; PRIOR FILING DATE: 2000-05-22  
; PRIOR APPLICATION NUMBER: US 60/218,950  
; PRIOR FILING DATE: 2000-07-14  
; PRIOR APPLICATION NUMBER: US 60/222,903  
; PRIOR FILING DATE: 2000-08-03  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 10979  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 8117  
; LENGTH: 542  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-040-862-8117

Query Match 100.0%; Score 24; DB 15; Length 542;  
Best Local Similarity 70.8%; Pred. No. 6.2e-05;  
Matches 17; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

Qy 1 UGAGUUUCACACAGAGUUGUC 24  
:||||:|||||:|||||:|||||:  
Db 432 TGGAGTTTCACACAGAGTTGGTC 409

RESULT 8  
US-10-154-884B-8117/c  
; Sequence 8117, Application US/10154884B  
; Publication No. US20040005561A1  
; GENERAL INFORMATION:  
; APPLICANT: Gaiger, Alexander  
; APPLICANT: Algate, Paul A.  
; APPLICANT: Mannion, Jane  
; APPLICANT: Retter, Marc W.  
; APPLICANT: Corixa Corporation  
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy  
; FILE REFERENCE: 014058-013521US

Db 432 TGGAGTTTCACACAGAGTTGGTC 409

RESULT 7  
US-10-057-475B-8117/c  
; Sequence 8117, Application US/10057475B  
; Publication No. US20040002068A1  
; GENERAL INFORMATION:  
; APPLICANT: Gaiger, Alexander  
; APPLICANT: Algate, Paul A.  
; APPLICANT: Mannion, Jane  
; APPLICANT: Clapper, Jonathan David  
; APPLICANT: Wang, Aijun  
; APPLICANT: Ordonez, Nadia  
; APPLICANT: Carter, Lauren  
; APPLICANT: McNeill, Patricia Dianne  
; APPLICANT: Corixa Corporation  
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy  
; FILE REFERENCE: 014058-014402US  
; CURRENT APPLICATION NUMBER: US/10/057,475B  
; CURRENT FILING DATE: 2002-01-22  
; PRIOR APPLICATION NUMBER: US 60/186,126  
; PRIOR FILING DATE: 2000-03-01  
; PRIOR APPLICATION NUMBER: US 60/190,479  
; PRIOR FILING DATE: 2000-03-17  
; PRIOR APPLICATION NUMBER: US 60/200,545  
; PRIOR FILING DATE: 2000-04-27  
; PRIOR APPLICATION NUMBER: US 60/200,303  
; PRIOR FILING DATE: 2000-04-28  
; PRIOR APPLICATION NUMBER: US 60/200,779  
; PRIOR FILING DATE: 2000-04-28  
; PRIOR APPLICATION NUMBER: US 60/200,999  
; PRIOR FILING DATE: 2000-05-01  
; PRIOR APPLICATION NUMBER: US 60/202,084  
; PRIOR FILING DATE: 2000-05-04  
; PRIOR APPLICATION NUMBER: US 60/206,201  
; PRIOR FILING DATE: 2000-05-22  
; PRIOR APPLICATION NUMBER: US 60/218,950  
; PRIOR FILING DATE: 2000-07-14  
; PRIOR APPLICATION NUMBER: US 60/222,903  
; PRIOR FILING DATE: 2000-08-03  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 10979  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 8117  
; LENGTH: 542  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-057-475B-8117

Query Match 100.0%; Score 24; DB 16; Length 542;  
Best Local Similarity 70.8%; Pred. No. 6.2e-05;  
Matches 17; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

Qy 1 UGAGUUUCACACAGAGUUGUC 24  
:||||:|||||:|||||:|||||:  
Db 432 TGGAGTTTCACACAGAGTTGGTC 409

RESULT 8  
US-10-154-884B-8117/c  
; Sequence 8117, Application US/10154884B  
; Publication No. US20040005561A1  
; GENERAL INFORMATION:  
; APPLICANT: Gaiger, Alexander  
; APPLICANT: Algate, Paul A.  
; APPLICANT: Mannion, Jane  
; APPLICANT: Retter, Marc W.  
; APPLICANT: Corixa Corporation  
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy  
; FILE REFERENCE: 014058-013521US

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; CURRENT APPLICATION NUMBER: US/10/154,884B
; CURRENT FILING DATE: 2002-05-23
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 11290
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8117
; LENGTH: 542
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-154-884B-8117

Query Match      100.0%; Score 24; DB 16; Length 542;
Best Local Similarity 70.8%; Pred.No. 6.2e-05;
Matches 17; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY      1 UGGAGUUUCACACACGAGUUGUC 24
       :||||:|||||:||||:|
Db      432 TGGAGTTTCACACACGAGTTGGTC 409

RESULT 9
US-09-796-692-8967/c
; Sequence 8967, Application US/09796692
; Publication No. US20020198362A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY
; TITLE OF INVENTION: HEMATOLOGICAL MALIGNANCIES
; FILE REFERENCE: 2077.001200
; CURRENT APPLICATION NUMBER: US/09/796,692
; CURRENT FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/222,903
; PRIOR FILING DATE: 2000-08-03
; US-09-796-692-8967

; PRIOR APPLICATION NUMBER: 60/223,416
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: 60/223,378
; PRIOR FILING DATE: 2000-08-07
; NUMBER OF SEQ ID NOS: 9597
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8967
; LENGTH: 596
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (13)
; OTHER INFORMATION: n=A,T,C or G
; NAME/KEY: unsure
; LOCATION: (47)
; OTHER INFORMATION: n=A,T,C or G
; NAME/KEY: unsure
; LOCATION: (49)
; OTHER INFORMATION: n=A,T,C or G
; NAME/KEY: unsure
; LOCATION: (56)
; OTHER INFORMATION: n=A,T,C or G
; NAME/KEY: unsure
; LOCATION: (63)
; OTHER INFORMATION: n=A,T,C or G
; NAME/KEY: unsure
; LOCATION: (81)
; OTHER INFORMATION: n=A,T,C or G
; NAME/KEY: unsure
; LOCATION: (155)
; OTHER INFORMATION: n=A,T,C or G
; NAME/KEY: unsure
; LOCATION: (196)
; OTHER INFORMATION: n=A,T,C or G
; NAME/KEY: unsure
; LOCATION: (211)
; OTHER INFORMATION: n=A,T,C or G
; NAME/KEY: unsure
; LOCATION: (267)
; OTHER INFORMATION: n=A,T,C or G
; NAME/KEY: unsure
; LOCATION: (281)
; OTHER INFORMATION: n=A,T,C or G
; NAME/KEY: unsure
; LOCATION: (282)
; OTHER INFORMATION: n=A,T,C or G
; NAME/KEY: unsure
; LOCATION: (332)
; OTHER INFORMATION: n=A,T,C or G
; NAME/KEY: unsure
; LOCATION: (372)
; OTHER INFORMATION: n=A,T,C or G
; NAME/KEY: unsure
; LOCATION: (520)
; OTHER INFORMATION: n=A,T,C or G
; NAME/KEY: unsure
; LOCATION: (521)
; OTHER INFORMATION: n=A,T,C or G
; NAME/KEY: unsure
; LOCATION: (551)
; OTHER INFORMATION: n=A,T,C or G
; NAME/KEY: unsure
; LOCATION: (579)
; OTHER INFORMATION: n=A,T,C or G
; NAME/KEY: unsure
; LOCATION: (585)
; OTHER INFORMATION: n=A,T,C or G
; NAME/KEY: unsure
; LOCATION: (586)
; OTHER INFORMATION: n=A,T,C or G
; US-09-796-692-8967
```



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Query Match      100.0%; Score 24; DB 9; Length 596;
Best Local Similarity 70.8%; Pred. No. 6.2e-05;
Matches 17; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 UGGAGUUUCACACACGAGUUGUC 24
    :||||:|||||:|||||:|||||:
Db 432 TGGAGTTTCACACGAGTTGGTC 409

RESULT 10
US-10-040-862-8967/c
; Sequence 8967, Application US/10040862
; Publication No. US20030078396A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; TITLE OF INVENTION: Hematological Malignancies
; FILE REFERENCE: 014058-013520US
; CURRENT APPLICATION NUMBER: US/10/040,862
; CURRENT FILING DATE: 2001-11-06
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: US 60/223,416
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: US 60/223,378
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: US 09/796,692
; PRIOR FILING DATE: 2001-03-01
; NUMBER OF SEQ ID NOS: 10467
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8967
; LENGTH: 596
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (13)
; OTHER INFORMATION: n=A,T,C or G
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (47)
; OTHER INFORMATION: n=A,T,C or G
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (49)
; OTHER INFORMATION: n=A,T,C or G
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (58)
; OTHER INFORMATION: n=A,T,C or G
; FEATURE:

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; NAME/KEY: unsure
; LOCATION: (63)
; OTHER INFORMATION: n=A,T,C or G
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (81)
; OTHER INFORMATION: n=A,T,C or G
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (155)
; OTHER INFORMATION: n=A,T,C or G
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (196)
; OTHER INFORMATION: n=A,T,C or G
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (211)
; OTHER INFORMATION: n=A,T,C or G
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (267)
; OTHER INFORMATION: n=A,T,C or G
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (281)
; OTHER INFORMATION: n=A,T,C or G
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (282)
; OTHER INFORMATION: n=A,T,C or G
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (332)
; OTHER INFORMATION: n=A,T,C or G
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (372)
; OTHER INFORMATION: n=A,T,C or G
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (520)
; OTHER INFORMATION: n=A,T,C or G
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (521)
; OTHER INFORMATION: n=A,T,C or G
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (551)
; OTHER INFORMATION: n=A,T,C or G
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (579)
; OTHER INFORMATION: n=A,T,C or G
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (585)
; OTHER INFORMATION: n=A,T,C or G
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (586)
; OTHER INFORMATION: n=A,T,C or G
; FEATURE:
US-10-040-862-8967

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Query Match      100.0%; Score 24; DB 15; Length 596;
Best Local Similarity 70.8%; Pred. No. 6.2e-05;
Matches 17; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 UGGAGUUUCACACACGAGUUGUC 24
    :||||:|||||:|||||:|||||:
Db 432 TGGAGTTTCACACGAGTTGGTC 409

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RESULT 11
US-10-057-475B-8967/c
; Sequence 8967, Application US/10057475B
; Publication No. US20040002068A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Clapper, Jonathan David
; APPLICANT: Wang, Aijun
; APPLICANT: Ordonez, Nadia
; APPLICANT: Carter, Lauren
; APPLICANT: McNeill, Patricia Dianne
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; TITLE OF INVENTION: Hematological Malignancies
; FILE REFERENCE: 014058-014402US
; CURRENT APPLICATION NUMBER: US/10/057,475B
; CURRENT FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 10979
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8967
; LENGTH: 596
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(596)
; OTHER INFORMATION: n = g, a, c or t
US-10-057-475B-8967
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; TITLE OF INVENTION: Hematological Malignancies
; FILE REFERENCE: 014058-014402US
; CURRENT APPLICATION NUMBER: US/10/057,475B
; CURRENT FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 10979
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8967
; LENGTH: 596
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(596)
; OTHER INFORMATION: n = g, a, c or t
US-10-057-475B-8967
Query Match 100.0%; Score 24; DB 16; Length 596;
Best Local Similarity 70.8%; Pred. No. 6.2e-05;
Matches 17; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 UGAGUUUACACACGAGUUGUC 24
:||||:|||||:|||||:|||||:
Db 432 TGGAGTTTCACACGAGTTGGTC 409

RESULT 12
US-10-154-884B-8967/c
; Sequence 8967, Application US/10154884B
; Publication No. US20040005561A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc W.
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; TITLE OF INVENTION: Hematological Malignancies
; FILE REFERENCE: 014058-014402US
; CURRENT APPLICATION NUMBER: US/10/057,475B
; CURRENT FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 10979
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8967
; LENGTH: 596
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(596)
; OTHER INFORMATION: n = g, a, c or t
US-10-057-475B-8967
Query Match 100.0%; Score 24; DB 16; Length 596;
Best Local Similarity 70.8%; Pred. No. 6.2e-05;
Matches 17; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 UGAGUUUACACACGAGUUGUC 24
:||||:|||||:|||||:|||||:
Db 432 TGGAGTTTCACACGAGTTGGTC 409

RESULT 13
US-10-228-811-1/c
; Sequence 1, Application US/10228811
; Publication No. US20030054392A1
; GENERAL INFORMATION:
; APPLICANT: Wittig, Prof. Burghardt
; APPLICANT: Junghans, Claas
; TITLE OF INVENTION: Design Principle for Constructing Expression Constructs for Gene
; TITLE OF INVENTION: Therapy
; FILE REFERENCE: XI 597/99
; CURRENT APPLICATION NUMBER: US/10/228,811
; CURRENT FILING DATE: 2002-08-27
; PRIOR APPLICATION NUMBER: DE 196 48 625.4
; PRIOR FILING DATE: 1996-11-13
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1078
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: gene
; LOCATION: (1)..(1078)
; OTHER INFORMATION: bcr3=abl2; Oligo DNA Dumbbell
; FEATURE:
; NAME/KEY: misc binding
; LOCATION: (1)..(2)

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; TITLE OF INVENTION: Hematological Malignancies
; FILE REFERENCE: 014058-013521US
; CURRENT APPLICATION NUMBER: US/10/154,884B
; CURRENT FILING DATE: 2002-05-23
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 11290
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8967
; LENGTH: 596
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(596)
; OTHER INFORMATION: n = g, a, c or t
US-10-154-884B-8967
Query Match 100.0%; Score 24; DB 16; Length 596;
Best Local Similarity 70.8%; Pred. No. 6.2e-05;
Matches 17; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 UGAGUUUACACACGAGUUGUC 24
:||||:|||||:|||||:|||||:
Db 432 TGGAGTTTCACACGAGTTGGTC 409

RESULT 13
US-10-228-811-1/c
; Sequence 1, Application US/10228811
; Publication No. US20030054392A1
; GENERAL INFORMATION:
; APPLICANT: Wittig, Prof. Burghardt
; APPLICANT: Junghans, Claas
; TITLE OF INVENTION: Design Principle for Constructing Expression Constructs for Gene
; TITLE OF INVENTION: Therapy
; FILE REFERENCE: XI 597/99
; CURRENT APPLICATION NUMBER: US/10/228,811
; CURRENT FILING DATE: 2002-08-27
; PRIOR APPLICATION NUMBER: DE 196 48 625.4
; PRIOR FILING DATE: 1996-11-13
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1078
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: gene
; LOCATION: (1)..(1078)
; OTHER INFORMATION: bcr3=abl2; Oligo DNA Dumbbell
; FEATURE:
; NAME/KEY: misc binding
; LOCATION: (1)..(2)

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; OTHER INFORMATION: intramolecular binding site; the T-nucleotides at position 1 to  
; OTHER INFORMATION: 2 can be modified with amino or caroxy features  
; FEATURE:  
; NAME/KEY: misc.binding  
; LOCATION: (1077)..(1078)  
; OTHER INFORMATION: intramolecular binding site; the T-nucleotides at position 1077  
; OTHER INFORMATION: to 1078 can be modified with amino or caroxy features  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Strandness: both; nucleic  
; OTHER INFORMATION: acid (linear), hypothetical: No. US20030054392A1 anti-sense: No  
US-10-228-811-1

Query Match 100.0%; Score 24; DB 15; Length 1078;  
Best Local Similarity 70.8%; Pred. No. 6.1e-05;  
Matches 17; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 UGGAGUUUCACACACGAGUUGGUC 24  
:||||:|||||:|||||:|||||:|||||:  
Db 661 TGGAGTTTCACACGAGTTGGTC 638

## RESULT 14

US-09-954-531-586/c  
; Sequence 586, Application US/09954531  
; Patent No. US20020165180A1  
; GENERAL INFORMATION:  
; APPLICANT: Weaver, Zoe  
; TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Cand  
; FILE REFERENCE: 689290-77  
; CURRENT APPLICATION NUMBER: US/09/954,531  
; CURRENT FILING DATE: 2002-05-02  
; PRIOR APPLICATION NUMBER: US/60/233,133  
; PRIOR FILING DATE: 2000-09-18  
; PRIOR APPLICATION NUMBER: US/60/234,009  
; PRIOR FILING DATE: 2000-09-20  
; PRIOR APPLICATION NUMBER: US/60/234,034  
; PRIOR FILING DATE: 2000-09-20  
; PRIOR APPLICATION NUMBER: US/60/234,509  
; PRIOR FILING DATE: 2000-09-22  
; PRIOR APPLICATION NUMBER: US/60/234,567  
; PRIOR FILING DATE: 2000-09-22  
; NUMBER OF SEQ ID NOS: 1392  
; SOFTWARE: Patent in version 3.0  
; SEQ ID NO 586  
; LENGTH: 4739  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-954-531-586

Query Match 100.0%; Score 24; DB 9; Length 4739;  
Best Local Similarity 70.8%; Pred. No. 5.9e-05;  
Matches 17; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 UGGAGUUUCACACGAGUUGGUC 24  
:||||:|||||:|||||:|||||:|||||:  
Db 3157 TGGAGTTTCACACGAGTTGGTC 3134

## RESULT 15

US-10-193-651-22/c  
; Sequence 22, Application US/10193651  
; Publication No. US20030064061A1  
; GENERAL INFORMATION:  
; APPLICANT: Zhao, Xun  
; APPLICANT: Ghaffari, Saghi  
; APPLICANT: Lodish, Harvey F.  
; APPLICANT: Malashkevich, Vladimir N.  
; APPLICANT: Kim, Peter S.  
; TITLE OF INVENTION: Bcr-Abl Oligomerization Domain  
; TITLE OF INVENTION: Polypeptides and Uses Therefor  
; FILE REFERENCE: 0399.2031-001  
; CURRENT APPLICATION NUMBER: US/10/193,651

; CURRENT FILING DATE: 2002-11-19  
; PRIOR APPLICATION NUMBER: US 60/303,857  
; PRIOR FILING DATE: 2001-07-09  
; NUMBER OF SEQ ID NOS: 22  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 22  
; LENGTH: 4739  
; TYPE: DNA  
; ORGANISM: Homo Sapiens  
; FEATURE:  
; OTHER INFORMATION: Bcr nucleic acid  
US-10-193-651-22

Query Match 100.0%; Score 24; DB 13; Length 4739;  
Best Local Similarity 70.8%; Pred. No. 5.9e-05;  
Matches 17; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 UGGAGUUUCACACGAGUUGGUC 24  
:||||:|||||:|||||:|||||:|||||:  
Db 3157 TGGAGTTTCACACGAGTTGGTC 3134

Search completed: May 27, 2004, 14:58:26  
Job time : 126.301 secs

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: May 26, 2004, 15:22:41 ; Search time 847.385 Seconds  
(without alignments)  
845.770 Million cell updates/sec

Title: US-09-121-239-8  
Perfect score: 24  
Sequence: 1 UGAGUUUACACACAGUUGUC 24

Scoring table: OLIGO\_NUC  
Gapop\_60.0 , Gapext 60.0

Searched: 27513289 seqs, 14931090276 residues

Word size : 0

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

EST:

1: em\_estba.\*

2: em\_esthum.\*

3: em\_estin.\*

4: em\_estmu.\*

5: em\_estov.\*

6: em\_estpl.\*

7: em\_estro.\*

8: em\_estc.\*

9: gb\_est1.\*

10: gb\_est2.\*

11: gb\_est3.\*

12: gb\_est4.\*

13: gb\_est5.\*

14: gb\_est6.\*

15: em\_estfun.\*

16: em\_estom.\*

17: em\_gss\_hum.\*

18: em\_gss\_inv.\*

19: em\_gss\_pin.\*

20: em\_gss\_vrt.\*

21: em\_gss\_fun.\*

22: em\_gss\_mam.\*

23: em\_gss\_mus.\*

24: em\_gss\_pro.\*

25: em\_gss\_rod.\*

26: em\_gss\_phg.\*

27: em\_gss\_vrl.\*

28: gb\_gss1.\*

29: gb\_gss2.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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C 2	24	100.0	314	14	D79153 HUM532H11B
C 3	24	100.0	377	10	BF800308 CM4-C1006
C 4	24	100.0	401	14	RS4267 y974h05.r1

#### ALIGNMENTS

RESULT 1  
H55545/c  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
MEDLINE  
PUBMED  
COMMENT

H55545  
CHR220484 Chromosome 22 exon Homo sapiens cDNA clone C22\_652 5',  
mRNA sequence.  
H55545  
H55545.1 GI:1108411  
EST.  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 181)  
Trotter, J.A., Long, K.R., Murrell, J.R., Stotler, C.J., Gusella, J.F.  
and Buckler, A.J.  
An expression-independent catalog of genes from human chromosome 22  
Genome Res. 5 (3), 214-224 (1995)  
96159527  
8593609  
Contact: Buckler AJ  
Molecular Neurogenetics Unit  
Massachusetts General Hospital  
Building 149, 13th St., Charlestown MA 02129  
Tel: 6177249616  
Fax: 6177265736  
Email: buckler@helix.mgh.harvard.edu  
Seq primer: T3.

C 5 24 100.0 417 9. A1126116  
6 24 100.0 437 10 BF873838  
7 24 100.0 438 10 BE938059  
C 8 24 100.0 443 10 AW452440  
9 24 100.0 531 12 BG927169  
10 24 100.0 588 10 BF380221  
C 11 24 100.0 588 10 BF094682  
C 12 24 100.0 597 10 BE396942  
C 13 24 100.0 599 9 A1132798  
C 14 24 100.0 605 10 AW961897  
C 15 24 100.0 621 10 BE267891  
C 16 24 100.0 637 14 CB267185  
C 17 24 100.0 642 10 BE019411  
C 18 24 100.0 653 12 BG829045  
C 19 24 100.0 665 10 BE514596  
C 20 24 100.0 684 10 BF530440  
C 21 24 100.0 686 10 BF397010  
C 22 24 100.0 712 10 BE397695  
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C 24 24 100.0 741 10 BE265121  
C 25 24 100.0 750 10 BE513994  
C 26 24 100.0 770 12 B1226004  
C 27 24 100.0 785 12 BG393462  
C 28 24 100.0 813 12 BM050194  
C 29 24 100.0 819 14 CF242964  
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C 32 24 100.0 875 10 BF241073  
C 33 24 100.0 878 10 BF338795  
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C 38 24 100.0 903 13 BQ41890  
C 39 24 100.0 918 13 BQ212925  
C 40 24 100.0 936 13 BX350695  
C 41 24 100.0 955 13 BQ945725  
C 42 24 100.0 975 12 BG392048  
C 43 24 100.0 1021 13 BQ896733  
C 44 19 79.2 544 10 BF901573  
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BE938059 MRI-TN004  
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BF380221 MR3-UT005  
BF094682 MR3-UT005  
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AW961897 EST373970  
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BE019411 bb55b12.y  
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BM050194 603632267  
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CD652568 AGENCOURT  
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AG178980 Pan trogl

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FEATURES
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      /clone_lib="Chromosome 22 exon"
      /note="Vector: pBluescriptIIKS+; Site 1: Sal I; Site 2: Bam HI (destroyed); Exons were isolated from human chromosome 22 specific cosmids using a modification of the method of exon amplification (Proc. Natl. Acad. Sci. USA 88:4005-4009, 1991). Amplified exons were digested with Sal I and Bgl II and subsequently cloned into pBluescriptIIKS+ at the Sal I and Bam HI sites."

ORIGIN
Query Match      100.0%; Score 24; DB 14; Length 181;
Best Local Similarity 70.8%; Pred. No. 0.0007;
Matches 17; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 UGGAGUUUCACACACGAGUUGUC 24
   :||||:|||||:|||||:|||||:
Db 143 TGGAGTTTCACACGAGTTGTC 120

RESULT 2
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LOCUS
DEFINITION
HUM532H11B Human placenta polyA+ (TFujiwara) Homo sapiens cDNA
clone GEN-532H11 5', mRNA sequence.
ACCESSION
D79153
VERSION
D79153.1 GI:1181026
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 314)
AUTHORS
Fujiwara, T., Hirano, H., Katagiri, T., Kawai, A., Kuga, Y., Nagata, M., Okuno, S., Ozaki, K., Shimizu, F., Shimada, Y., Shinomiya, H., Takaichi, A., Takeda, S., Watanabe, T., Takahashi, E., Hirai, Y., Maekawa, H., Shin, S. and Nakamura, Y.
TITLE
Fujiwara et al. (1995)
JOURNAL
Unpublished (1995)
COMMENT
Contact: Tsutomu Fujiwara
Otsuka GEN Research Institute
Otsuka Pharmaceutical Co., Ltd
463-10 Kagasuno Kawauchi-cho, Tokushima, Tokushima, 771-01 Japan
Tel: 0886-65-2888
Fax: 0886-37-1035.

FEATURES
source
  Location/Qualifiers
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      /db_xref="taxon:9606"
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      /tissue_type="placenta"
      /clone_lib="Human placenta polyA+ (TFujiwara)"

ORIGIN
Query Match      100.0%; Score 24; DB 14; Length 314;
Best Local Similarity 70.8%; Pred. No. 0.00079;
Matches 17; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 UGGAGUUUCACACACGAGUUGUC 24
   :||||:|||||:|||||:|||||:
Db 52 TGGAGTTTCACACGAGTTGTC 29

RESULT 3
BF800308/c
LOCUS
DEFINITION
CM4-CI0062-181000-370-b10 CI0062 Homo sapiens cDNA, mRNA sequence.
ACCESSION
BF800308
VERSION
BF800308.1 GI:12129297
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 377)
AUTHORS
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
TITLE
Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
JOURNAL
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE
20202663
PUBMED
10737800
COMMENT
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CM4&t2=CM4-CI0062-181000-370-b10&t3=2000-10-18&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 18
High quality sequence stop: 377.

FEATURES
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      /clone_lib="CI0062"
      /note="Organ: colon ins; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN
Query Match      100.0%; Score 24; DB 10; Length 377;
Best Local Similarity 70.8%; Pred. No. 0.00083;
Matches 17; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 UGGAGUUUCACACACGAGUUGUC 24
   :||||:|||||:|||||:|||||:
Db 249 TGGAGTTTCACACGAGTTGTC 226

RESULT 4
R54267/c
LOCUS
DEFINITION
Y974h05.r1 Soares infant brain IN1B Homo sapiens cDNA clone IMAGE:39270 5', similar to gb:U01147 BREAKPOINT CLUSTER REGION PROTEIN (HUMAN); mRNA sequence.
ACCESSION
R54267
VERSION
R54267.1 GI:816169
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

```



Email: asimpson@ludwig.org.br  
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL  
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=IL3&t2=IL3-FT0114-071100-338-C02&t3=2000-11-07&t4=1)  
Seq primer: puc 18 forward  
High quality sequence stop: 390.

FEATURES

source  
1. .437  
Location/Qualifiers

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/dev\_stage="Adult"  
/clone\_lib="FT0114"  
/note="Organ: lung tumor; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN

Query Match 100.0%; Score 24; DB 10; Length 437;  
Best Local Similarity 70.8%; Pred. No. 0.00085;  
Matches 17; Conservative 7; Mismatches 0; Indels 0; Gaps 0;  
QY 1 UGGAGUUUCCACACGAGUUGUC 24  
:||||:|||||:|||||:|||||:  
Db 319 TGGAGTTTCACACGAGTTGTC 342

RESULT 7

BE938059  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
COMMENT  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 438)  
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.  
Shotgun sequencing of the human transcriptome with ORF expressed sequence tags  
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
20202663  
10737800  
Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: asimpson@ludwig.org.br  
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL  
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=IL3&t2=MR1-TN0045-290  
800-003-e03&t3=2000-08-29&t4=1)  
Seq primer: puc 18 forward  
High quality sequence stop: 297.

FEATURES

source  
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Location/Qualifiers

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/dev\_stage="Adult"  
/clone\_lib="TN0045"  
/note="Organ: testis normal; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN

Query Match 100.0%; Score 24; DB 10; Length 438;  
Best Local Similarity 70.8%; Pred. No. 0.00086;  
Matches 17; Conservative 7; Mismatches 0; Indels 0; Gaps 0;  
QY 1 UGGAGUUUCCACACGAGUUGUC 24  
:||||:|||||:|||||:|||||:  
Db 145 TGGAGTTTCACACGAGTTGTC 168

RESULT 8

AW452440/c  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 443)  
NCI-CCGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapps@mail.nih.gov  
Oligo-dr track not found, Not I site shown in beginning of sequence is likely internal to the message. cDNA Library Preparation: M.B. Soares Lab Clone distribution: NCI-CCGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www.bio.llnl.gov/bbrp/image/image.html The following repetitive elements were found in this cDNA sequence: 147-207, >HSR1T  
Seq primer: M13 Forward  
POLYA=No.

FEATURES

source

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/clone\_lib="NCI CCGAP Subs"  
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; NCI CCGAP Subs is a subtracted library derived from NCI\_CGAP\_Sub4. The NCI\_CGAP\_Sub5 library had 3 million recombinants. A single-stranded DNA preparation of NCI\_CGAP\_Sub4 was used as a tracer in a subtractive hybridization with a driver comprising: the IMAGE pool (NCI\_CGAP\_kid3 pool 1 LLAM 3334-3337, 3682-3693, 3798-3803 (IMAGE CloneIDs 1322376-1323911, 1456008-1456775, 1500552-1502855); NCI\_CGAP\_kid3 pool 1 LLAM 3338-3342, 3722-3725, 3776-3778 (IMAGE CloneIDs 1323912-1325831, 1471368-1472903, 1492104-1493255); NCI\_CGAP\_Lu5 pool 1 LLAM 3575-3582, 3851-3854 (IMAGE CloneIDs 1414920-1417991, 1520904-1522439); NCI\_CGAP\_GC4 pool 1 LLAM 3164-3167, 3716-3720, 3733-3735 (IMAGE CloneIDs 1257096-1258631, 1469064-1470983, 1475592-1476743); NCI\_CGAP\_Pr22 pool 1 LLAM 2457-2459, 2758-2759, 3062-3068



(IMAGE CloneIds 985608-986759,1101192-1101959,  
1219788-1220615); NCI CGAP\_Colo pool 1 LUAM 2644-2653,  
2871-2872 (IMAGE CGAPs  
1057416-1061255,1144594-1145351). (10% of the driver  
population), plus a pool of 3,840 arrayed clones from  
NCI CGAP Sub1 (IMAGE CloneIds 2708616-2710535) and  
NCI CGAP Sub2 (IMAGE CloneIds 2710536-2712455) (10% of  
the driver population), plus a pool of 11,136 clones from  
NCI CGAP Sub3 (IMAGE CloneIds 2712456-2723391) (10% of the  
driver population), plus a pool of 5,472 clones from  
NCI CGAP Sub4 (IMAGE CloneIds 2723592-2728969) (70% of the  
driver population). Subtraction was performed as  
previously described [Bonaldo, Lennon & Soares (1996):  
Normalization and Subtraction: Two Approaches To  
Facilitate Gene Discovery. Genome Research 6, 791-806.  
TAG TISSUE=germ cell  
TAG LIB=NCI CGAP  
TAG\_SEQ=AAATCC"

## ORIGIN

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Query Match      100.0%;   Score 24;   DB 10;   Length 443;
Best Local Similarity 70.8%;   Pred. NO. 0.00086;
Matches 17; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

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Db      355  TGGAGTTTCAACACGAGTTGGTC 332

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RESULT 9	531 bp	linear	EST 06-NOV-2001
BG927169/c		mRNA	
LOCUS			
DEFINITION	HNC18-1-D3.R HNC (Human Normal Cartilage) Homo sapiens cDNA, mRNA		
ACCESSION	BG927169		
VERSION	BG927169.1		
KEYWORDS	GI:14321692		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
REFERENCE	1 (bases 1 to 531)		
AUTHORS	Kumar, S., Connor, J.R., Dodds, R.A., Halsey, W., Van Horn, M., Mao, J., Sathe, G., Mui, P., Agarwal, P., Badger, A.M., Lee, J.C., Gowen, M. and Lark, M.W.		

TITLE	Identification and initial characterization of 5000 expressed sequenced tags (ESTs) each from adult human normal and osteoarthritic cartilage cDNA libraries
JOURNAL	Osteoarthritis Cartil. 9 (7), 641-653 (2001)
MEDLINE	21482651
PUBMED	11597177
COMMENT	Contact: Sanjay Kumar UW2109 Glaxosmithkline 709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA Tel: 610-270-7245 Fax: 610-270-5598 Email: sanjay.kumar-l@gsk.com Seq primer: 77

## FEATURES

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Directional"

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## ORIGIN

Query Match	100.0%;	Score 24;	DB 12;	Length 531;
Best Local Similarity	70.8%;	Pred. No. 0.00089;		

Matches	17;	Conservative	7;	Mismatches	0;	Indels	0;	Gaps	0;
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Db 438 TGGAGTTTCACACAGATTGGTC 415

RESULT 10  
BF380221/c  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

BF380221 588 bp mRNA linear EST 27-NOV-2000  
MR3-UT0050-250900-003-g03 UT0050 Homo sapiens cDNA, mRNA sequence.  
BF380221  
BF380221.1 GI:11369346  
EST.  
Homo sapiens (human)  
Homo sapiens  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (base 1 to 588)  
REFERENCE

## REFERENCE

TITLE	ADDITIONAL AUTHORS
Shotgun sequencing of the human transcriptome with ORF expressed sequence tags	Wang, M., et al.
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)	Wang, M., et al.
20202663	Wang, M., et al.
PUBMED	Wang, M., et al.
10737800	Wang, M., et al.
COMMENT	Wang, M., et al.

10737800	<p>Contact: Simpson A.J.G.  Laboratory of Cancer Genetics  Ludwig Institute for Cancer Research  Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil  Tel: +55-11-2704922  Fax: +55-11-2707001  Email: asimpson@ludwig.org.br</p> <p>This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL  (<a href="http://www.ludwig.org.br/scripts/gethtml2.pl?t1=MR3&amp;t2=MR3-UT0050-250900-003-q03&amp;t3=2000-09-25&amp;t4=1">http://www.ludwig.org.br/scripts/gethtml2.pl?t1=MR3&amp;t2=MR3-UT0050-250900-003-q03&amp;t3=2000-09-25&amp;t4=1</a>)</p>
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**FEATURES**  
**source**

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/notes="Organ: uterus; tumor; Vector: puc18; Site_1: SmaI;
Site_2: SmaI; A mini-library was made by cloning products
derived from OPSTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
source

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## ORIGIN

Query Match	100.0%;	Score 24;	DB 10;	Length 588;
Best Local Similarity	70.8%;	Pred. No. 0.00092;		
Matches 17;	Conservative	7;	Mismatches 0;	Indels 0;
Gaps 0;				

QY  
D6  
Db

1 UGGAGUUUCACACACGAGUUGGUC 24  
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.452 TGGAGTTTCACACACGAGTTGGTC 429

## RESULT 11

LOCUS	BF094682	588 bp	mRNA	linear	EST 19-OCT-2000
DEFINITION	MR3-UT0050-130900-003-g03	UT0050	Homo sapiens	cDNA, mRNA sequence.	

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ACCESSION      BF094682
VERSION        BF094682.1  GI:109003392
KEYWORDS
SOURCE         Homo sapiens (human)
ORGANISM       Homo sapiens
REFERENCE      1 (bases 1 to 588)
AUTHORS        Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
TITLE          Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
JOURNAL        Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE        20202663
PUBMED         10737800
COMMENT        Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=MR3-UT0050-130
900-003-g03&t3=2000-09-13&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 586.
FEATURES       source
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                insert size 1.8kb. Library constructed by Ling Hong in
                the laboratory of Gerald M. Rubin (University of
                California, Berkeley) using ZAP-cDNA synthesis kit
                (Stratagene) and Superscript II RT (Life Technologies)."
```

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JOURNAL        Unpublished (1999)
COMMENT        Contact: Robert Strausberg, Ph.D.
Email: cgabbs@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arranged by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
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                cloned into EcoRI/XhoI sites using the following 5'
                adaptor: GGCACGAG(G). Size-selected >500bp for average
                insert size 1.8kb. Library constructed by Ling Hong in
                the laboratory of Gerald M. Rubin (University of
                California, Berkeley) using ZAP-cDNA synthesis kit
                (Stratagene) and Superscript II RT (Life Technologies)."
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Query Match    100.0%; Score 24; DB 10; Length 597;
Best Local Similarity 70.8%; Pred. No. 0.00092;
Matches 17; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

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RESULT 13
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LOCUS          AUI32798 NT2RP4 Homo sapiens cDNA clone NT2RP4000561 5', mRNA
DEFINITION     sequence.
ACCESSION      AUI32798
VERSION        AUI32798.1  GI:10993337
KEYWORDS       EST.
SOURCE         Homo sapiens (human)
ORGANISM       Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 599)
AUTHORS        Ota,T., Sugiyama,T., Ishii,S., Suzuki,Y., Saito,K., Yamamoto,J.,
Nishikawa,T., Nakamura,Y., Nagai,T., Sugano,S., Masuho,Y. and
Isogai,T.
TITLE          HRI human cDNA project (Ota,T., Sugiyama,T., Ishii,S., Suzuki,Y.,
Saito,K., Yamamoto,J., Nishikawa,T., Nakamura,Y., Nagai,T.,
Sugano,S., Masuho,Y., Isogai,T.)
JOURNAL        Unpublished (2000)
COMMENT        Contact: Takao Isogai
Genomics Laboratory
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3986
Email: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
FEATURES       source
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Db 452 TGGAGTTTCACACACGAGTTGGTC 429

RESULT 12
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LOCUS          BE396942 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3621156 5',
DEFINITION     mRNA sequence.
ACCESSION      BE396942
VERSION        BE396942.1  GI:9342307
KEYWORDS       EST.
SOURCE         Homo sapiens (human)
ORGANISM       Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 597)
AUTHORS        NIH-MGC http://mgc.nci.nih.gov/
TITLE          National Institutes of Health, Mammalian Gene Collection (MGC)
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Matches 17; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

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Db 406 TGGAGTTTCACACGAGTTGGTC 383

RESULT 14
AW961897/C
LOCUS      605 bp mRNA linear EST 01-JUN-2000
DEFINITION EST373970 MAGE resequencences, MAGG Homo sapiens cDNA, mRNA sequence.
ACCESSION  AW961897
VERSION     AW961897.1 GI:8151583
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 605)
AUTHORS   Hegde,P., Qi,R., Abernathy,K., Dharap,S., Gaspard,R., Gay,C.,
          Holt,I.E., Saeed,A.I., Sharov,V., Lee,N.H., Yeatman,T.J. and
          Quackenbush,J.
          Assessment of gene expression patterns in a model of colon tumor
          metastasis using a 19,200 element cDNA microarray
          Unpublished (2000)
          Contact: John Quackenbush
          The Institute for Genomic Research
          9712 Medical Center Dr., Rockville, MD 20850, USA
          Tel: 301 838 3528
          Fax: 301 838 0208
          Email: johnq@tigr.org
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Db 412 TGGAGTTTCACACGAGTTGGTC 389

RESULT 15
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LOCUS      621 bp mRNA linear EST 13-JUL-2000
DEFINITION G01125452F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3345084 5',
          mRNA sequence.
ACCESSION  BE267891
VERSION     BE267891.1 GI:9141488
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 621)
AUTHORS   NIH-MGC http://mgc.mci.nih.gov/.
          National Institutes of Health, Mammalian Gene Collection (MGC)
          Unpublished (1999)
          Contact: Robert Strausberg, Ph.D.
          Email: cgapbs@mail.nih.gov
          Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
          cDNA Library Preparation: Ling Hong/Rubin Laboratory
          cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
          DNA Sequencing by: Incyte Genomics, Inc.
          Clone distribution: MGC clone distribution information can be
          found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
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              cloned into EcoRI/XhoI sites using the following 5'
              adaptor: GGCACGAG(G). Size-selected >500bp for average
              insert size 1.8kb. Library constructed by Ling Hong in
              the laboratory of Gerald M. Rubin (University of
              California, Berkeley) using ZAP-cDNA synthesis kit
              (Stratagene) and Superscript II RT (Life Technologies)."
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## ORIGIN

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Query Match      100.0%; Score 24; DB 10; Length 621;
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Db 183 TGGAGTTTCACACGAGTTGGTC 160

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Job time : 847.385 secs
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REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENTFEATURES  
source

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 26, 2004, 16:00:31 ; Search time 532.065 Seconds  
(without alignments)  
2036.547 Million cell updates/sec

Title: US-09-121-239-9

Perfect score: 25

Sequence: 1 GACTGTCACAGCATTCGCTGACC 25

Scoring table:

OLIGO NUC

Gapop 60.0 , Gapext 60.0

Searched: 3470272 seqs, 21671516995 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

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2: gb\_hgt.\*

3: gb\_in.\*

4: gb\_om.\*

5: gb\_ov.\*

6: gb\_pat.\*

7: gb\_ph.\*

8: gb\_pl.\*

9: gb\_pr.\*

10: gb\_ro.\*

11: gb\_sts.\*

12: gb\_sy.\*

13: gb\_un.\*

14: gb\_vl.\*

15: em\_ba.\*

16: em\_fun.\*

17: em\_hum.\*

18: em\_in.\*

19: em\_mu.\*

20: em\_om.\*

21: em\_or.\*

22: em\_ov.\*

23: em\_pat.\*

24: em\_ph.\*

25: em\_pl.\*

26: em\_ro.\*

27: em\_sts.\*

28: em\_un.\*

29: em\_vl.\*

30: em\_hgt\_hum.\*

31: em\_hgt\_inv.\*

32: em\_hgt\_other.\*

33: em\_hgt\_mus.\*

34: em\_hgt\_pln.\*

35: em\_hgt\_rtd.\*

36: em\_hgt\_mam.\*

37: em\_hgt\_vrt.\*

38: em\_sy.\*

39: em\_hgt\_hum.\*

40: em\_hgt\_mus.\*

41: em\_hgt\_other.\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

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2	25	100.0	25	6	BD222532	BD222532 Methods f
3	25	100.0	25	6	BD222533	BD222533 Methods f
4	25	100.0	25	6	BD222534	BD222534 Methods f
5	25	100.0	56	6	I12447	I12447 Sequence 17
6	25	100.0	56	6	I14509	I14509 Sequence 17
7	25	100.0	210	9	AY043457	AY043457 Homo sapi
8	25	100.0	250	9	AF321981	AF321981 Homo sapi
9	25	100.0	305	9	AF192533	AF192533 Homo sapi
10	25	100.0	350	6	BD222546	BD222546 Methods f
11	25	100.0	561	9	HUMMK562B	M19695 Human myelo
12	25	100.0	679	9	HUMABLB	M30832 Human bcr/a
13	25	100.0	854	9	HUMABLD	M30829 Human bcr/a
14	25	100.0	922	9	HSAL131467	AJ131467 Homo sapi
15	25	100.0	997	9	HSAL131466	AJ131466 Homo sapi
16	25	100.0	1078	6	A92081	A92081 Sequence 5
17	25	100.0	1078	6	AR230688	AR230688 Sequence
18	25	100.0	1157	6	BD177069	BD177069 Standard
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20	25	100.0	2255	6	I04527	I04527 Sequence 1
21	25	100.0	2541	9	HUMBCRX	M5395 Human break
22	25	100.0	2811	6	AX780333	AX780333 Sequence
23	25	100.0	3481	9	AK128501	AK128501 Homo sapi
24	25	100.0	4714	9	HSBCR	Y0661 Human bcr m
25	25	100.0	4739	6	AX331144	AX331144 Sequence
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27	25	100.0	5000	9	HUMBCRE	L02935 Human major
28	25	100.0	111249	9	AP000343	AP000343 Homo sapi
29	25	100.0	152141	9	HS007000	U07000 Human break
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35	21	84.0	240115	2	AC138021	AC138021 Pan trogl
36	18	72.0	22	6	I58643	I58643 Sequence 11
37	18	72.0	62	6	AR100681	AR100681 Sequence
38	18	72.0	81	6	AR100682	AR100682 Sequence
39	18	72.0	205	6	I02402	I02402 Sequence 1
40	18	72.0	257	6	I58633	I58633 Sequence 1
41	18	72.0	257	6	I96199	I96199 Sequence 36
42	17	68.0	60	6	A50293	A50293 Sequence 13
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ALIGNMENTS

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LOCUS BD222531 25 bp DNA linear PAT 17-JUL-2003  
DEFINITION Methods for detecting and measuring spliced nucleic acids.  
ACCESSION BD222531  
VERSION BD222531.1 GI:33032301  
KEYWORDS JP 2002521037-A/9,  
SOURCE synthetic construct  
ORGANISM artificial sequences.  
REFERENCE 1 (bases 1 to 25)  
AUTHORS Harvey,R.C. and Eastman,P.S.  
TITLES Methods for detecting and measuring spliced nucleic acids  
JOURNAL Patent: JP 2002521037-A 9 16-JUL-2002;  
GEN PROBE INC

```
COMMENT OS Artificial Sequence
PN JP 2002521037-A/9
PD 16-JUL-2002
PF 23-JUL-1999 JP 2000561364
PR 23-JUL-1998 US 09/121239
PT RICHARD C HARVEY, PAUL S EASTMAN
PC C12Q1/68, C12N15/09, C12N15/00
CC Description of Artificial Sequence: Probe for bcr b2 sequence
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BD222532 25 bp RNA linear PAT 17-JUL-2003
LOCUS Methods for detecting and measuring spliced nucleic acids.
DEFINITION
ACCESSION BD222532
VERSION BD222532.1 GI:33032302
KEYWORDS synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 25)
AUTHORS Harvey, R.C. and Eastman, P.S.
TITLE Methods for detecting and measuring spliced nucleic acids
JOURNAL Patent: JP 2002521037-A 10 16-JUL-2002;
COMMENT OS Artificial Sequence
PN JP 2002521037-A/10
PD 16-JUL-2002
PF 23-JUL-1999 JP 2000561364
PR 23-JUL-1998 US 09/121239
PT RICHARD C HARVEY, PAUL S EASTMAN
PC C12Q1/68, C12N15/09, C12N15/00
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LOCUS Methods for detecting and measuring spliced nucleic acids.
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ACCESSION BD222533
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KEYWORDS synthetic construct
SOURCE synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 25)
AUTHORS Harvey, R.C. and Eastman, P.S.
TITLE Methods for detecting and measuring spliced nucleic acids
JOURNAL Patent: JP 2002521037-A 11 16-JUL-2002;
COMMENT OS Artificial Sequence
PN JP 2002521037-A/11
PD 16-JUL-2002
PF 23-JUL-1999 JP 2000561364
PR 23-JUL-1998 US 09/121239
PT RICHARD C HARVEY, PAUL S EASTMAN
PC C12Q1/68, C12N15/09, C12N15/00
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DB 25 GACTGTCCACAGCATTCGCGTGACC 1
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LOCUS Methods for detecting and measuring spliced nucleic acids.
DEFINITION
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VERSION BD222534.1 GI:33032304
KEYWORDS synthetic construct
SOURCE synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 25)
AUTHORS Harvey, R.C. and Eastman, P.S.
TITLE Methods for detecting and measuring spliced nucleic acids
JOURNAL Patent: JP 2002521037-A 12 16-JUL-2002;
COMMENT OS Artificial Sequence
PN JP 2002521037-A/12
PD 16-JUL-2002
PF 23-JUL-1999 JP 2000561364
PR 23-JUL-1998 US 09/121239
PT RICHARD C HARVEY, PAUL S EASTMAN
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RESULT 5
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DEFINITION Sequence 17 from patent US 5424413.
ACCESSION I12447
VERSION I12447.1 GI:909831
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 56)
AUTHORS Hogan,J.J., Arnold,L.J. Jr., Nelson,N.C. and Bezverkov,R.
TITLE Branched nucleic acid probes
JOURNAL Patent: US 5424413-A 17 13-JUN-1995;
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DEFINITION Sequence 17 from patent US 5451503.
ACCESSION I14509
VERSION I14509.1 GI:996992
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 56)
AUTHORS Hogan,J.J., Arnold,L.J. Jr., Nelson,N.C. and Bezverkov,R.
TITLE Method for use of branched nucleic acid probes
JOURNAL Patent: US 5451503-A 17 19-SEP-1995;
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Best Local Similarity 100.0%; Pred. No. 4e-05;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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    |||||
Db 3 GACTGTCCACAGCATTCCGCTGACC 27

RESULT 7
LOCUS AY043457 210 bp mRNA linear PRI 27-JUN-2003
DEFINITION Homo sapiens BCR-ABL fusion protein (BCR-ABL fusion) mRNA, partial cds.
ACCESSION AY043457

Query Match      100.0%; Score 25; DB 6; Length 56;
Best Local Similarity 100.0%; Pred. No. 4e-05;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DEFINITION Homo sapiens BCR-ABL fusion transcript e15a2 mRNA sequence.
ACCESSION AF321981
VERSION AF321981.1 GI:13021894
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 250)
AUTHORS Moreno,M.P., Cortinas,M.N., Bonomi,R., Cardeza,A. and Uriarte,M.R.
TITLE A novel BCR-ABL fusion transcript (e15a2) in two patients with atypical Chronic Myeloproliferative Syndrome
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 250)
AUTHORS Moreno,M.P., Cortinas,M.N., Bonomi,R., Cardeza,A. and Uriarte,M.R.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2000) Biologia Molecular, Asociacion Espanola, Bulevar Artigas 1465, Montevideo 11200, Uruguay
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VERSION AY043457.1 GI:22073966
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ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 210)
AUTHORS Otazu,I.B., Belen Rivero,M., Olicio,R., Pinto,A., Zalcborg,I. and Seunanez,H.N.
TITLE A rare, in-frame BCR-ABL fusion (e13a3) in a patient with an aggressive chronic myeloid leukaemia
JOURNAL Acta Haematol. 108 (3), 150-153 (2002)
MEDLINE 22559050
PUBMED 12373087
REFERENCE 2 (bases 1 to 210)
AUTHORS Otazu,I.B., Rivero,M.B. and Olicio,R.
TITLE Direct Submission
JOURNAL Submitted (03-JUL-2001) Genetics Division, Instituto Nacional de Cancer, Praca da Cruz Vermelha, 23, sexto andar, Rio de Janeiro, RJ 21230-130, Brazil
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Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 67 GACTGTCCACAGCATTCCGCTGACC 91

RESULT 8
LOCUS AF321981 250 bp mRNA linear PRI 21-FEB-2001
DEFINITION Homo sapiens BCR-ABL fusion transcript e15a2 mRNA sequence.
ACCESSION AF321981
VERSION AF321981.1 GI:13021894
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
REFERENCE 1 (bases 1 to 250)
AUTHORS Moreno,M.P., Cortinas,M.N., Bonomi,R., Cardeza,A. and Uriarte,M.R.
TITLE A novel BCR-ABL fusion transcript (e15a2) in two patients with atypical Chronic Myeloproliferative Syndrome
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 250)
AUTHORS Moreno,M.P., Cortinas,M.N., Bonomi,R., Cardeza,A. and Uriarte,M.R.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2000) Biologia Molecular, Asociacion Espanola, Bulevar Artigas 1465, Montevideo 11200, Uruguay
FEATURES
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 DB 41 GACTGTCCACAGCATTCCGCTGACC 65

## RESULT 9

AF192533  
 LOCUS Homo sapiens BCR-ABL fusion protein (BCR-ABL fusion) mRNA, partial cds.  
 DEFINITION  
 ACCESSION AF192533 GI:7406986  
 VERSION  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM

REFERENCE 1 (bases 1 to 305)  
 AUTHORS Cortinas,M.N., Uriarte,M.R. and Moreno,M.P.  
 TITLE Identification of a novel BCR ABL fusion transcript in two patients with persistent neutrophilia in absence of Philadelphia chromosome Unpublished  
 JOURNAL  
 REFERENCE 2 (bases 1 to 305)  
 AUTHORS Cortinas,M.N., Uriarte,M.R. and Moreno,M.P.  
 TITLE Direct Submission  
 JOURNAL Primera de Socorros Mutuos, Bvar. Artigas 1465, Montevideo 11200, Uruguay

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## source

## source

## gene

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 DB 88 GACTGTCCACAGCATTCCGCTGACC 112

## RESULT 10

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 DEFINITION  
 ACCESSION BD222546  
 VERSION  
 KEYWORDS JP 2002521037-A/24.  
 SOURCE Homo sapiens (human)  
 ORGANISM  
 REFERENCE 1 (bases 1 to 350)  
 AUTHORS Harvey,R.C. and Eastman,P.S.  
 TITLE Methods for detecting and measuring spliced nucleic acids  
 JOURNAL Patent: JP 2002521037-A 24 16-JUL-2002;  
 GEN PROBE INC  
 COMMENT OS Homo sapiens (human)  
 PN JP 2002521037-A/24  
 PD 16-JUL-2002  
 PF 23-JUL-1999 JP 2000561364  
 PR 23-JUL-1998 US 09/121239  
 PI RICHARD C HARVEY,PAUL S EASTMAN  
 PC C12Q1/68,C12N15/09,C12N15/00  
 CC Methods for detecting and measuring spliced nucleic acids FH  
 KEY Location/Qualifiers  
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 DB 89 GACTGTCCACAGCATTCCGCTGACC 113

## RESULT 11

HUMMK562B  
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 DEFINITION  
 ACCESSION M19695  
 VERSION M19695.1 GI:188567  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM  
 REFERENCE 1 (bases 1 to 561)  
 AUTHORS Grosfeld,G., Verwoerd,T., van Aghoven,T., de Klein,A., Ramachandran,K.L., Heisterkamp,N., Stam,K. and Groffen,J.  
 TITLE The chronic myelocytic cell line K562 contains a breakpoint in bcr and produces a chimeric bcr/c-abl transcript  
 JOURNAL Mol. Cell. Biol. 6 (2), 607-616 (1986)  
 MEDLINE 87064346  
 PUBMED 3023859  
 COMMENT Original source text: Human myelocytic Ph(1)-positive CML K562 cell



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line, cDNA to mRNA, clone 8E.
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        Best Local Similarity 100.0%; Pred. No. 4.1e-05;
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QY 1 GACTGTCCACAGCATTCGCTGACC 25
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Db 84 GACTGTCCACAGCATTCGCTGACC 108
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RESULT 12
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LOCUS
DEFINITION
    Human bcr/abl fusion protein, partial cds, clone E3.
ACCESSION
    M30832.1 GI:177944
VERSION
    Philadelphia chromosome; abl proto-oncogene; translocation.
KEYWORDS
    Homo sapiens (human)
ORGANISM
    Homo sapiens
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
    1 (bases 1 to 679)
AUTHORS
    Shtivelman,E., Lifshitz,B., Gale,R.P. and Canaani,E.
TITLES
    Fused transcript of abl and bcr genes in chronic myelogenous
    leukaemia
JOURNAL
    Nature 315 (6020), 550-554 (1985)
MEDLINE
    85240529
PUBMED
    2989692
COMMENT
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RESULT 13
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DEFINITION
    Human bcr/abl fusion protein mRNA, partial cds, clone K28.

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ACCESSION
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VERSION
    M30829.1 GI:177953
KEYWORDS
    Philadelphia chromosome; abl proto-oncogene; translocation.
SOURCE
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ORGANISM
    Homo sapiens
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
    1 (bases 1 to 854)
AUTHORS
    Shtivelman,E., Lifshitz,B., Gale,R.P. and Canaani,E.
TITLES
    Fused transcript of abl and bcr genes in chronic myelogenous
    leukaemia
JOURNAL
    Nature 315 (6020), 550-554 (1985)
MEDLINE
    85240529
PUBMED
    2989692
COMMENT
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RESULT 14
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DEFINITION
    Homo sapiens mRNA for BCR/ABL chimeric fusion peptide, partial.
ACCESSION
    AJ131467.1 GI:4033556
VERSION
    BCR/ABL chimeric fusion peptide; bcr/abl gene.
KEYWORDS
    Homo sapiens (human)
ORGANISM
    Homo sapiens
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
    1
AUTHORS
    Burmeister,T., Maurer,J., Aivado,M., Elmaagacli,A.H., Grunebach,F.,
    Held,K.R., Hees,G., Hochhaus,A., Hoppner,W., Lentz,K.U.,
    Lubbert,M., Schafer,K.L., Schafhausen,P., Schmidt,C.A., Schuler,F.,
    Seeger,K., Seelig,R., Thiede,C., Viehmann,S., Weber,C., Wilhelm,S.,
    Christmann,A., Clement,J.H., Ebener,U., Enczmann,J., Leo,R.,
    Schleuning,M., Schoch,R. and Thiel,E.
TITLES
    Quality assurance in RT-PCR-based BCR/ABL diagnostics--results of
    an interlaboratory test and a standardization approach
JOURNAL
    Leukemia 14 (10), 1850-1856 (2000)
MEDLINE
    20471781
PUBMED
    11021760
REFERENCE
    2 (bases 1 to 922)
AUTHORS
    Burmeister,T.
TITLES
    Direct Submission
JOURNAL
    Submitted (04-DEC-1998) Burmeister T., Medizinische Klinik III, FU
    Berlin, Hindenburgdamm 30, Berlin, Germany 12200, Germany

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

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Sequence: 1 GACTGTCCAGACATTCGCTGACC 25

Scoring table: OLIGO NUC  
Gapop 60.0 , Gapext 60.0

Searched: 3373863 seqs, 2124099041 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

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8: Geneseqn2003bs:\*  
9: Geneseqn2003cs:\*  
10: Geneseqn2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 4	25	100.0	25	3	AZ60848	Aaz60848 Oligonucleotide
5	25	100.0	45	9	ADC38532	Aac38532 Template
6	25	100.0	56	2	AAQ46951	Aat46951 Branched
7	25	100.0	200	2	AAT88785	Aat88785 Leukaemic
8	25	100.0	250	6	ABS73175	Abs73175 Human tra
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11	25	100.0	504	5	AAS85023	Aas85023 DNA encod
12	25	100.0	504	8	ACH38242	Ach38242 Human tra
13	25	100.0	561	6	ABS73169	Abs73169 Human tra
14	25	100.0	679	5	ABS73172	Abs73172 DNA encod
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18	25	100.0	921	5	AAS85025	Aas85025 DNA encod
19	25	100.0	922	6	ABS73180	Abs73180 DNA encod
20	25	100.0	997	6	ABS73173	Abs73173 DNA encod
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30	25	100.0	5795	5	AAS85031	Aas85031 DNA encod
31	25	100.0	152141	7	ACA64961	Ac64961 Human BCR
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37	18	72.0	22	2	AAQ34635	Aaq34635 Human bcr
38	18	72.0	62	2	AAQ66774	Aaq66774 L6(1)31 r
C 39	18	72.0	81	2	AAQ66775	Aaq66775 L6(1)31 r
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ALIGNMENTS

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XX  
AC AAZ60850;  
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DT 16-MAY-2000 (first entry)  
XX  
DE Oligonucleotide used to detect bcr b3-abl fusion transcripts.  
XX  
KW Fusion transcript; translocation; bcr b3 region; abl gene;  
KW amplification assay; detection assay; medical diagnosis;  
KW clinical monitoring; chimeric RNA; fusion RNA; condition marker;  
KW disease marker; cancer; leukemia; ss.  
XX  
OS Synthetic.  
XX  
PN WO200005418-A1.  
XX  
PD 03-FEB-2000.  
XX  
PF 23-JUL-1999; 99WO-US016832.  
XX  
PR 23-JUL-1998; 98US-00121239.  
XX  
PA (GENP-) GEN-PROBE INC.  
XX  
PI Harvey RC, Eastman PS;  
XX  
DR WPI; 2000-182730/16.  
XX  
PT Novel methods for preparing RNA from biological samples, used for the  
PT detection and measurement of nucleic acids and fusion nucleic acids.  
XX  
PS Claim 19; Page 41; 49pp; English.  
XX  
CC Oligonucleotides AAZ60840-62 and AAZ60865-66 are used in the method of  
CC the invention to detect fusion transcripts produced from a translocation  
CC between the bcr b3 region and the abl gene. The specification describes a  
CC method for detecting a fusion nucleic acid (particularly chimeric mRNA  
CC species), in a biological sample. The method comprises contacting a  
CC sample of fusion nucleic acid with primers, amplifying the hybridized  
CC fusion nucleic acid, and detecting the target hybrid. The method is used  
CC for the sample and rapid preparation of RNA from a biological sample,  
CC particularly from the cytoplasm of eukaryotic cells, which is suitable  
CC for use in an amplification and detection assay. The methods are used for

CC the analysis and detection of nucleic acids in biological samples. The  
 CC methods are useful in the human medical and veterinary fields, for  
 CC medical diagnoses and clinical monitoring of a patient's response to  
 CC therapy where a disease or medical condition is associated with a  
 CC particular type and/or level of mRNA present in the sample. The methods  
 CC are also useful for detecting or quantifying fusion or chimeric RNA  
 CC species, and for detecting a translocation as a marker for a given  
 CC condition or disease, e.g. translocations associate with cancers,  
 CC particularly forms of leukemia

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 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 AC AAZ60849;  
 XX  
 DT 16-MAY-2000 (first entry)  
 XX  
 DE Oligonucleotide used to detect bcr b3-abl fusion transcripts.  
 XX  
 KW Fusion transcript; translocation; bcr b3 region; abl gene;  
 KW amplification assay; detection assay; medical diagnosis;  
 KW clinical monitoring; chimeric RNA; fusion RNA; condition marker;  
 KW disease marker; cancer; leukemia; ss.  
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 PN WO200005418-A1.  
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 PD 03-FEB-2000.  
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 PF 23-JUL-1999; 99WO-US016832.  
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 PR 23-JUL-1998; 98US-00121239.  
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 PA (GENP-) GEN-PROBE INC.  
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 PI Harvey RC, Eastman PS;  
 XX  
 WPI; 2000-182730/16.  
 XX  
 PT Novel methods for preparing RNA from biological samples, used for the  
 PT detection and measurement of nucleic acids and fusion nucleic acids.  
 XX  
 PS Claim 19; Page 41; 49pp; English.  
 XX  
 CC Oligonucleotides AAZ60840-62 and AAZ60865-66 are used in the method of  
 CC the invention to detect fusion transcripts produced from a translocation  
 CC between the bcr b3 region and the abl gene. The specification describes a  
 CC method for detecting a fusion nucleic acid (particularly chimeric mRNA  
 CC species), in a biological sample. The method comprises contacting a  
 CC sample of fusion nucleic acid with primers, amplifying the hybridized  
 CC fusion nucleic acid, and detecting the target hybrid. The method is used  
 CC for the simple and rapid preparation of RNA from a biological sample,  
 CC particularly from the cytoplasm of eukaryotic cells, which is suitable  
 CC for use in an amplification and detection assay. The methods are used for  
 CC the analysis and detection of nucleic acids in biological samples. The  
 CC methods are useful in the human medical and veterinary fields, for  
 CC medical diagnoses and clinical monitoring of a patient's response to  
 CC therapy where a disease or medical condition is associated with a  
 CC particular type and/or level of mRNA present in the sample. The methods  
 CC are also useful for detecting or quantifying fusion or chimeric RNA  
 CC species, and for detecting a translocation as a marker for a given  
 CC condition or disease, e.g. translocations associate with cancers,  
 CC particularly forms of leukemia

CC species, and for detecting a translocation as a marker for a given  
 CC condition or disease, e.g. translocations associate with cancers,  
 CC particularly forms of leukemia

XX SQ Sequence 25 BP; 5 A; 10 C; 5 G; 0 T; 5 U; 0 Other;  
 Query Match 100.0%; Score 25; DB 3; Length 25;  
 Best Local Similarity 80.0%; Pred. No. 0.00021;  
 Matches 20; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 GACTGTCCACAGCATTCGCTGACC 25  
 DB 1 GACTGTCCACAGCATTCGCTGACC 25

RESULT 3  
 AAZ60851/c  
 ID AAZ60851 standard; RNA; 25 BP.  
 XX  
 AC AAZ60851;  
 XX  
 DT 16-MAY-2000 (first entry)  
 XX  
 DE Oligonucleotide used to detect bcr b3-abl fusion transcripts.  
 XX  
 KW Fusion transcript; translocation; bcr b3 region; abl gene;  
 KW amplification assay; detection assay; medical diagnosis;  
 KW clinical monitoring; chimeric RNA; fusion RNA; condition marker;  
 KW disease marker; cancer; leukemia; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200005418-A1.  
 XX  
 PD 03-FEB-2000.  
 XX  
 PF 23-JUL-1999; 99WO-US016832.  
 XX  
 PR 23-JUL-1998; 98US-00121239.  
 XX  
 PA (GENP-) GEN-PROBE INC.  
 XX  
 PI Harvey RC, Eastman PS;  
 XX  
 WPI; 2000-182730/16.  
 XX  
 PT Novel methods for preparing RNA from biological samples, used for the  
 PT detection and measurement of nucleic acids and fusion nucleic acids.  
 XX  
 PS Claim 19; Page 41; 49pp; English.  
 XX  
 CC Oligonucleotides AAZ60840-62 and AAZ60865-66 are used in the method of  
 CC the invention to detect fusion transcripts produced from a translocation  
 CC between the bcr b3 region and the abl gene. The specification describes a  
 CC method for detecting a fusion nucleic acid (particularly chimeric mRNA  
 CC species), in a biological sample. The method comprises contacting a  
 CC sample of fusion nucleic acid with primers, amplifying the hybridized  
 CC fusion nucleic acid, and detecting the target hybrid. The method is used  
 CC for the simple and rapid preparation of RNA from a biological sample,  
 CC particularly from the cytoplasm of eukaryotic cells, which is suitable  
 CC for use in an amplification and detection assay. The methods are used for  
 CC the analysis and detection of nucleic acids in biological samples. The  
 CC methods are useful in the human medical and veterinary fields, for  
 CC medical diagnoses and clinical monitoring of a patient's response to  
 CC therapy where a disease or medical condition is associated with a  
 CC particular type and/or level of mRNA present in the sample. The methods  
 CC are also useful for detecting or quantifying fusion or chimeric RNA  
 CC species, and for detecting a translocation as a marker for a given  
 CC condition or disease, e.g. translocations associate with cancers,  
 CC particularly forms of leukemia

XX SQ Sequence 25 BP; 5 A; 5 C; 10 G; 0 T; 5 U; 0 Other;

Query Match 100.0%; Score 25; DB 3; Length 25;  
 Best Local Similarity 100.0%; Pred. No. 0.00021;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GACTGTCCACAGCATTCGCTGACC 25  
 |||||  
 DB 25 GACTGTCCACAGCATTCGCTGACC 1

RESULT 4  
 AAZ60848  
 ID AAZ60848 standard; DNA; 25 BP.  
 XX  
 AC AAZ60848;  
 XX  
 DT 16-MAY-2000 (first entry)  
 XX  
 DE Oligonucleotide used to detect bcr b3-abl fusion transcripts.  
 XX  
 KW Fusion transcript; translocation; bcr b3 region; abl gene;  
 KW amplification assay; detection assay; medical diagnosis;  
 KW clinical monitoring; chimeric RNA; fusion RNA; condition marker;  
 KW disease marker; cancer; leukemia; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200005418-A1.  
 XX  
 PD 03-FEB-2000.  
 XX  
 PF 23-JUL-1999; 99WO-US016832.  
 XX  
 PR 23-JUL-1999; 98US-00121239.  
 XX  
 PA (GENP-) GEN-PROBE INC.  
 XX  
 PI Harvey RC, Eastman PS;  
 XX  
 DR WPI; 2000-182730/16.  
 XX  
 PT Novel methods for preparing RNA from biological samples, used for the  
 PT detection and measurement of nucleic acids and fusion nucleic acids.  
 XX  
 PS Claim 19; Page 41; 49pp; English.  
 CC  
 CC Oligonucleotides AAZ60840-62 and AAZ60865-66 are used in the method of  
 CC the invention to detect fusion transcripts produced from a translocation  
 CC between the bcr b3 region and the abl gene. The specification describes a  
 CC method for detecting a fusion nucleic acid (particularly chimeric mRNA  
 CC species), in a biological sample. The method comprises contacting a  
 CC sample of fusion nucleic acid with primers, amplifying the hybridized  
 CC fusion nucleic acid, and detecting the target hybrid. The method is used  
 CC for the simple and rapid preparation of RNA from a biological sample,  
 CC particularly from the cytoplasm of eukaryotic cells, which is suitable  
 CC for use in an amplification and detection assay. The methods are used for  
 CC the analysis and detection of nucleic acids in biological samples. The  
 CC methods are useful in the human medical and veterinary fields, for  
 CC medical diagnoses and clinical monitoring of a patient's response to  
 CC therapy where a disease or medical condition is associated with a  
 CC particular type and/or level of mRNA present in the sample. The methods  
 CC are also useful for detecting or quantifying fusion or chimeric RNA  
 CC species, and for detecting a translocation as a marker for a given  
 CC condition or disease, e.g. translocations associate with cancers,  
 CC particularly forms of leukemia  
 XX  
 SQ Sequence 25 BP; 5 A; 10 C; 5 G; 5 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 3; Length 25;  
 Best Local Similarity 100.0%; Pred. No. 0.00021;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GACTGTCCACAGCATTCGCTGACC 25  
 |||||  
 DB 25 GACTGTCCACAGCATTCGCTGACC 1

RESULT 4  
 AAZ60848  
 ID AAZ60848 standard; DNA; 25 BP.  
 XX  
 AC AAZ60848;  
 XX  
 DT 16-MAY-2000 (first entry)  
 XX  
 DE Oligonucleotide used to detect bcr b3-abl fusion transcripts.  
 XX  
 KW Fusion transcript; translocation; bcr b3 region; abl gene;  
 KW amplification assay; detection assay; medical diagnosis;  
 KW clinical monitoring; chimeric RNA; fusion RNA; condition marker;  
 KW disease marker; cancer; leukemia; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200005418-A1.  
 XX  
 PD 03-FEB-2000.  
 XX  
 PF 23-JUL-1999; 99WO-US016832.  
 XX  
 PR 23-JUL-1999; 98US-00121239.  
 XX  
 PA (GENP-) GEN-PROBE INC.  
 XX  
 PI Harvey RC, Eastman PS;  
 XX  
 DR WPI; 2000-182730/16.  
 XX  
 PT Novel methods for preparing RNA from biological samples, used for the  
 PT detection and measurement of nucleic acids and fusion nucleic acids.  
 XX  
 PS Claim 19; Page 41; 49pp; English.  
 CC  
 CC Oligonucleotides AAZ60840-62 and AAZ60865-66 are used in the method of  
 CC the invention to detect fusion transcripts produced from a translocation  
 CC between the bcr b3 region and the abl gene. The specification describes a  
 CC method for detecting a fusion nucleic acid (particularly chimeric mRNA  
 CC species), in a biological sample. The method comprises contacting a  
 CC sample of fusion nucleic acid with primers, amplifying the hybridized  
 CC fusion nucleic acid, and detecting the target hybrid. The method is used  
 CC for the simple and rapid preparation of RNA from a biological sample,  
 CC particularly from the cytoplasm of eukaryotic cells, which is suitable  
 CC for use in an amplification and detection assay. The methods are used for  
 CC the analysis and detection of nucleic acids in biological samples. The  
 CC methods are useful in the human medical and veterinary fields, for  
 CC medical diagnoses and clinical monitoring of a patient's response to  
 CC therapy where a disease or medical condition is associated with a  
 CC particular type and/or level of mRNA present in the sample. The methods  
 CC are also useful for detecting or quantifying fusion or chimeric RNA  
 CC species, and for detecting a translocation as a marker for a given  
 CC condition or disease, e.g. translocations associate with cancers,  
 CC particularly forms of leukemia  
 XX  
 SQ Sequence 25 BP; 5 A; 10 C; 5 G; 5 T; 0 U; 0 Other;

Db 1 GACTGTCCACAGCATTCGCTGACC 25

RESULT 5  
 ADC38532  
 ID ADC38532 standard; DNA; 45 BP.  
 XX  
 AC ADC38532;  
 XX  
 DT 18-DEC-2003 (first entry)  
 XX  
 DE Template translocation oligonucleotide SEQ ID 9.  
 XX  
 KW Chromosome translocation; cancer; leukaemia; lymphoma; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN WO2003044486-A2.  
 XX  
 PD 30-MAY-2003.  
 XX  
 PF 20-NOV-2002; 2002WO-US037507.  
 XX  
 PR 20-NOV-2001; 2001US-0335716P.  
 XX  
 PA (REGC ) UNIV CALIFORNIA.  
 XX  
 PI Nolan JP, Zhou F;  
 XX  
 DR WPI; 2003-468806/44.  
 XX  
 PT Detecting chromosome translocations in a target nucleic acid sequence for  
 PT diagnosing cancers associated with chromosome translocations, by using  
 PT microsphere arrays.  
 XX  
 PS Claim 52; Fig 7; 57pp; English.  
 XX  
 CC The present invention relates to a method (M) for detecting chromosome  
 CC translocation. The method comprises amplifying a target nucleic acid  
 CC sequence from a sample, hybridizing oligonucleotides (ONTs) specific for  
 CC regions of the translocation to the amplified target, where the ONTs  
 CC comprise capture tags, extending the ONTs to produce labelled and extended  
 CC ONTs, hybridizing the ONTs to address tags on solid support and detecting  
 CC the presence of labelled extended ONTs on the solid support. (M) is  
 CC useful for detecting a chDNA from a biological sample from a human. The  
 CC chromosome translocation is associated with cancer (e.g. leukaemia) and  
 CC this method is especially useful for diagnosing cancer, especially  
 CC leukaemia, and also lymphoma. The present sequence is a template  
 CC translocation oligonucleotide used to illustrate the invention.  
 XX  
 SQ Sequence 45 BP; 15 A; 14 C; 8 G; 8 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 9; Length 45;  
 Best Local Similarity 100.0%; Pred. No. 0.00021;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GACTGTCCACAGCATTCGCTGACC 25  
 |||||  
 DB 7 GACTGTCCACAGCATTCGCTGACC 31

RESULT 6  
 AAQ46951  
 ID AAQ46951 standard; DNA; 56 BP.  
 XX  
 AC AAQ46951;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 21-JAN-1994 (first entry)  
 XX  
 DE Branched probe to CMLb translocation region of chromosome 22.  
 XX

KW Chronic myelogenous leukaemia; CMLb; abl region;  
 KW acute lymphocytic leukaemia; ALL; genetic translocation; chromosome 22;  
 KW target sequence; universal detection oligomer; branched probe;  
 KW chemiluminescent acridinium ester; ss.  
 XX  
 OS Synthetic.  
 XX  
 XX  
 FH Key Location/Qualifiers  
 FT misc\_feature 1..40  
 FT /tag= a  
 FT /note= "complementary to region of chromosome 22  
 FT associated with CMLb translocation"  
 FT 41..56  
 FT /tag= b  
 FT /note= "complementary to nucleotides 16-1 of universal  
 FT detection probe AAQ46949"  
 FT  
 XX  
 PN EP52931-A1.  
 XX  
 XX  
 PD 28-JUL-1993.  
 XX  
 XX  
 PF 20-JAN-1993; 93EP-00300377.  
 XX  
 XX 22-JAN-1992; 92US-00827021.  
 XX (GENP-) GEN PROBE INC.  
 XX  
 PI Hogan JJ, Arnold LJ, Nelson NC, Bezverkov R;  
 XX WPI; 1993-236606/30.  
 XX  
 XX Nucleic acid molecules which hybridise in presence of target nucleic acid  
 PT - are used as probes in hybridisation assays or as therapeutic agents for  
 PT diseases.  
 XX  
 PS Example 6; Fig 12B; 58pp; English.  
 XX  
 CC Chimeric targets were synthesised homologous to 3 different genetic  
 CC translocations between a constant abl region of chromosome 9 and various  
 CC regions of chromosome 22; two are the most common translocations  
 CC associated with chronic myelogenous leukaemia (CMLa and CMLb) and the  
 CC other is associated with acute lymphocytic leukaemia (ALL). An AB-  
 CC labelled universal detection oligomer (AAQ46949) specific for the abl  
 CC region was synthesised. Three different strands were designed to contain  
 CC a probe region specific for one of the translocated chromosome 22 regions  
 CC as well as an arm region complementary to part of the universal probe  
 CC (AAQ46950-2). The probe mixes were found to detect only the correct  
 CC chimeric targets and did not cross-react significantly with the other  
 CC targets. (Updated on 25-MAR-2003 to correct PN field.) (Updated on 25-MAR  
 CC -2003 to correct PA field.)  
 XX  
 SQ Sequence 56 BP; 18 A; 18 C; 9 G; 11 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 25; DB 2; Length 56;  
 Best Local Similarity 100.0%; Pred. No. 0.00021;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GACTGTCCACAGCATTCGCTGACC 25  
 Db 3 GACTGTCCACAGCATTCGCTGACC 27  
 RESULT 7  
 AAT88785  
 ID AAT88785 standard; DNA; 200 BP.  
 XX  
 XX AAT88785;  
 XX  
 DT 23-MAR-1998 (first entry)  
 XX  
 DE Leukaemic cell BCR-ABL mRNA PCR product target sequence.  
 XX  
 KW Leukaemia; BCR-ABL; cell line K562; target; immunoassay; probe;

KW hybridisation; diagnostic; luciferase; genetic disease; ss.  
 XX Unidentified.  
 XX  
 PN CA2186998-A.  
 XX  
 PD 31-MAY-1997.  
 XX  
 XX 02-OCT-1996; 96CA-02186998.  
 XX  
 PR 30-NOV-1995; 95US-00565055.  
 XX (UYWI-) UNIV WINDSOR.  
 XX  
 XX Christopoulos TK;  
 XX WPI; 1997-415964/39.  
 XX  
 PT Immunoassays and nucleic acid hybridisation assays - using protein-  
 PT encoding nucleic acid fragments as labels.  
 XX  
 PS Disclosure; Page 26; 39pp; English.  
 XX  
 CC A novel assay has been developed for determining an analyte. The assay  
 CC comprises labelling the analyte with a nucleic acid fragment that encodes  
 CC a protein, expressing the nucleic acid, and detecting the protein. The  
 CC present sequence represents a target sequence from a leukaemic cell (cell  
 CC line K562), used in an example of the present assay. The assay is used  
 CC for the determination of antigens or nucleic acids for diagnostic or  
 CC research purposes, e.g. detecting low levels of tumour markers, analysing  
 CC nucleic acid mutations associated with genetic diseases, diagnosing and  
 CC monitoring pathogen infections, or searching for new disease markers. The  
 CC immunoassay when using a luciferase for detection is more sensitive than  
 CC an enzyme-amplified, time-resolved fluorometric immunoassay and does not  
 CC require preparation of a luciferase-antibody conjugate  
 XX  
 SQ Sequence 200 BP; 49 A; 52 C; 51 G; 48 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 25; DB 2; Length 200;  
 Best Local Similarity 100.0%; Pred. No. 0.0002;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GACTGTCCACAGCATTCGCTGACC 25  
 Db 40 GACTGTCCACAGCATTCGCTGACC 64  
 RESULT 8  
 ABS73175  
 ID ABS73175 standard; DNA; 250 BP.  
 XX  
 XX ABS73175;  
 AC  
 DT 04-DEC-2002 (first entry)  
 XX  
 XX Human translocation (9: 22) (q34: q11) #3.  
 DE  
 XX  
 KW Chromosome aberration; oncogenic fusion protein; cancer;  
 KW proliferative disease; cellular protein isoform; heat shock protein 90;  
 KW HSP-90; rheumatoid arthritis; cancer; haematopoietic disorder;  
 KW T cell lymphoma; B cell lymphoma; chronic myeloid leukaemia; CML;  
 KW acute myeloid leukaemia; AML; chronic myelomonocytic leukaemia; CMML;  
 KW acute lymphoblastic leukaemia; ALL; APL; solid tumour;  
 KW papillary thyroid carcinoma; Ewing's sarcoma; melanoma; liposarcoma;  
 KW rhabdomyosarcoma; synovial sarcoma; viral infection; gene; ds.  
 XX  
 XX Homo sapiens.  
 OS  
 XX WO200269900-A2.  
 PN  
 XX 12-SEP-2002.  
 PD  
 XX 01-MAR-2002; 2002WO-US006518.



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XX 01-MAR-2001; 2001US-0272751P.
XX (CONF-) CONFORMA THERAPEUTICS CORP.
XX Fritz LC, Burrows FJ;
XX WPI; 2002-698710/75.
XX P-PSDB; ABG95013.
XX Treating genetically-defined disease associated with chromosomal
XX aberrations yielding oncogenic fusion proteins, e.g. cell proliferative
XX diseases, involves administering an inhibitor of heat shock protein 90.
XX Disclosure; Page 97; 389pp; English.
XX The invention describes a method of treating genetically-defined disease
XX associated with chromosomal aberrations yielding oncogenic fusion
XX proteins (I), treating cancerous cells containing (I) in a heterogeneous
XX cell population, treating proliferative diseases associated with mutant
XX protein or cellular protein isoforms (II) dependent on heat shock protein
XX (HSP)-90, or selectively treating cells expressing (II) involving
XX administering HSP90-inhibitor. The method is useful for treating
XX genetically-defined disease with chromosomal aberration yielding
XX oncogenic fusion protein, treating cancerous cells containing fusion
XX protein in heterogeneous cell population, treating proliferative disease
XX (e.g. rheumatoid arthritis or cancer) associated with mutant protein or
XX cellular protein isoform dependent on heat shock protein (HSP)-90 (e.g.
XX p53), or selectively treating cells expressing mutant protein or cellular
XX protein isoform in a patient heterozygous for (II). The method is useful
XX for treating a disease e.g. haematopoietic disorder such as T or B cell
XX lymphoma, chronic myeloid leukaemia (CML), APL, ALL, NHL and CMMML,
XX or a disease characterised by a solid tumour such as papillary thyroid
XX carcinoma, Ewing's sarcoma, melanoma, liposarcoma, rhabdomyosarcoma and
XX synovial sarcoma. The method is also useful for treating viral
XX infections. This represents the DNA sequence of a chromosome aberration
XX Sequence 250 BP; 65 A; 62 C; 63 G; 60 T; 0 U; 0 Other;
XX Query Match 100.0%; Score 25; DB 6; Length 250;
XX Best Local Similarity 100.0%; Pred. No. 0.0002;
XX Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GACTGTCCACAGCATTCGCTGACC 25
DB 41 GACTGTCCACAGCATTCGCTGACC 65
RESULT 9
ABS73174
ID ABS73174 standard; DNA; 305 BP.
XX AC ABS73174;
XX DT 04-DEC-2002 (first entry)
XX DE DNA encoding human translocation (9: 22) (q34: q11) protein #5.
XX Chromosome aberration; oncogenic fusion protein; cancer;
XX proliferative disease; cellular protein isoform; heat shock protein 90;
XX HSP-90; rheumatoid arthritis; cancer; haematopoietic disorder;
XX T cell lymphoma; B cell lymphoma; chronic myeloid leukaemia; CML;
XX acute myeloid leukaemia; AML; chronic myelomonocytic leukaemia; CMMML;
XX acute lymphoblastic leukaemia; ALL; APL; NHL; solid tumour;
XX papillary thyroid carcinoma; Ewing's sarcoma; melanoma; liposarcoma;
XX rhabdomyosarcoma; synovial sarcoma; viral infection; gene; ds.
XX OS Homo sapiens.
XX PN WO200269900-A2.
XX PD 12-SEP-2002.
XX PF 01-MAR-2002; 2002WO-US006518.
XX
XX 01-MAR-2001; 2001US-0272751P.
XX (CONF-) CONFORMA THERAPEUTICS CORP.
XX Fritz LC, Burrows FJ;
XX WPI; 2002-698710/75.
XX P-PSDB; ABG95013.
XX Treating genetically-defined disease associated with chromosomal
XX aberrations yielding oncogenic fusion proteins, e.g. cell proliferative
XX diseases, involves administering an inhibitor of heat shock protein 90.
XX Disclosure; Page 97; 389pp; English.
XX The invention describes a method of treating genetically-defined disease
XX associated with chromosomal aberrations yielding oncogenic fusion
XX proteins (I), treating cancerous cells containing (I) in a heterogeneous
XX cell population, treating proliferative diseases associated with mutant
XX protein or cellular protein isoforms (II) dependent on heat shock protein
XX (HSP)-90, or selectively treating cells expressing (II) involving
XX administering HSP90-inhibitor. The method is useful for treating
XX genetically-defined disease with chromosomal aberration yielding
XX oncogenic fusion protein, treating cancerous cells containing fusion
XX protein in heterogeneous cell population, treating proliferative disease
XX (e.g. rheumatoid arthritis or cancer) associated with mutant protein or
XX cellular protein isoform dependent on heat shock protein (HSP)-90 (e.g.
XX p53), or selectively treating cells expressing mutant protein or cellular
XX protein isoform in a patient heterozygous for (II). The method is useful
XX for treating a disease e.g. haematopoietic disorder such as T or B cell
XX lymphoma, chronic myeloid leukaemia (CML), APL, ALL, NHL and CMMML,
XX or a disease characterised by a solid tumour such as papillary thyroid
XX carcinoma, Ewing's sarcoma, melanoma, liposarcoma, rhabdomyosarcoma and
XX synovial sarcoma. The method is also useful for treating viral
XX infections. This represents the DNA sequence of a chromosome aberration
XX Sequence 305 BP; 77 A; 79 C; 77 G; 72 T; 0 U; 0 Other;
XX Query Match 100.0%; Score 25; DB 6; Length 305;
XX Best Local Similarity 100.0%; Pred. No. 0.0002;
XX Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GACTGTCCACAGCATTCGCTGACC 25
DB 88 GACTGTCCACAGCATTCGCTGACC 112
RESULT 10
AAZ60863
ID AAZ60863 standard; DNA; 350 BP.
XX AC AAZ60863;
XX DT 16-MAY-2000 (first entry)
XX DE Region surrounding a bcr-able splice junction.
XX Fusion transcript; translocation; bcr b3 region; abl gene;
XX amplification assay; detection assay; medical diagnosis;
XX clinical monitoring; chimeric RNA; fusion RNA; condition marker;
XX disease marker; cancer; leukemia; ss.
XX OS Unidentified.
XX PN WO200005418-A1.
XX PD 03-FEB-2000.
XX PF 23-JUL-1999; 99WO-US016832.
XX PR 23-JUL-1998; 98US-00121239.
XX

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PA (GENP-) GEN-PROBE INC.  
 XX Harvey RC, Eastman PS;  
 XX WPI; 2000-192730/16.  
 DR  
 XX Novel methods for preparing RNA from biological samples, used for the  
 PT detection and measurement of nucleic acids and fusion nucleic acids.  
 PT  
 XX Disclosure; Fig 2; 49pp; English.  
 XX  
 CC The present sequence represents a region surrounding a bcr-able splice  
 CC junction. The specification describes oligonucleotides which are used to  
 CC detect fusion transcripts produced from a translocation between the bcr  
 CC b3 region and the abl gene. The specification also describes a method for  
 CC detecting a fusion nucleic acid (particularly chimeric mRNA species), in  
 CC a biological sample. The method comprises contacting a sample of fusion  
 CC nucleic acid with primer, amplifying the hybridized fusion nucleic acid,  
 CC and detecting the target hybrid. The method is used for the simple and  
 CC rapid preparation of RNA from a biological sample, particularly from the  
 CC cytoplasm of eukaryotic cells, which is suitable for use in an  
 CC amplification and detection assay. The methods are used for the analysis  
 CC and detection of nucleic acids in biological samples. The methods are  
 CC useful in the human medical and veterinary fields, for medical diagnoses  
 CC and clinical monitoring of a patient's response to therapy where a disease  
 CC or medical condition is associated with a particular type and/or level of  
 CC mRNA present in the sample. The methods are also useful for detecting or  
 CC quantifying fusion or chimeric RNA species, and for detecting a  
 CC translocation as a marker for a given condition or disease, e.g.  
 CC translocations associate with cancers, particularly forms of leukemia  
 XX  
 SQ Sequence 350 BP; 85 A; 92 C; 89 G; 84 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 25; DB 3; Length 350;  
 Best Local Similarity 100.0%; Pred. No. 0.0002;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GACTGTCCACAGCATTCGCTGACC 25  
 DB 89 GACTGTCCACAGCATTCGCTGACC 113  
 RESULT 11  
 AAS85023  
 ID AAS85023 standard; cDNA; 504 BP.  
 AC AAS85023;  
 XX  
 DT 13-FEB-2002 (first entry)  
 DE  
 XX DNA encoding novel human diagnostic protein #20827.  
 XX  
 KW Human; chromosome mapping; gene mapping; gene therapy; forensic;  
 KW food supplement; medical imaging; diagnostic; genetic disorder; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200175067-A2.  
 XX  
 PD 11-OCT-2001.  
 XX  
 XX 30-MAR-2001; 2001WO-US0008631.  
 XX  
 PR 31-MAR-2000; 2000US-00540217.  
 PR 23-AUG-2000; 2000US-00649167.  
 XX  
 PA (HYSE-) HYSEQ INC.  
 XX  
 XX Drmanac RT, Liu C, Tang YT;  
 PI  
 XX WPI; 2001-639362/73.  
 DR P-PSDB; ABG20836.  
 DR  
 XX

PT New isolated polynucleotide and encoded polypeptides, useful in  
 PT diagnostics, forensics, gene mapping, identification of mutations  
 PT responsible for genetic disorders or other traits and to assess  
 PT biodiversity.  
 XX  
 PS Claim 1; SEQ ID NO 20827; 103pp; English.  
 XX  
 CC The invention relates to isolated polynucleotide (I) and polypeptide (II)  
 CC sequences. (I) is useful as hybridisation probes, polymerase chain  
 CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,  
 CC and in recombinant production of (II). The polynucleotides are also used  
 CC in diagnostics as expressed sequence tags for identifying expressed  
 CC genes. (I) is useful in gene therapy techniques to restore normal  
 CC activity of (II) or to treat disease states involving (II). (II) is  
 CC useful for generating antibodies against it, detecting or quantitating a  
 CC polypeptide in tissue, as molecular weight markers and as a food  
 CC supplement. (II) and its binding partners are useful in medical imaging  
 CC of sites expressing (II). (I) and (II) are useful for treating disorders  
 CC involving aberrant protein expression or biological activity. The  
 CC polypeptide and polynucleotide sequences have applications in  
 CC diagnostics, forensics, gene mapping, identification of mutations  
 CC responsible for genetic disorders or other traits to assess biodiversity  
 CC and to produce other types of data and products dependent on DNA and  
 CC amino acid sequences. AAS64197-AAS94584 represent novel human diagnostic  
 CC coding sequences of the invention. Note: The sequence data for this  
 CC patent did not appear in the printed specification, but was obtained in  
 CC electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 504 BP; 119 A; 122 C; 144 G; 117 T; 0 U; 2 Other;  
 Query Match 100.0%; Score 25; DB 5; Length 504;  
 Best Local Similarity 100.0%; Pred. No. 0.0002;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GACTGTCCACAGCATTCGCTGACC 25  
 DB 239 GACTGTCCACAGCATTCGCTGACC 263  
 RESULT 12  
 ACH38242  
 ID ACH38242 standard; cDNA; 504 BP.  
 XX  
 AC ACH38242;  
 XX  
 DT 13-OCT-2003 (first entry)  
 DE  
 XX Human endothelial cell cDNA #6375.  
 XX  
 KW Human; ss; sequencing by hybridisation; SBH; expressed sequence tag; EST;  
 KW genome mapping; biodiversity; genetic disorder.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US2003073623-A1.  
 XX  
 PD 17-APR-2003.  
 XX  
 XX 30-JUL-2001; 2001US-00918995.  
 PF  
 XX 30-JUL-2001; 2001US-00918995.  
 PR  
 XX (DRMA/) DRMANAC R T.  
 PA (LABA/) LABAT I.  
 PA (STAC/) STACHE-CRAIN B.  
 PA (DICK/) DICKSON M C.  
 PA (JONE/) JONES L W.  
 XX  
 XX Drmanac RT, Labat I, Stache-Crain B, Dickson MC, Jones LW;  
 PI  
 XX WPI; 2003-615964/58.  
 DR  
 XX

PT New polynucleotide sequences obtained from various cDNA libraries, useful  
PT as hybridization probes, as oligomers for PCR, for chromosome and gene  
PT mapping, in the recombinant production of protein, or in generating  
PT antisense DNA or RNA.

PS Claim 1; SEQ ID NO 25454; 44pp; English.

XX The invention relates to an isolated polynucleotide comprising any one of  
CC 38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence was  
CC determined by the technique of SBH (sequencing by hybridisation). Also  
CC included is a purified polypeptide comprising a sequence corresponding to  
CC a reading frame of the novel polynucleotide. The nucleic acid sequences  
CC are useful in diagnostics as expressed sequence tags (EST) for  
CC identifying expressed genes or for physical mapping of the human genome,  
CC in forensics, in assessing biodiversity, or in identifying mutations  
CC responsible for genetic disorders and other traits. The nucleotide  
CC sequences are also useful as hybridisation probes, as oligomers for PCR,  
CC for chromosome and gene mapping, in the recombinant production of  
CC protein, or in generating antisense DNA or RNA. The purified polypeptide  
CC is useful for generating antibodies specific for it. The present sequence  
CC is one of the 38043 isolated cDNA/EST sequences. Note: The sequence data  
CC for this patent did not form part of the printed specification, but was  
CC obtained in electronic format directly from USPTO at  
CC seqdata.uspto.gov/sequence.html?DocID=20030073623

XX Sequence 504 BP; 119 A; 122 C; 144 G; 117 T; 0 U; 2 Other;

Query Match 100.0%; Score 25; DB 8; Length 504;  
Best Local Similarity 100.0%; Pred. No. 0.0002;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GACTGTCCACAGCATTCGCTGACC 25  
|||  
DB 239 GACTGTCCACAGCATTCGCTGACC 263

RESULT 13

ABS73169  
ID ABS73169 standard; DNA; 561 BP.

AC ABS73169;

DT 04-DEC-2002 (first entry)

XX Human translocation (9: 22) (q34: q11) #1.

XX Chromosome aberration; oncogenic fusion protein; cancer;  
KW proliferative disease; cellular protein isoform; heat shock protein 90;  
KW HSP-90; rheumatoid arthritis; cancer; haematopoietic disorder;  
KW T cell lymphoma; B cell lymphoma; chronic myeloid leukaemia; CML;  
KW acute myeloid leukaemia; AML; chronic myelomonocytic leukaemia; CMML;  
KW acute lymphoblastic leukaemia; ALL; APL; NHL; solid tumour;  
KW papillary thyroid carcinoma; Ewing's sarcoma; melanoma; liposarcoma;  
KW rhabdomyosarcoma; synovial sarcoma; viral infection; gene; ds.

OS Homo sapiens.

XX WO200269900-A2.

PD 12-SEP-2002.

PF 01-MAR-2002; 2002WO-US006518.

PR 01-MAR-2001; 2001US-0272751P.

XX (CONF-) CONFORMA THERAPEUTICS CORP.

XX Fritz LC, Burrows FU;

DR WPI; 2002-698710/75.

XX Treating genetically-defined disease associated with chromosomal

PT aberrations yielding oncogenic fusion proteins, e.g. cell proliferative

PT diseases, involves administering an inhibitor of heat shock protein 90.  
XX Disclosure; Page 91-92; 389pp; English.

XX The invention describes a method of treating genetically-defined disease  
CC associated with chromosomal aberrations yielding oncogenic fusion  
CC proteins (I), treating cancerous cells containing (I) in a heterogeneous  
CC cell population, treating proliferative diseases associated with mutant  
CC protein or cellular protein isoforms (II) dependent on heat shock protein  
CC (HSP)-90, or selectively treating cells expressing (II) involving  
CC administering HSP90-inhibitor. The method is useful for treating  
CC genetically-defined disease with chromosomal aberration yielding  
CC oncogenic fusion protein, treating cancerous cells containing fusion  
CC protein in heterogeneous cell population, treating proliferative disease  
CC (e.g. rheumatoid arthritis or cancer) associated with mutant protein or  
CC cellular protein isoform dependent on heat shock protein (HSP)-90 (e.g.  
CC p53), or selectively treating cells expressing mutant protein or cellular  
CC protein isoform in a patient heterozygous for (II). The method is useful  
CC for treating a disease e.g. haematopoietic disorder such as T or B cell  
CC lymphoma, chronic myeloid leukaemia (CML), APL, ALL, NHL and CMML,  
CC or a disease characterised by a solid tumour such as papillary thyroid  
CC carcinoma, Ewing's sarcoma, melanoma, liposarcoma, rhabdomyosarcoma and  
CC synovial sarcoma. The method is also useful for treating viral  
CC infections. This represents the DNA sequence of a chromosome aberration

XX Sequence 561 BP; 134 A; 134 C; 136 G; 157 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 6; Length 561;  
Best Local Similarity 100.0%; Pred. No. 0.0002;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GACTGTCCACAGCATTCGCTGACC 25  
|||  
DB 84 GACTGTCCACAGCATTCGCTGACC 108

RESULT 14

ABS73172  
ID ABS73172 standard; DNA; 679 BP.

AC ABS73172;

DT 04-DEC-2002 (first entry)

XX DNA encoding human translocation (9: 22) (q34: q11) protein #3.

XX Chromosome aberration; oncogenic fusion protein; cancer;  
KW proliferative disease; cellular protein isoform; heat shock protein 90;  
KW HSP-90; rheumatoid arthritis; cancer; haematopoietic disorder;  
KW T cell lymphoma; B cell lymphoma; chronic myeloid leukaemia; CML;  
KW acute myeloid leukaemia; AML; chronic myelomonocytic leukaemia; CMML;  
KW acute lymphoblastic leukaemia; ALL; APL; NHL; solid tumour;  
KW papillary thyroid carcinoma; Ewing's sarcoma; melanoma; liposarcoma;  
KW rhabdomyosarcoma; synovial sarcoma; viral infection; gene; ds.

OS Homo sapiens.

XX WO200269900-A2.

PD 12-SEP-2002.

PF 01-MAR-2002; 2002WO-US006518.

PR 01-MAR-2001; 2001US-0272751P.

XX (CONF-) CONFORMA THERAPEUTICS CORP.

XX Fritz LC, Burrows FU;

DR WPI; 2002-698710/75.

XX P-PSDB; ABC95011.

XX Treating genetically-defined disease associated with chromosomal

PT aberrations yielding oncogenic fusion proteins, e.g. cell proliferative

PT aberrations yielding oncogenic fusion proteins, e.g. cell proliferative  
PT diseases, involves administering an inhibitor of heat shock protein 90.  
XX  
PS Disclosure; Page 94-95; 389pp; English.  
XX  
CC The invention describes a method of treating genetically-defined disease  
CC associated with chromosomal aberrations yielding oncogenic fusion  
CC proteins (I), treating cancerous cells containing (I) in a heterogeneous  
CC cell population, treating proliferative diseases associated with mutant  
CC protein or cellular protein isoforms (II) dependent on heat shock protein  
CC (HSP)-90, or selectively treating cells expressing (II) involving  
CC administering HSP90-inhibitor. The method is useful for treating  
CC genetically-defined disease with chromosomal aberration yielding  
CC oncogenic fusion protein, treating cancerous cells containing fusion  
CC protein in heterogeneous cell population, treating proliferative disease  
CC (e.g. rheumatoid arthritis or cancer) associated with mutant protein or  
CC cellular protein isoform dependent on heat shock protein (HSP)-90 (e.g.  
CC p53), or selectively treating cells expressing mutant protein or cellular  
CC protein isoform in a patient heterozygous for (II). The method is useful  
CC for treating a disease e.g. haematopoietic disorder such as T or B cell  
CC lymphoma, chronic myeloid leukaemia (CML), APL, ALL, AML, NHL and CML,  
CC or a disease characterised by a solid tumour such as papillary thyroid  
CC carcinoma, Ewing's sarcoma, melanoma, liposarcoma, rhabdomyosarcoma and  
CC synovial sarcoma. The method is also useful for treating viral  
CC infections. This represents the DNA sequence of a chromosome aberration  
XX  
SQ Sequence 679 BP; 186 A; 165 C; 184 G; 144 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 6; Length 679;  
Best Local Similarity 100.0%; Pred. No. 0.0002;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GACTGTCCACAGCATTCCGCTGACC 25  
DB 302 GACTGTCCACAGCATTCCGCTGACC 326

RESULT 15  
ABV29306/c  
ID ABV29306 standard; cDNA; 766 BP.  
XX AC ABV29306;  
XX  
DT 16-SEP-2002 (first entry)  
XX  
DE Human prostate expression marker cDNA 29297.  
XX  
KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;  
KW pharmacogenomic marker; gene; ss.  
XX  
OS Homo sapiens.  
XX  
FN WO200160860-A2.  
XX  
PD 23-AUG-2001.  
XX  
PF 20-FEB-2001; 2001WO-US005171.  
XX  
PR 17-FEB-2000; 2000US-0183319P.  
PR 16-MAR-2000; 2000US-0189862P.  
PR 25-MAY-2000; 2000US-0207454P.  
PR 09-JUN-2000; 2000US-0211314P.  
PR 18-JUL-2000; 2000US-0219007P.  
PR 13-DEC-2000; 2000US-0255281P.  
XX  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
XX  
PI Schlegel R, Endege WO, Monahan JE;  
XX  
DX WFI; 2001-662795/76.  
XX  
PT Novel isolated nucleic acid molecule associated with cancerous state of  
PT prostate cells and correlating with presence of prostate cancer, useful

PT for detecting presence of prostate cancer, stage of prostate cancer.  
XX  
PS Claim 1; Page 6267; 11750pp; English.  
XX  
CC The invention relates to an isolated nucleic acid molecule (I) comprising  
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the  
CC specification or its complement. (I) is useful for: (a) assessing whether  
CC a patient is afflicted with prostate cancer; (b) monitoring the  
CC progression of prostate cancer in a patient; (c) assessing the efficacy  
CC of a test compound to inhibit prostate cancer in a patient; (d) assessing  
CC the efficacy of a therapy for inhibiting prostate cancer in a patient;  
CC (e) selecting a composition for inhibiting prostate cancer in a patient;  
CC (f) assessing the prostate cell carcinogenic potential of a compound; (g)  
CC determining whether prostate cancer has metastasized in a patient; (h)  
CC assessing the aggressiveness or indolence of prostate cancer in a patient  
CC ; (I) is also useful as a pharmacodynamic or pharmacogenomic marker  
XX  
SQ Sequence 766 BP; 166 A; 237 C; 193 G; 170 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 5; Length 766;  
Best Local Similarity 100.0%; Pred. No. 0.0002;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GACTGTCCACAGCATTCCGCTGACC 25  
DB 553 GACTGTCCACAGCATTCCGCTGACC 529

Search completed: May 26, 2004, 16:52:17  
Job time : 112.497 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: May 26, 2004, 16:02:51 ; Search time 21.0702 Seconds  
(without alignments)  
658.454 Million cell updates/sec

Title: US-09-121-239-9

Perfect score: 25

Sequence: 1 GACTGTCCACAGCATTCGCTGACC 25

Scoring table: OLIGO NUC

Gapop 60.0 , Gapext 60.0

Searched: 682709 seqs, 277475446 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents NA:  
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2: /cgn2\_6/ptodata/2/ina/5B\_COMB.seq:  
3: /cgn2\_6/ptodata/2/ina/6A\_COMB.seq:  
4: /cgn2\_6/ptodata/2/ina/6B\_COMB.seq:  
5: /cgn2\_6/ptodata/2/ina/PTUS\_COMB.seq:  
6: /cgn2\_6/ptodata/2/ina/backfiles1.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	25	100.0	56	1	US-07-940-652-17
2	25	100.0	56	1	US-08-255-553-17
3	25	100.0	1078	4	US-09-310-842-1
4	24	96.0	26	1	US-08-363-233B-6
5	18	72.0	22	1	US-08-152-621-11
6	18	72.0	22	5	PCT-US92-05035-11
7	18	72.0	62	3	US-08-448-446B-1
8	18	72.0	81	3	US-08-448-448B-2
9	18	72.0	257	1	US-08-152-621-1
10	18	72.0	257	1	US-08-306-691B-36
11	18	72.0	257	5	PCT-US92-05035-1
12	16	64.0	28	3	US-09-341-955-2
13	16	64.0	28	4	US-09-779-881-2
14	16	64.0	864	4	US-09-489-039A-2414
15	14	56.0	61	3	US-08-448-448B-19
16	14	56.0	363	3	US-08-905-223-206
17	14	56.0	500	4	US-09-621-976-9874
18	14	56.0	930	4	US-09-252-991A-11373
19	14	56.0	981	4	US-09-252-991A-11296
20	14	56.0	1094	4	US-09-280-116-243
21	14	56.0	1197	4	US-09-252-991A-6737
22	14	56.0	1269	4	US-09-149-476-143
23	14	56.0	1272	4	US-09-252-991A-6952
24	14	56.0	1361	4	US-09-280-116-197
25	14	56.0	1427	4	US-09-907-794A-152
26	14	56.0	1427	4	US-09-905-125A-152
27	14	56.0	1427	4	US-09-902-775A-152

c 28	14	56.0	1620	1	US-07-616-022C-9	Sequence 9, Appli
c 29	14	56.0	1869	4	US-09-406-045-2	Sequence 2, Appli
c 30	14	56.0	2346	4	US-09-252-991A-6782	Sequence 6782, Ap
c 31	14	56.0	3041	4	US-09-339-159B-31	Sequence 31, Appl
c 32	14	56.0	36519	3	US-08-923-137-2	Sequence 2, Appli
c 33	14	56.0	786431	4	US-09-751-389-3	Sequence 3, Appli
c 34	13	52.0	277	4	US-09-313-234A-1791	Sequence 1791, Ap
c 35	13	52.0	288	4	US-09-134-000C-2182	Sequence 2182, Ap
c 36	13	52.0	396	4	US-09-621-976-16576	Sequence 16576, A
c 37	13	52.0	403	4	US-09-621-976-16577	Sequence 16577, A
c 38	13	52.0	437	4	US-09-221-017B-243	Sequence 243, App
c 39	13	52.0	444	4	US-09-252-991A-6828	Sequence 6828, Ap
c 40	13	52.0	458	4	US-09-621-976-16578	Sequence 16578, A
c 41	13	52.0	477	4	US-09-489-039A-1314	Sequence 1314, Ap
c 42	13	52.0	489	4	US-09-252-991A-12619	Sequence 12619, A
c 43	13	52.0	504	3	US-09-328-111-120	Sequence 120, App
c 44	13	52.0	792	4	US-09-489-039A-1358	Sequence 1358, Ap
c 45	13	52.0	857	4	US-09-660-176-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1  
US-07-940-652-17  
; Sequence 17, Application US/07940652  
; Patent No. 5424413  
; GENERAL INFORMATION:  
; APPLICANT: James J. Hogan et al.  
; TITLE OF INVENTION: BRANCHED NUCLEIC ACID PROBES  
; NUMBER OF SEQUENCES: 31  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 611 West Sixth Street  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: USA  
; ZIP: 90017  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: IBM P.C. DOS Version 3.30  
; SOFTWARE: WordPerfect (Version 5.1)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/940.652  
; FILING DATE: 19920904  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/07/827.021  
; FILING DATE: 22-JAN-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Warburg, Richard J.  
; REGISTRATION NUMBER: 32,327  
; REFERENCE/DOCKET NUMBER: 199/201  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (213) 489-1600  
; TELEFAX: (213) 955-0440  
; TELEX: 67-3510  
; INFORMATION FOR SEQ ID NO: 17:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 56  
; TYPE: NUCLEIC ACID  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-07-940-652-17

Query Match 100.0%; Score 25; DB 1; Length 56;  
Best Local Similarity 100.0%; Pred. No. 6.5e-06;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GACTGTCCACAGCATTCGCTGACC 25  
DB 3 GACTGTCCACAGCATTCGCTGACC 27

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RESULT 2
US-08-255-553-17
; Sequence 17, Application US/08255553
; Patent No. 5451503
; GENERAL INFORMATION:
; APPLICANT: James J. Hogan et al.
; TITLE OF INVENTION: BRANCHED NUCLEIC ACID PROBES
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 611 West Sixth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90017
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS Version 3.30
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/255,553
; FILING DATE: 07-JUN-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/940,652
; FILING DATE: 04-SEP-1992
; APPLICATION NUMBER: US/07/827,021
; FILING DATE: 22-JAN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 199/201
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 56
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-255-553-17

Query Match 100.0%; Score 25; DB 1; Length 56;
Best Local Similarity 100.0%; Pred. No. 6.5e-06;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GACTGTCCACAGCATTCGCGTGACC 25
DB 3 GACTGTCCACAGCATTCGCGTGACC 27

RESULT 3
US-09-310-842-1
; Sequence 1, Application US/09310842A
; Patent No. 6451593
; GENERAL INFORMATION:
; APPLICANT: Wittig, Prof. Burghardt
; APPLICANT: Junghans, Claas
; TITLE OF INVENTION: Design Principle for Constructing Expression Constructs for Gene
; FILE REFERENCE: XI 597/99
; CURRENT APPLICATION NUMBER: US/09/310,842A
; CURRENT FILING DATE: 1999-05-12
; EARLIER APPLICATION NUMBER: DE 196 48 625.4
; EARLIER FILING DATE: 1996-11-13
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1
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LENGTH: 1078
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: gene
LOCATION: (1)..(1078)
OTHER INFORMATION: bcr3=abl2; Oligo DNA Dumbbell
FEATURE:
NAME/KEY: misc_binding
LOCATION: (1)..(2)
OTHER INFORMATION: intramolecular binding site; the T-nucleotides at position 1 to
OTHER INFORMATION: 2 can be modified with amino or caroxy features
FEATURE:
NAME/KEY: misc_binding
LOCATION: (1077)..(1078)
OTHER INFORMATION: intramolecular binding site; the T-nucleotides at position 1077
OTHER INFORMATION: to 1078 can be modified with amino or caroxy features
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Strandness: both; nucleic
OTHER INFORMATION: acid (linear), hypothetical: No. 6451593 anti-sense: No
US-09-310-842-1

Query Match 100.0%; Score 25; DB 4; Length 1078;
Best Local Similarity 100.0%; Pred. No. 6.5e-06;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GACTGTCCACAGCATTCGCGTGACC 25
DB 662 GACTGTCCACAGCATTCGCGTGACC 686

RESULT 4
US-08-363-233B-6
; Sequence 6, Application US/08363233B
; Patent No. 5714383
; GENERAL INFORMATION:
; APPLICANT: Thompson, James D.
; TITLE OF INVENTION: METHOD AND REAGENT FOR TREATING CHRONIC
; TITLE OF INVENTION: MYELOGENOUS LEUKEMIA
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: Suite 4700
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/363,233B
; FILING DATE: December 23, 1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION DATA: including application
; PRIOR APPLICATION DATA: described below: 2
; APPLICATION NUMBER: 07/882,822
; FILING DATE: May 14, 1992
; APPLICATION NUMBER: 08/193,922
; FILING DATE: February 7, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 209/165
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
```

INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 26 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-363-233B-6

Query Match 96.0%; Score 24; DB 1; Length 26;  
Best Local Similarity 79.2%; Pred. No. 2.5e-05;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GACTGTCACAGCATTCGCTGACC 24  
|||:|||||:|||||:|||||:  
DB 3 GACUGUCCACAGCAUUCGCGUGAC 26

## RESULT 5

US-08-152-621-11  
Sequence 11, Application US/08152621  
Patent No. 5652222  
GENERAL INFORMATION:  
APPLICANT: Calabretta, Bruno  
TITLE OF INVENTION: Selective Inhibition of  
Leukemic Cell Proliferation by bcr-abl  
TITLE OF INVENTION: Antisense Oligonucleotides  
NUMBER OF SEQUENCES: 34  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SEIDEL, GONDA, LAVORGNA  
STREET: 1800 Two Penn Center  
CITY: Philadelphia  
STATE: Pennsylvania  
COUNTRY: U.S.A.  
ZIP: 19102

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb  
COMPUTER: IBM PS/2  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: WordPerfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/152,621  
FILING DATE: No. 5652222ember 15, 1993  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/718,302  
FILING DATE: June 18, 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Monaco, Daniel A.  
REGISTRATION NUMBER: 30,480  
REFERENCE/DOCKET NUMBER: 6056-120 (CT.) 1  
TELEPHONE: (215) 568-8383  
TELEFAX: (215) 568-5549  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 22 Nucleotides  
TYPE: nucleic acid  
STRANDEDNESS: double stranded  
TOPOLOGY: linear  
US-08-152-621-11

Query Match 72.0%; Score 18; DB 1; Length 22;  
Best Local Similarity 100.0%; Pred. No. 0.082;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CACAGCATTCGCTGACC 25  
|||||:|||||:|||||:  
DB 1 CACAGCATTCGCTGACC 18

## RESULT 6

PCT-US92-05035-11  
Sequence 11, Application PC/TUS9205035  
GENERAL INFORMATION:  
APPLICANT: Calabretta, Bruno  
TITLE OF INVENTION: Selective Inhibition of  
Leukemic Cell Proliferation by bcr-abl  
TITLE OF INVENTION: Antisense Oligonucleotides  
NUMBER OF SEQUENCES: 34  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Temple University - Of The Common-  
wealth System of Higher Education  
STREET: 406 University Services Building  
CITY: Philadelphia  
STATE: Pennsylvania  
COUNTRY: U.S.A.  
ZIP: 19122

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb  
COMPUTER: IBM PS/2  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: WordPerfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US92/05035  
FILING DATE: 19920615  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/718,302  
FILING DATE: June 18, 1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/869,911  
FILING DATE: April 14, 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Monaco, Daniel A.  
REGISTRATION NUMBER: 30,480  
REFERENCE/DOCKET NUMBER: 6056-120 (CIP) 1  
TELEPHONE: (215) 568-8383  
TELEFAX: (215) 568-5549  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 22 Nucleotides  
TYPE: NUCLEIC ACID  
STRANDEDNESS: double stranded  
TOPOLOGY: linear  
PCT-US92-05035-11

Query Match 72.0%; Score 18; DB 5; Length 22;  
Best Local Similarity 100.0%; Pred. No. 0.082;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CACAGCATTCGCTGACC 25  
|||||:|||||:|||||:  
DB 1 CACAGCATTCGCTGACC 18

## RESULT 7

US-08-448-446B-1  
Sequence 1, Application US/08448446B  
Patent No. 6080851  
GENERAL INFORMATION:  
APPLICANT: Pachuk et al.  
TITLE OF INVENTION: Compounds and Methods for the Treatment  
of Leukemias  
TITLE OF INVENTION: Of Leukemias  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Woodcock Washburn  
STREET: One Liberty Place - 46th Floor  
CITY: Philadelphia  
STATE: PA

COUNTRY: USA  
ZIP: 19103  
COMPUTER READABLE FORM:  
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE  
COMPUTER: IBM PS/2  
OPERATING SYSTEM: PC-DOS  
SOFTWARE: WORDPERFECT 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/448,446B  
FILING DATE: July 10, 1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/989,852  
FILING DATE: December 4, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Doreen Yanko Trujillo  
REGISTRATION NUMBER: 35,719  
REFERENCE/DOCKET NUMBER: APOL-0020  
TELECOMMUNICATION INFORMATION: C  
TELEPHONE: (215) 568-3100  
TELEFAX: (215) 568-3439  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 62  
TYPE: Nucleic Acid  
STRANDEDNESS: Single  
TOPOLOGY: Linear  
ANTI-SENSE: NO  
US-08-448-446B-1

Query Match 72.0%; Score 18; DB 3; Length 62;  
Best Local Similarity 83.3%; Pred. No. 0.082;  
Matches 15; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 8 CACAGCATTCGCTGACC 25  
|||||:|||||  
Db 1 CACAGCAUUCGCGUACC 18

RESULT 8  
US-08-448-446B-2/c  
Sequence 2, Application US/08448446B  
Patent No. 6080851  
GENERAL INFORMATION:  
APPLICANT: Pachuk et al.  
TITLE OF INVENTION: Compounds and Methods for the Treatment  
OF INVENTION: of Leukemias  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Woodcock Washburn  
ADDRESSEE: Kurtz Mackiewicz & No. 6080851ris  
STREET: One Liberty Place - 46th Floor  
CITY: Philadelphia  
STATE: PA  
COUNTRY: USA  
ZIP: 19103  
COMPUTER READABLE FORM:  
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE  
COMPUTER: IBM PS/2  
OPERATING SYSTEM: PC-DOS  
SOFTWARE: WORDPERFECT 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/448,446B  
FILING DATE: July 10, 1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/989,852  
FILING DATE: December 4, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Doreen Yanko Trujillo  
REGISTRATION NUMBER: 35,719  
REFERENCE/DOCKET NUMBER: APOL-0020  
TELECOMMUNICATION INFORMATION: C

TELEPHONE: (215) 568-3100  
TELEFAX: (215) 568-3439  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 81  
TYPE: Nucleic Acid  
STRANDEDNESS: Single  
TOPOLOGY: Linear  
ANTI-SENSE:  
US-08-448-446B-2  
Query Match 72.0%; Score 18; DB 3; Length 81;  
Best Local Similarity 100.0%; Pred. No. 0.082;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 8 CACAGCATTCGCTGACC 25  
|||||:|||||  
Db 81 CACAGCATTCGCTGACC 64

RESULT 9  
US-08-152-621-1  
Sequence 1, Application US/08152621  
Patent No. 5652222  
GENERAL INFORMATION:  
APPLICANT: Calabretta, Bruno  
APPLICANT: Gewirtz, Alan M.  
TITLE OF INVENTION: Selective Inhibition of  
Leukemic Cell Proliferation by bcr-abl  
TITLE OF INVENTION: Antisense Oligonucleotides  
NUMBER OF SEQUENCES: 34  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SEIDEL, GONDA, LAVORGNA  
ADDRESSEE: & MONACO, P.C.  
STREET: 1800 Two Penn Center  
CITY: Philadelphia  
STATE: Pennsylvania  
COUNTRY: U.S.A.  
ZIP: 19102

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb  
COMPUTER: IBM PS/2  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: WordPerfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/152,621  
FILING DATE: No. 5652222ember 15, 1993  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/718,302  
FILING DATE: June 18, 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Monaco, Daniel A.  
REGISTRATION NUMBER: 30,480  
REFERENCE/DOCKET NUMBER: 6056-120 (CT.) 1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (215) 568-8383  
TELEFAX: (215) 568-5549  
TELEX: No. 5652222e  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 257 Nucleotides  
TYPE: nucleic acid  
STRANDEDNESS: single stranded  
TOPOLOGY: linear  
US-08-152-621-1

Query Match 72.0%; Score 18; DB 1; Length 257;  
Best Local Similarity 100.0%; Pred. No. 0.082;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CACAGCATTCGCTGACC 25  
|||||:|||||



Db 1 CACAGCATTCGCTGACC 18

## RESULT 10

US-08-306-691B-36

; Sequence 36, Application US/08306691B

; Patent No. 5734039

; GENERAL INFORMATION:

; APPLICANT: Calabretta, Bruno

; APPLICANT: Skorski, Tomasz

; TITLE OF INVENTION: ANTISENSE

; TITLE OF INVENTION: OLIGONUCLEOTIDES TARGETING COOPERATING ONCOGENES

; NUMBER OF SEQUENCES: 55

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Seidel, Gonda, Lavorigna & Monaco, P.C.

; STREET: Two Penn Center, Suite 1800

; CITY: Philadelphia

; STATE: Pennsylvania

; COUNTRY: U.S.A.

; ZIP: 19102

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb

; COMPUTER: IBM PS/2

; OPERATING SYSTEM: MS-DOS

; SOFTWARE: WordPerfect 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/306,691B

; FILING DATE: September 15, 1994

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Monaco, Daniel A.

; REGISTRATION NUMBER: 30,480

; REFERENCE/DOCKET NUMBER: 8321-8

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (215) 568-8383

; TELEFAX: (215) 568-5549

; TELEX: No. 5734039e

; INFORMATION FOR SEQ ID NO: 36:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 257 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

US-08-306-691B-36

Query Match 72.0%; Score 18; DB 1; Length 257;

Best Local Similarity 100.0%; Pred. No. 0.082;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CACAGCATTCGCTGACC 25

|||||

Db 1 CACAGCATTCGCTGACC 18

## RESULT 11

PCT-US92-05035-1

; Sequence 1, Application PC/TUS9205035

; GENERAL INFORMATION:

; APPLICANT: Calabretta, Bruno

; APPLICANT: Gewirtz, Alan M.

; TITLE OF INVENTION: Selective Inhibition of

; TITLE OF INVENTION: Leukemic Cell Proliferation by bcr-abl

; TITLE OF INVENTION: Antisense Oligonucleotides

; NUMBER OF SEQUENCES: 34

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Temple University - Of The Common-

; ADDRESSEE: wealth System of Higher Education

; STREET: 406 University Services Building

; CITY: Philadelphia

; STATE: Pennsylvania

COUNTRY: U.S.A.

ZIP: 19122

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb

COMPUTER: IBM PS/2

OPERATING SYSTEM: MS-DOS

SOFTWARE: WordPerfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US92/05035

FILING DATE: 19920615

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/718,302

FILING DATE: June 18, 1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/869,911

FILING DATE: April 14, 1991

ATTORNEY/AGENT INFORMATION:

NAME: Monaco, Daniel A.

REGISTRATION NUMBER: 30,480

REFERENCE/DOCKET NUMBER: 6056-120 (CIP) 1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (215) 568-8383

TELEFAX: (215) 568-5549

TELEX: None

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 257 Nucleotides

TYPE: NUCLEIC ACID

STRANDEDNESS: single stranded

TOPOLOGY: linear

PCT-US92-05035-1

Query Match

Best Local Similarity 72.0%; Score 18; DB 5; Length 257;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CACAGCATTCGCTGACC 25

|||||

Db 1 CACAGCATTCGCTGACC 18

## RESULT 12

US-09-341-955-2/c

; Sequence 2, Application US/09341955

; Patent No. 6251690

; GENERAL INFORMATION:

; APPLICANT: Kulmala, Sakari

; APPLICANT: Ala-Kieme, Timo

; APPLICANT: Eskola, Jarkko

; APPLICANT: Korpela, Timo

; TITLE OF INVENTION: ELECTRICAL EXCITATION OF LABEL SUBSTANCES AT COATED

; TITLE OF INVENTION: ELECTRODES

; FILE REFERENCE: TUR-080

; CURRENT APPLICATION NUMBER: US/09/341,955

; CURRENT FILING DATE: 1999-07-21

; EARLIER APPLICATION NUMBER: PCT/FI98/00114

; EARLIER FILING DATE: 1999-02-10

; NUMBER OF SEQ ID NOS: 2

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 2

; LENGTH: 28

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence:

; OTHER INFORMATION: oligonucleotide containing an amino group

US-09-341-955-2

Query Match

Best Local Similarity 64.0%; Score 16; DB 3; Length 28;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: May 27, 2004, 11:30:47 ; Search time 131.564 Seconds  
(without alignments)  
864.392 Million cell updates/sec

Title: US-09-121-239-9  
Perfect score: 25  
Sequence: 1 GACTGTCCACAGCATTCGCTGACC 25

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 2960401 seqs, 2274450654 residues

Word size : 0  
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Minimum DB seq length: 0  
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15: /cgn2\_6/ptodata/2/pubpna/US10C\_PUBCOMB.seq.\*  
16: /cgn2\_6/ptodata/2/pubpna/US10C\_PUBCOMB.seq.\*  
17: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq.\*  
18: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq.\*  
19: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match %	ID	Description
1	25	100.0	504 10	US-09-918-995-25454
2	25	100.0	542 9	US-09-796-692-8117
3	25	100.0	542 15	US-10-040-862-8117
4	25	100.0	542 16	US-10-057-475B-8117
5	25	100.0	542 16	US-10-154-884B-8117
6	25	100.0	596 9	US-09-796-692-8967
7	25	100.0	596 15	US-10-040-862-8967
8	25	100.0	596 16	US-10-057-475B-8967
9	25	100.0	596 16	US-10-154-884B-8967
10	25	100.0	1078 15	US-10-228-811-1
11	25	100.0	4739 9	US-09-954-531-586
12	25	100.0	4739 13	US-10-193-651-22
13	17	68.0	3664 15	US-10-128-714-206
14	17	68.0	3750 15	US-10-128-714-5206

c 15 64.0 28 9 US-09-779-881-2  
c 16 64.0 285 11 US-09-864-408A-4649  
c 17 60.0 383 9 US-09-960-352-9070  
c 18 60.0 483 9 US-09-974-300-8116  
c 19 60.0 501 9 US-09-974-300-8143  
c 20 60.0 765 16 US-10-369-433-39879  
c 21 60.0 804 16 US-10-369-433-39128  
c 22 60.0 804 16 US-10-369-433-39497  
c 23 60.0 828 16 US-10-388-934-133  
c 24 60.0 837 13 US-10-282-122A-25393  
c 25 60.0 933 9 US-09-974-300-2109  
c 26 60.0 3076 15 US-10-128-714-495  
c 27 60.0 3076 15 US-10-128-714-5495  
c 28 60.0 203264 13 US-10-087-132-988  
c 29 56.0 16 9 US-09-068-817-9  
c 30 56.0 21 10 US-09-864-636A-1953  
c 31 56.0 21 11 US-09-864-426A-1953  
c 32 56.0 21 15 US-10-084-839-1953  
c 33 56.0 28 9 US-09-747-163-7  
c 34 56.0 80 12 US-10-384-245-179  
c 35 56.0 134 15 US-10-029-386-26303  
c 36 56.0 268 13 US-10-052-283-149  
c 37 56.0 335 9 US-09-815-343-156  
c 38 56.0 335 13 US-10-097-105-156  
c 39 56.0 430 10 US-09-918-995-2118  
c 40 56.0 460 9 US-09-969-347-68  
c 41 56.0 461 10 US-09-918-995-14682  
c 42 56.0 462 10 US-09-918-995-9876  
c 43 56.0 474 16 US-10-369-433-38733  
c 44 56.0 493 13 US-10-052-283-38  
c 45 501 15 US-10-060-036-3547

## ALIGNMENTS

## RESULT 1

US-09-918-995-25454  
; Sequence 25454, Application US/09918995  
; Publication No. US20030073623A1  
; GENERAL INFORMATION:  
; APPLICANT: Hyseq, Inc.  
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED  
; FILE REFERENCE: 20411-756  
; CURRENT APPLICATION NUMBER: US/09/918,995  
; CURRENT FILING DATE: 2001-07-30  
; PRIOR APPLICATION NUMBER: US/09/235,076  
; PRIOR FILING DATE: 1999-01-20  
; NUMBER OF SEQ ID NOS: 38054  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 25454  
; LENGTH: 504  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1)..(504)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-918-995-25454

Query Match 100.0%; Score 25; DB 10; Length 504;  
Best Local Similarity 100.0%; Pred. No. 2.6e-05;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GACTGTCCACAGCATTCGCTGACC 25

DB 239 GACTGTCCACAGCATTCGCTGACC 263

## RESULT 2

US-09-796-692-8117  
; Sequence 8117, Application US/09796692

```
; Publication No. US20020198362A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY
; TITLE OF INVENTION: HEMATOLOGICAL MALIGNANCIES
; FILE REFERENCE: 2077.001200
; CURRENT APPLICATION NUMBER: US/09/796,692
; CURRENT FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/222,903
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 60/223,416
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: 60/223,378
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: US 09/796,692
; PRIOR FILING DATE: 2001-03-01
; NUMBER OF SEQ ID NOS: 10467
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8117
; LENGTH: 542
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-796-692-8117

Query Match      100.0%; Score 25; DB 9; Length 542;
Best Local Similarity 100.0%; Pred. No. 2.6e-05;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GACTGTCCACAGCATTCGCTGACC 25
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DB      433 GACTGTCCACAGCATTCGCTGACC 457

RESULT 3
US-10-040-862-8117
; Sequence 8117, Application US/10040862
; Publication No. US20030078396A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; TITLE OF INVENTION: Hematological Malignancies
; FILE REFERENCE: 014058-013200S
; CURRENT APPLICATION NUMBER: US/10/040,862
; CURRENT FILING DATE: 2001-11-06
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
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; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: US 60/223,416
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: US 60/223,378
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: US 09/796,692
; PRIOR FILING DATE: 2001-03-01
; NUMBER OF SEQ ID NOS: 10467
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8117
; LENGTH: 542
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-040-862-8117

Query Match      100.0%; Score 25; DB 15; Length 542;
Best Local Similarity 100.0%; Pred. No. 2.6e-05;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GACTGTCCACAGCATTCGCTGACC 25
        |||||
DB      433 GACTGTCCACAGCATTCGCTGACC 457

RESULT 4
US-10-057-475B-8117
; Sequence 8117, Application US/10057475B
; Publication No. US20040002068A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Clapper, Jonathan David
; APPLICANT: Wang, Aljun
; APPLICANT: Ordonez, Nadia
; APPLICANT: Carter, Lauren
; APPLICANT: McNeill, Patricia Dianne
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; TITLE OF INVENTION: Hematological Malignancies
; FILE REFERENCE: 014058-014402US
; CURRENT APPLICATION NUMBER: US/10/057,475B
; CURRENT FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
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; PRIOR APPLICATION NUMBER: US 60/222,903  
 ; PRIOR FILING DATE: 2000-08-03  
 ; Remaining Prior Application data removed - See File Wrapper or PALM.  
 ; NUMBER OF SEQ ID NOS: 10979  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 8117  
 ; LENGTH: 542  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-10-057-475B-8117

Query Match 100.0%; Score 25; DB 16; Length 542;  
 Best Local Similarity 100.0%; Pred. No. 2.6e-05;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GACTGTCCACAGCATTCGCTGACC 25  
 |||||  
 Db 433 GACTGTCCACAGCATTCGCTGACC 457

RESULT 5

US-10-154-884B-8117  
 ; Sequence 8117, Application US/10154884B  
 ; Publication No. US20040005561A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Gaiger, Alexander  
 ; APPLICANT: Algate, Paul A.  
 ; APPLICANT: Mannion, Jane  
 ; APPLICANT: Retter, Marc W.  
 ; APPLICANT: Corixa Corporation  
 ; TITLE OF INVENTION: Hematological Malignancies  
 ; FILE REFERENCE: 014058-013521US  
 ; CURRENT APPLICATION NUMBER: US/10/154,884B  
 ; CURRENT FILING DATE: 2002-05-23  
 ; PRIOR APPLICATION NUMBER: US 60/186,126  
 ; PRIOR FILING DATE: 2000-03-01  
 ; PRIOR APPLICATION NUMBER: US 60/190,479  
 ; PRIOR FILING DATE: 2000-03-17  
 ; PRIOR APPLICATION NUMBER: US 60/200,545  
 ; PRIOR FILING DATE: 2000-04-27  
 ; PRIOR APPLICATION NUMBER: US 60/200,303  
 ; PRIOR FILING DATE: 2000-04-28  
 ; PRIOR APPLICATION NUMBER: US 60/200,779  
 ; PRIOR FILING DATE: 2000-04-28  
 ; PRIOR APPLICATION NUMBER: US 60/200,999  
 ; PRIOR FILING DATE: 2000-05-01  
 ; PRIOR APPLICATION NUMBER: US 60/202,084  
 ; PRIOR FILING DATE: 2000-05-04  
 ; PRIOR APPLICATION NUMBER: US 60/218,950  
 ; PRIOR FILING DATE: 2000-07-14  
 ; PRIOR APPLICATION NUMBER: US 60/222,903  
 ; PRIOR FILING DATE: 2000-08-03  
 ; PRIOR APPLICATION NUMBER: US 60/223,416  
 ; PRIOR FILING DATE: 2000-08-04  
 ; PRIOR APPLICATION NUMBER: 60/223,378  
 ; PRIOR FILING DATE: 2000-08-07  
 ; NUMBER OF SEQ ID NOS: 11290  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 8117  
 ; LENGTH: 542  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-10-154-884B-8117

Query Match 100.0%; Score 25; DB 16; Length 542;  
Best Local Similarity 100.0%; Pred. No. 2.6e-05;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GACTGTCCACAGCATTCGCTGACC 25  
 |||||  
 Db 433 GACTGTCCACAGCATTCGCTGACC 457

RESULT 6

US-09-796-692-8967  
 ; Sequence 8967, Application US/09796692  
 ; Publication No. US20020198362A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Gaiger, Alexander  
 ; APPLICANT: Algate, Paul A.  
 ; APPLICANT: Mannion, Jane  
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY  
 ; FILE REFERENCE: 2077.001200  
 ; CURRENT APPLICATION NUMBER: US/09/796,692  
 ; CURRENT FILING DATE: 2001-03-01  
 ; PRIOR APPLICATION NUMBER: 60/186,126  
 ; PRIOR FILING DATE: 2000-03-01  
 ; PRIOR APPLICATION NUMBER: 60/190,479  
 ; PRIOR FILING DATE: 2000-03-17  
 ; PRIOR APPLICATION NUMBER: 60/200,545  
 ; PRIOR FILING DATE: 2000-04-27  
 ; PRIOR APPLICATION NUMBER: 60/200,303  
 ; PRIOR FILING DATE: 2000-04-28  
 ; PRIOR APPLICATION NUMBER: 60/200,779  
 ; PRIOR FILING DATE: 2000-04-28  
 ; PRIOR APPLICATION NUMBER: 60/200,999  
 ; PRIOR FILING DATE: 2000-05-01  
 ; PRIOR APPLICATION NUMBER: 60/202,084  
 ; PRIOR FILING DATE: 2000-05-04  
 ; PRIOR APPLICATION NUMBER: 60/206,201  
 ; PRIOR FILING DATE: 2000-05-22  
 ; PRIOR APPLICATION NUMBER: 60/218,950  
 ; PRIOR FILING DATE: 2000-07-14  
 ; PRIOR APPLICATION NUMBER: 60/222,903  
 ; PRIOR FILING DATE: 2000-08-03  
 ; PRIOR APPLICATION NUMBER: 60/223,416  
 ; PRIOR FILING DATE: 2000-08-04  
 ; PRIOR APPLICATION NUMBER: 60/223,378  
 ; PRIOR FILING DATE: 2000-08-07  
 ; NUMBER OF SEQ ID NOS: 9597  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 8967  
 ; LENGTH: 596  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens

; FEATURE:  
 ; NAME/KEY: unsure  
 ; LOCATION: (13)  
 ; OTHER INFORMATION: n=A, T, C or G  
 ; NAME/KEY: unsure  
 ; LOCATION: (47)  
 ; OTHER INFORMATION: n=A, T, C or G  
 ; NAME/KEY: unsure  
 ; LOCATION: (49)  
 ; OTHER INFORMATION: n=A, T, C or G  
 ; NAME/KEY: unsure  
 ; LOCATION: (58)  
 ; OTHER INFORMATION: n=A, T, C or G  
 ; NAME/KEY: unsure  
 ; LOCATION: (63)  
 ; OTHER INFORMATION: n=A, T, C or G  
 ; NAME/KEY: unsure  
 ; LOCATION: (81)  
 ; OTHER INFORMATION: n=A, T, C or G  
 ; NAME/KEY: unsure  
 ; LOCATION: (155)  
 ; OTHER INFORMATION: n=A, T, C or G  
 ; NAME/KEY: unsure  
 ; LOCATION: (196)  
 ; OTHER INFORMATION: n=A, T, C or G  
 ; NAME/KEY: unsure  
 ; LOCATION: (211)  
 ; OTHER INFORMATION: n=A, T, C or G  
 ; NAME/KEY: unsure  
 ; LOCATION: (267)

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; OTHER INFORMATION: n=A,T,C or G
; NAME/KEY: unsure
; LOCATION: (281)
; OTHER INFORMATION: n=A,T,C or G
; NAME/KEY: unsure
; LOCATION: (282)
; OTHER INFORMATION: n=A,T,C or G
; NAME/KEY: unsure
; LOCATION: (332)
; OTHER INFORMATION: n=A,T,C or G
; NAME/KEY: unsure
; LOCATION: (372)
; OTHER INFORMATION: n=A,T,C or G
; NAME/KEY: unsure
; LOCATION: (520)
; OTHER INFORMATION: n=A,T,C or G
; NAME/KEY: unsure
; LOCATION: (521)
; OTHER INFORMATION: n=A,T,C or G
; NAME/KEY: unsure
; LOCATION: (551)
; OTHER INFORMATION: n=A,T,C or G
; NAME/KEY: unsure
; LOCATION: (579)
; OTHER INFORMATION: n=A,T,C or G
; NAME/KEY: unsure
; LOCATION: (585)
; OTHER INFORMATION: n=A,T,C or G
; NAME/KEY: unsure
; LOCATION: (586)
; OTHER INFORMATION: n=A,T,C or G
; US-09-796-692-8967

Query Match      100.0%; Score 25; DB 9; Length 596;
Best Local Similarity 100.0%; Pred. No. 2.6e-05;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GACTGTCCACAGCATTCGCGTGACC 25
Db 433 GACTGTCCACAGCATTCGCGTGACC 457

RESULT 7
US-10-040-862-8967
; Sequence 8967, Application US/10040862
; Publication No. US20030078396A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; FILE OF INVENTION: Hematological Malignancies
; FILE REFERENCE: 014058-013520US
; CURRENT APPLICATION NUMBER: US/10/040,862
; CURRENT FILING DATE: 2001-11-06
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: US 60/223,416
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: US 60/223,378
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: US 09/796,692
; PRIOR FILING DATE: 2001-03-01
; NUMBER OF SEQ ID NOS: 10467
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8967
; LENGTH: 596
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (13)
; OTHER INFORMATION: n=A,T,C or G
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (47)
; OTHER INFORMATION: n=A,T,C or G
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (49)
; OTHER INFORMATION: n=A,T,C or G
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (58)
; OTHER INFORMATION: n=A,T,C or G
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (63)
; OTHER INFORMATION: n=A,T,C or G
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (81)
; OTHER INFORMATION: n=A,T,C or G
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (155)
; OTHER INFORMATION: n=A,T,C or G
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (196)
; OTHER INFORMATION: n=A,T,C or G
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (211)
; OTHER INFORMATION: n=A,T,C or G
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (267)
; OTHER INFORMATION: n=A,T,C or G
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (281)
; OTHER INFORMATION: n=A,T,C or G
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (282)
; OTHER INFORMATION: n=A,T,C or G
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (332)
; OTHER INFORMATION: n=A,T,C or G
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (372)
; OTHER INFORMATION: n=A,T,C or G
; FEATURE:

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; NAME/KEY: unsure  
; LOCATION: (520)  
; OTHER INFORMATION: n=A,T,C or G  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (521)  
; OTHER INFORMATION: n=A,T,C or G  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (551)  
; OTHER INFORMATION: n=A,T,C or G  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (579)  
; OTHER INFORMATION: n=A,T,C or G  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (585)  
; OTHER INFORMATION: n=A,T,C or G  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (586)  
; OTHER INFORMATION: n=A,T,C or G  
US-10-040-862-8967

Query Match 100.0%; Score 25; DB 15; Length 596;  
Best Local Similarity 100.0%; Pred. No. 2.6e-05;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GACTGTCCACAGCATTCGCGTGACC 25  
Db 433 GACTGTCCACAGCATTCGCGTGACC 457

## RESULT 8

US-10-057-475B-8967  
; Sequence 8967, Application US/10057475B  
; Publication No. US20040002068A1  
; GENERAL INFORMATION:  
; APPLICANT: Gaiger, Alexander  
; APPLICANT: Algate, Paul A.  
; APPLICANT: Mannion, Jane  
; APPLICANT: Clapper, Jonathan David  
; APPLICANT: Wang, Aijun  
; APPLICANT: Carder, Lauren  
; APPLICANT: Ordonez, Nadia  
; APPLICANT: McNeill, Patricia Dianne  
; APPLICANT: Corixa Corporation  
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy  
; FILE REFERENCE: 014058-014402US  
; CURRENT APPLICATION NUMBER: US/10/057,475B  
; CURRENT FILING DATE: 2002-01-22  
; PRIOR APPLICATION NUMBER: US 60/186,126  
; PRIOR FILING DATE: 2000-03-01  
; PRIOR APPLICATION NUMBER: US 60/190,479  
; PRIOR FILING DATE: 2000-03-17  
; PRIOR APPLICATION NUMBER: US 60/200,545  
; PRIOR FILING DATE: 2000-04-27  
; PRIOR APPLICATION NUMBER: US 60/200,303  
; PRIOR FILING DATE: 2000-04-28  
; PRIOR APPLICATION NUMBER: US 60/200,779  
; PRIOR FILING DATE: 2000-04-28  
; PRIOR APPLICATION NUMBER: US 60/202,084  
; PRIOR FILING DATE: 2000-05-04  
; PRIOR APPLICATION NUMBER: US 60/206,201  
; PRIOR FILING DATE: 2000-05-22  
; PRIOR APPLICATION NUMBER: US 60/218,950  
; PRIOR FILING DATE: 2000-07-14  
; PRIOR APPLICATION NUMBER: US 60/222,903  
; PRIOR FILING DATE: 2000-08-03  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 11290  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 8967  
; LENGTH: 596  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)...(596)  
; OTHER INFORMATION: n = g, a, c or t  
US-10-154-884B-8967

Query Match 100.0%; Score 25; DB 15; Length 596;  
Best Local Similarity 100.0%; Pred. No. 2.6e-05;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 10979  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 8967  
; LENGTH: 596  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)...(596)  
; OTHER INFORMATION: n = g, a, c or t  
US-10-057-475B-8967

Query Match 100.0%; Score 25; DB 16; Length 596;  
Best Local Similarity 100.0%; Pred. No. 2.6e-05;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GACTGTCCACAGCATTCGCGTGACC 25  
Db 433 GACTGTCCACAGCATTCGCGTGACC 457

## RESULT 9

US-10-154-884B-8967  
; Sequence 8967, Application US/10154884B  
; Publication No. US20040005561A1  
; GENERAL INFORMATION:  
; APPLICANT: Gaiger, Alexander  
; APPLICANT: Algate, Paul A.  
; APPLICANT: Mannion, Jane  
; APPLICANT: Retter, Marc W.  
; APPLICANT: Corixa Corporation  
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy  
; FILE REFERENCE: 014058-013521US  
; CURRENT APPLICATION NUMBER: US/10/154,884B  
; CURRENT FILING DATE: 2002-05-23  
; PRIOR APPLICATION NUMBER: US 60/186,126  
; PRIOR FILING DATE: 2000-03-01  
; PRIOR APPLICATION NUMBER: US 60/190,479  
; PRIOR FILING DATE: 2000-03-17  
; PRIOR APPLICATION NUMBER: US 60/200,545  
; PRIOR FILING DATE: 2000-04-27  
; PRIOR APPLICATION NUMBER: US 60/200,303  
; PRIOR FILING DATE: 2000-04-28  
; PRIOR APPLICATION NUMBER: US 60/200,779  
; PRIOR FILING DATE: 2000-04-28  
; PRIOR APPLICATION NUMBER: US 60/200,999  
; PRIOR FILING DATE: 2000-05-01  
; PRIOR APPLICATION NUMBER: US 60/202,084  
; PRIOR FILING DATE: 2000-05-04  
; PRIOR APPLICATION NUMBER: US 60/206,201  
; PRIOR FILING DATE: 2000-05-22  
; PRIOR APPLICATION NUMBER: US 60/218,950  
; PRIOR FILING DATE: 2000-07-14  
; PRIOR APPLICATION NUMBER: US 60/222,903  
; PRIOR FILING DATE: 2000-08-03  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 11290  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 8967  
; LENGTH: 596  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)...(596)  
; OTHER INFORMATION: n = g, a, c or t  
US-10-154-884B-8967

Query Match 100.0%; Score 25; DB 16; Length 596;  
Best Local Similarity 100.0%; Pred. No. 2.6e-05;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GACTGTCCACAGCATTCGCGTGACC 25  
 Db 433 GACTGTCCACAGCATTCGCGTGACC 457

RESULT 10  
 US-10-228-811-1  
 ; Sequence 1, Application US/10228811  
 ; Publication No. US20030054392A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Wittig, Prof. Blaushardt  
 ; APPLICANT: Jungmans, Claas  
 ; TITLE OF INVENTION: Design Principle for Constructing Expression Constructs for Gene  
 ; FILE REFERENCE: XI 597/99  
 ; CURRENT APPLICATION NUMBER: US/10/228,811  
 ; CURRENT FILING DATE: 2002-08-27  
 ; PRIOR APPLICATION NUMBER: DE 196 48 625.4  
 ; PRIOR FILING DATE: 1996-11-13  
 ; NUMBER OF SEQ ID NOS: 13  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 1  
 ; LENGTH: 1078  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; NAME/KEY: gene  
 ; LOCATION: (1)..(1078)  
 ; OTHER INFORMATION: bcr3=abl2; Oligo DNA Dumbbell  
 ; FEATURE:  
 ; NAME/KEY: misc binding  
 ; LOCATION: (1)..(2)  
 ; OTHER INFORMATION: intramolecular binding site; the T-nucleotides at position 1 to  
 ; OTHER INFORMATION: 2 can be modified with amino or caroxy features  
 ; FEATURE:  
 ; NAME/KEY: misc binding  
 ; LOCATION: (1077)..(1078)  
 ; OTHER INFORMATION: intramolecular binding site; the T-nucleotides at position 1077  
 ; OTHER INFORMATION: to 1078 can be modified with amino or caroxy features  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: Strandness: both; nucleic  
 ; OTHER INFORMATION: acid (linear), hypothetical: No. US20030054392A1 anti-sense: No  
 US-10-228-811-1

Query Match 100.0%; Score 25; DB 15; Length 1078;  
 Best Local Similarity 100.0%; Pred. No. 2.4e-05;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GACTGTCCACAGCATTCGCGTGACC 25  
 Db 662 GACTGTCCACAGCATTCGCGTGACC 686

RESULT 11  
 US-09-954-531-586  
 ; Sequence 586, Application US/09954531  
 ; Patent No. US20020165180A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Weaver, Zoe  
 ; TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Cand  
 ; FILE REFERENCE: 689290-77  
 ; CURRENT APPLICATION NUMBER: US/09/954,531  
 ; CURRENT FILING DATE: 2002-05-02  
 ; PRIOR APPLICATION NUMBER: US/60/233,133  
 ; PRIOR FILING DATE: 2000-09-18  
 ; PRIOR APPLICATION NUMBER: US/60/234,009  
 ; PRIOR FILING DATE: 2000-09-20  
 ; PRIOR APPLICATION NUMBER: US/60/234,034  
 ; PRIOR FILING DATE: 2000-09-20  
 ; PRIOR APPLICATION NUMBER: US/60/234,509  
 ; PRIOR FILING DATE: 2000-09-22

; PRIOR APPLICATION NUMBER: US/60/234,567  
 ; PRIOR FILING DATE: 2000-09-22  
 ; NUMBER OF SEQ ID NOS: 1392  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 586  
 ; LENGTH: 4739  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-09-954-531-586

Query Match 100.0%; Score 25; DB 9; Length 4739;  
 Best Local Similarity 100.0%; Pred. No. 2e-05;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GACTGTCCACAGCATTCGCGTGACC 25  
 Db 3158 GACTGTCCACAGCATTCGCGTGACC 3182

RESULT 12  
 US-10-193-651-22  
 ; Sequence 22, Application US/10193651  
 ; Publication No. US20030064061A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Zhao, Xun  
 ; APPLICANT: Ghaffari, Saghi  
 ; APPLICANT: Lodish, Harvey F.  
 ; APPLICANT: Malashkevich, Vladimir N.  
 ; APPLICANT: Kim, Peter S.  
 ; TITLE OF INVENTION: Bcr-Abl Oligomerization Domain  
 ; TITLE OF INVENTION: Polypeptides and Uses Therefor  
 ; FILE REFERENCE: 0399,2031-001  
 ; CURRENT APPLICATION NUMBER: US/10/193,651  
 ; CURRENT FILING DATE: 2002-11-19  
 ; PRIOR APPLICATION NUMBER: US 60/303,857  
 ; PRIOR FILING DATE: 2001-07-09  
 ; NUMBER OF SEQ ID NOS: 22  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 22  
 ; LENGTH: 4739  
 ; TYPE: DNA  
 ; ORGANISM: Homo Sapiens  
 ; FEATURE:  
 ; OTHER INFORMATION: Bcr nucleic acid  
 US-10-193-651-22

Query Match 100.0%; Score 25; DB 13; Length 4739;  
 Best Local Similarity 100.0%; Pred. No. 2e-05;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GACTGTCCACAGCATTCGCGTGACC 25  
 Db 3158 GACTGTCCACAGCATTCGCGTGACC 3182

RESULT 13  
 US-10-128-714-206  
 ; Sequence 206, Application US/10128714  
 ; Publication No. US20030119013A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Jiang, Bo  
 ; APPLICANT: Hu, Wengi  
 ; APPLICANT: Tishkoff, Daniel  
 ; APPLICANT: Zamudio, Carlos  
 ; APPLICANT: Eroskin, Alexey M  
 ; APPLICANT: Lemieux, Sebastien M  
 ; TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and  
 ; TITLE OF INVENTION: Methods of Use  
 ; FILE REFERENCE: 10182-018-999  
 ; CURRENT APPLICATION NUMBER: US/10/128,714  
 ; CURRENT FILING DATE: 2002-04-23  
 ; PRIOR APPLICATION NUMBER: US 60/285,697  
 ; PRIOR FILING DATE: 2001-04-23



; PRIOR APPLICATION NUMBER: US 60/287,066  
 ; PRIOR FILING DATE: 2001-04-27  
 ; PRIOR APPLICATION NUMBER: US 60/295,890  
 ; PRIOR FILING DATE: 2001-06-05  
 ; PRIOR APPLICATION NUMBER: US 60/303,899  
 ; PRIOR FILING DATE: 2001-07-09  
 ; PRIOR APPLICATION NUMBER: US 60/316,362  
 ; PRIOR FILING DATE: 2001-08-31  
 ; NUMBER OF SEQ ID NOS: 8603  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 206  
 ; LENGTH: 3664  
 ; TYPE: DNA  
 ; ORGANISM: Aspergillus fumigatus  
 US-10-128-714-206

Query Match 68.0%; Score 17; DB 15; Length 3664;  
 Best Local Similarity 100.0%; Pred. No. 1.2;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GTCCACAGCATTCCGCT 21  
 Db 3547 GTCCACAGCATTCCGCT 3563

RESULT 14  
 US-10-128-714-5206  
 ; Sequence 5206, Application US/10128714  
 ; Publication No. US20030119013A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Jiang, Bo  
 ; APPLICANT: Hu, Wenqi  
 ; APPLICANT: Tishkoff, Daniel  
 ; APPLICANT: Zamudio, Carlos  
 ; APPLICANT: Eroshkin, Alexey M  
 ; APPLICANT: Lemieux, Sebastien M  
 ; TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and  
 ; FILE REFERENCE: 10182-018-999  
 ; CURRENT APPLICATION NUMBER: US/10128,714  
 ; CURRENT FILING DATE: 2002-04-23  
 ; PRIOR APPLICATION NUMBER: US 60/285,697  
 ; PRIOR FILING DATE: 2001-04-23  
 ; PRIOR APPLICATION NUMBER: US 60/287,066  
 ; PRIOR FILING DATE: 2001-04-27  
 ; PRIOR APPLICATION NUMBER: US 60/295,890  
 ; PRIOR FILING DATE: 2001-06-05  
 ; PRIOR APPLICATION NUMBER: US 60/303,899  
 ; PRIOR FILING DATE: 2001-07-09  
 ; PRIOR APPLICATION NUMBER: US 60/316,362  
 ; PRIOR FILING DATE: 2001-08-31  
 ; NUMBER OF SEQ ID NOS: 8603  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 5206  
 ; LENGTH: 3750  
 ; TYPE: DNA  
 ; ORGANISM: Aspergillus fumigatus  
 US-10-128-714-5206

Query Match 68.0%; Score 17; DB 15; Length 3750;  
 Best Local Similarity 100.0%; Pred. No. 1.2;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GTCCACAGCATTCCGCT 21  
 Db 3636 GTCCACAGCATTCCGCT 3652

RESULT 15  
 US-09-779-881-2/c  
 ; Sequence 2, Application US/09779881  
 ; Patent No. US20020081749A1  
 ; GENERAL INFORMATION:

; APPLICANT: Kulmala, Sakari  
 ; APPLICANT: Ala-Kleme, Timo  
 ; APPLICANT: Eskola, Jarkko  
 ; APPLICANT: Korpela, Timo  
 ; TITLE OF INVENTION: ELECTRICAL EXCITATION OF LABEL SUBSTANCES AT COATED  
 ; FILE REFERENCE: TUR-080  
 ; CURRENT APPLICATION NUMBER: US/09/779,881  
 ; CURRENT FILING DATE: 2001-02-09  
 ; PRIOR APPLICATION NUMBER: 09/341,955  
 ; PRIOR FILING DATE: 1999-07-21  
 ; PRIOR APPLICATION NUMBER: PCT/FI98/00114  
 ; PRIOR FILING DATE: 1999-02-10  
 ; NUMBER OF SEQ ID NOS: 2  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 2  
 ; LENGTH: 28  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence:  
 ; OTHER INFORMATION: oligonucleotide containing an amino group  
 US-09-779-881-2

Query Match 64.0%; Score 16; DB 9; Length 28;  
 Best Local Similarity 100.0%; Pred. No. 8.6;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 CAGCATTCCGCTGACC 25  
 Db 28 CAGCATTCCGCTGACC 13

Search completed: May 27, 2004, 14:58:27  
 Job time : 132.564 secs

**THIS PAGE BLANK (USPTO)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 26, 2004, 15:22:41 ; Search time 882.692 Seconds  
(without alignments)  
845.770 Million cell updates/sec

Title: US-09-121-239-9

Perfect score: 25  
Sequence: 1 GACTGTCACACATTCCGCTGACC 25

Scoring table: OLIGO\_NUC  
Gapop\_60.0 , Gapext 60.0

Searched: 27513289 seqs, 14931090276 residues

Word size : 0

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

EST:\*

1: em\_estba:\*

2: em\_esthum:\*

3: em\_estin:\*

4: em\_estmu:\*

5: em\_estov:\*

6: em\_estpl:\*

7: em\_estro:\*

8: em\_estl:\*

9: gb\_estl:\*

10: gb\_est2:\*

11: gb\_hic:\*

12: gb\_est3:\*

13: gb\_est4:\*

14: gb\_est5:\*

15: em\_estfun:\*

16: em\_estom:\*

17: em\_gsa\_hum:\*

18: em\_gsa\_inv:\*

19: em\_gsa\_pln:\*

20: em\_gsa\_vrt:\*

21: em\_gsa\_fun:\*

22: em\_gsa\_nam:\*

23: em\_gsa\_mus:\*

24: em\_gsa\_pro:\*

25: em\_gsa\_rod:\*

26: em\_gsa\_phg:\*

27: em\_gsa\_vrl:\*

28: gb\_gsl1:\*

29: gb\_gae2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	25	100.0	181	14	H55545	H55545 CHR220484 C
2	25	100.0	314	14	D79153	D79153 HUM532H118
3	25	100.0	360	10	BE168421	BE168421 QV3-HT051
4	25	100.0	377	10	BF800308	BF800308 CM4-CI006

5	25	100.0	401	14	R54267	R54267 YG74h05.r1
6	25	100.0	437	10	BF873838	BF873838 IL3-ET011
7	25	100.0	443	10	AW452440	AW452440 UI-H-B13-
8	25	100.0	531	12	BG927169	BG927169 HNC18-1-D
9	25	100.0	588	10	BF380221	BF380221 MR3-UT005
10	25	100.0	588	10	BF094682	BF094682 MR3-UT005
11	25	100.0	590	10	BF953848	BF953848 MR0-NN117
12	25	100.0	597	10	BE396942	BE396942 601290652
13	25	100.0	605	10	AW961897	AW961897 EST373970
14	25	100.0	621	10	BE267891	BE267891 601125452
15	25	100.0	637	14	CB267185	CB267185 1006091.H
16	25	100.0	653	12	BG829045	BG829045 602753375
17	25	100.0	665	10	BE514596	BE514596 601316940
18	25	100.0	684	10	BF530440	BF530440 602071562
19	25	100.0	712	10	BE397010	BE397010 601289812
20	25	100.0	712	10	BE397695	BE397695 601289802
21	25	100.0	734	10	BE513555	BE513555 601315079
22	25	100.0	741	10	BE265121	BE265121 601193661
23	25	100.0	770	12	BI226004	BI226004 602950455
24	25	100.0	777	13	BU597369	BU597369 AGENCOURT
25	25	100.0	785	12	BG393462	BG393462 602411828
26	25	100.0	797	12	BI225128	BI225128 602949789
27	25	100.0	819	14	CF242964	CF242964 AGENCOURT
28	25	100.0	844	14	CD652568	CD652568 AGENCOURT
29	25	100.0	853	13	BQ227532	BQ227532 AGENCOURT
30	25	100.0	878	10	BF338795	BF338795 602036226
31	25	100.0	880	13	BQ422888	BQ422888 AGENCOURT
32	25	100.0	880	13	BU539742	BU539742 AGENCOURT
33	25	100.0	888	13	BU540933	BU540933 AGENCOURT
34	25	100.0	895	13	EX368536	EX368536 EX368536
35	25	100.0	903	13	BQ441890	BQ441890 AGENCOURT
36	25	100.0	918	13	BQ212925	BQ212925 AGENCOURT
37	25	100.0	936	13	EX350695	EX350695 EX350695
38	25	100.0	955	13	BQ945725	BQ945725 AGENCOURT
39	25	100.0	975	12	BG392048	BG392048 602410011
40	25	100.0	1021	13	BQ896733	BQ896733 AGENCOURT
41	24	96.0	104	10	AW998451	AW998451 PM2-BN006
42	24	96.0	796	10	BE743192	BE743192 601573879
43	24	96.0	813	12	BM050194	BM050194 603632267
44	22	88.0	438	10	BE938059	BE938059 MR1-TN004
45	20	80.0	750	10	BE513994	BE513994 601315851

## ALIGNMENTS

RESULT 1	H55545	CHR220484	Chromosome 22	181 bp	mRNA	linear	EST 07-DEC-1995
LOCUS	H55545	CHR220484	Chromosome 22	181 bp	mRNA	linear	EST 07-DEC-1995
DEFINITION	H55545	CHR220484	Chromosome 22	181 bp	mRNA	linear	EST 07-DEC-1995
ACCESSION	H55545	CHR220484	Chromosome 22	181 bp	mRNA	linear	EST 07-DEC-1995
VERSION	H55545.1	GI:1108411	Chromosome 22	181 bp	mRNA	linear	EST 07-DEC-1995
KEYWORDS	EST.	Chromosome 22	181 bp	mRNA	linear	EST 07-DEC-1995	
SOURCE	Homo sapiens (human)	Chromosome 22	181 bp	mRNA	linear	EST 07-DEC-1995	
ORGANISM	Homo sapiens	Chromosome 22	181 bp	mRNA	linear	EST 07-DEC-1995	
REFERENCE	1 (bases 1 to 181)	Chromosome 22	181 bp	mRNA	linear	EST 07-DEC-1995	
AUTHORS	Trofater, J.A., Long, K.R., Murrell, J.R., Stotler, C.J., Gusella, J.F. and Buckler, A.J.	Chromosome 22	181 bp	mRNA	linear	EST 07-DEC-1995	
TITLE	An expression-independent catalog of genes from human chromosome 22	Chromosome 22	181 bp	mRNA	linear	EST 07-DEC-1995	
JOURNAL	Genome Res. 5 (3), 214-224 (1995)	Chromosome 22	181 bp	mRNA	linear	EST 07-DEC-1995	
MEDLINE	96159527	Chromosome 22	181 bp	mRNA	linear	EST 07-DEC-1995	
PUBMED	8593609	Chromosome 22	181 bp	mRNA	linear	EST 07-DEC-1995	
COMMENT	Contact: Buckler AJ Molecular Neurogenetics Unit Massachusetts General Hospital Building 149, 13th St., Charlestown MA 02129 Tel: 6177249616 Fax: 6177265736 Email: buckler@helix.mgh.harvard.edu Seq primer: T3.	Chromosome 22	181 bp	mRNA	linear	EST 07-DEC-1995	

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      /organism="Homo sapiens"
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      /lab_host="E. coli DH5a"
      /clone_lib="Chromosome 22 exon"
      /note="Vector: pBluescriptIIKS+; Site_1: Sal I; Site_2:
      Bam HI (destroyed); Exons were isolated from human
      chromosome 22 specific cosmids using a modification of
      the method of exon amplification (Proc. Natl. Acad. Sci.
      USA 88:4005-4009, 1991). Amplified exons were digested
      with Sal I and Bgl II and subsequently cloned into
      pBluescriptIIKS+ at the Sal I and Bam HI sites."

ORIGIN
Query Match      100.0%; Score 25; DB 14; Length 181;
Best Local Similarity 100.0%; Pred. No. 0.0033;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GACTGTCCACAGCATTCGCTGACC 25
    |||||
Db 144 GACTGTCCACAGCATTCGCTGACC 168

RESULT 2
D79153
LOCUS       D79153          314 bp      mRNA      linear      EST 09-FEB-1996
DEFINITION HUM532H11B Human placenta polyA+ (TFujiwara) Homo sapiens cDNA
            clone GEN-532H11 5', mRNA sequence.
ACCESSION   D79153
VERSION     D79153.1 GI:1181026
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
REFERENCE   1 (bases 1 to 314)
AUTHORS     Fujiwara, T., Hirano, H., Katagiri, T., Kawai, A., Kuga, Y., Negata, M.,
            Okuno, S., Ozaki, K., Shimizu, F., Shimada, Y., Shinomiya, H.,
            Takaichi, A., Takeda, S., Watanabe, T., Takahashi, E., Hirai, Y.,
            Maekawa, H., Shin, S. and Nakamura, Y.
            Fujiwara et al. (1995)
            Unpublished (1995)
            Contact: Tsutomu Fujiwara
            Otsuka GEN Research Institute
            Otsuka Pharmaceutical Co., Ltd
            463-10 Kagasuno Kawauchi-cho, Tokushima, Tokushima, 771-01 Japan
            Tel: 0886-65-2888
            Fax: 0886-37-1035.

FEATURES
source
  Location/Qualifiers
    1..314
      /organism="Homo sapiens"
      /mol_type="mRNA"
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      /clone="GEN-532H11"
      /tissue_type="placenta"
      /clone_lib="Human placenta polyA+ (TFujiwara)"

ORIGIN
Query Match      100.0%; Score 25; DB 14; Length 314;
Best Local Similarity 100.0%; Pred. No. 0.0035;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GACTGTCCACAGCATTCGCTGACC 25
    |||||
Db 53 GACTGTCCACAGCATTCGCTGACC 77

RESULT 3
BE168421/c
LOCUS       BE168421      360 bp      mRNA      linear      EST 21-JUN-2000
DEFINITION QV3-HT0513-060400-148-b11 HT0513 Homo sapiens cDNA, mRNA sequence.
ACCESSION   BE168421
VERSION     BE168421.1 GI:8631051
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
REFERENCE   1 (bases 1 to 360)
AUTHORS     Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
            Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
            Goldman, G.H., Carvalho, F., Matsukuma, A., Baia, G.S., Simpson, D.H.,
            Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V.,
            O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
            Simpson, A.J.
            Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
            Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
            20202663
            10737800
            Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=et2=QV3-HT0513-060
            400-148-b11&t3=2000-04-06&t4=1)
            400-148-b11&t3=2000-04-06&t4=1)
            Seq primer: puc 18 forward
            High quality sequence start: 31
            High quality sequence stop: 359.

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      /clone_lib="HT0513"
      /dev_stage="Adult"
      /note="Organ: head neck; Vector: puc18; Site_1: SmaI;
      Site_2: SmaI; A mini-library was made by cloning products
      derived from ORESTES PCR (U.S. Letters Patent application
      No. 196,716 - Ludwig Institute for Cancer Research)
      profiles into the pUC 18 vector. Reverse transcription of
      tissue mRNA and cDNA amplification were performed under
      low stringency conditions."

ORIGIN
Query Match      100.0%; Score 25; DB 10; Length 360;
Best Local Similarity 100.0%; Pred. No. 0.0035;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GACTGTCCACAGCATTCGCTGACC 25
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Db 328 GACTGTCCACAGCATTCGCTGACC 304

RESULT 4
BF800308
LOCUS       BF800308      377 bp      mRNA      linear      EST 12-JAN-2001
DEFINITION CM4-CI0062-181000-370-b10 CI0062 Homo sapiens cDNA, mRNA sequence.
ACCESSION   BF800308
VERSION     BF800308.1 GI:12129297
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
REFERENCE   1 (bases 1 to 377)
AUTHORS     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
            Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,

```

Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldmann,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.

Shotgun sequencing of the human transcriptome with ORF expressed

sequence tags

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

20202663

10737800

#### TITLE

#### JOURNAL

#### MEDLINE

#### PUBMED

#### COMMENT

Contact: Simpson A.J.G.

Laboratory of Cancer Genetics

Ludwig Institute for Cancer Research

Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,

Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome

Project. This entry can be seen in the following URL

(<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CM4&t2=CM4-CI0062-181000-370-b10&t3=2000-10-18&t4=1>)

Seq primer: puc 18 forward

High quality sequence start: 18

High quality sequence stop: 377.

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/db\_xref="taxon:9606"

/dev\_stage="Adult"

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/note="Organ: colon ins; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

#### ORIGIN

Query Match 100.0%; Score 25; DB 10; Length 377;

Best Local Similarity 100.0%; Pred.No. 0.0035;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GACTGTCCACAGCATTCGCTGACC 25

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Db 250 GACTGTCCACAGCATTCGCTGACC 274

#### RESULT 5

##### LOCUS

R54267 401 bp mRNA linear EST 18-MAY-1995

Y974h05.r1 Soares infant brain lN1B Homo sapiens cDNA clone

IMAGE:39270 5' similar to gb:U01147 BREAKPOINT CLUSTER REGION

PROTEIN (HUMAN) ; mRNA sequence.

#### ACCESSION

R54267

R54267.1 GI:816169

EST.

KEYWORDS

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 401)

REFERENCE

AUTHORS

Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevisan,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.

The WashU-Merck EST Project

Unpublished (1995)

CONTACT: Wilson RK

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

Insert Size: 1872

High quality sequence stops: 342 Source: IMAGE Consortium, LNL  
This clone is available royalty-free through LNL; contact the  
IMAGE Consortium ([info@image.lnl.gov](mailto:info@image.lnl.gov)) for further information.

Insert Length: 1872 Std Error: 0.00

Seq primer: M13RP1

High quality sequence stop: 342.

#### FEATURES

##### source

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/clone\_lib="Soares infant brain lN1B"

/note="Organ: whole brain; Vector: Lfamid BA; Site 1: Not

I; Site 2: Hind III; 1st strand cDNA was primed with a Not

I - oligo(dt) primer [5'

AACTGGAAGAAATTCGCGCCGAGCAATTTTTTTTTTTT 3'];

double-stranded cDNA was ligated to Hind III adaptors  
(Pharmacia), digested with Not I and directionally cloned  
into the Not I and Hind III sites of the Lfamid BA vector.  
Library went through one round of normalization. Library  
constructed by Bento Soares and M.Fatima Bonaldo."

#### ORIGIN

Query Match 100.0%; Score 25; DB 14; Length 401;

Best Local Similarity 100.0%; Pred.No. 0.0035;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GACTGTCCACAGCATTCGCTGACC 25

|||||

Db 226 GACTGTCCACAGCATTCGCTGACC 250

#### RESULT 6

##### LOCUS

BF873838

IL3-ET0114-071100-338-C02 ET0114 Homo sapiens cDNA, mRNA sequence.

DEFINITION

BF873838

ACCESSION

BF873838.1 GI:12264007

VERSION

EST.

KEYWORDS

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 437)

REFERENCE

AUTHORS

Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldmann,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.

Shotgun sequencing of the human transcriptome with ORF expressed

sequence tags

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

20202663

10737800

CONTACT: Simpson A.J.G.

Laboratory of Cancer Genetics

Ludwig Institute for Cancer Research

Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,

Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL  
 (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=IL3&tl2=IL3-ET0114-071100-338-C02&t3=2000-11-07&t4=i1)  
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 High quality sequence stop: 390.

## FEATURES

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 /dev\_stage="Adult"  
 /clone\_lib="ET0114"

/notes="Organ: lung tumor; Vector: puc18; Site: 1: SmaI; Site: 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

## ORIGIN

Query Match 100.0%; Score 25; DB 10; Length 437;  
 Best Local Similarity 100.0%; Pred. No. 0.0036;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GACTGTCCACAGCATTCGCTGACC 25

Db 318 GACTGTCCACAGCATTCGCTGACC 294

## RESULT 7

AW452440

LOCUS

DEFINITION UI-H-B13-als-c-04-0-UI.s1 NCI\_CGAP\_Sub5 Homo sapiens cDNA clone IMAGE:3068526 3', mRNA sequence.

ACCESSION AW452440

VERSION AW452440.1

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 443)

AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

JOURNAL Unpublished (1997)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgaps@mail.nih.gov

Oligo-dT track not found. Not 1 site shown in beginning of sequence

is likely internal to the message. cDNA library Preparation: M.B.

Soares Lab Clone distribution: NCI-CGAP clone distribution

Information can be found through the I.M.A.G.E. Consortium/LINL at:

www.bio.lnl.gov/bbrp/image/image.html The following repetitive

elements were found in this cDNA sequence: 147-207, &gt;HSR17

Seq primer: M13 Forward

POLYA=No.

## FEATURES

source

1. .443  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:3068526"  
 /lab\_host="DHI08 (Life Technologies)"  
 /clone\_lib="NCI\_CGAP\_Sub5"

/notes="Vector: pT73D-pac (Pharmacia) with a modified polylinker; Site 1: Not 1; Site 2: Eco RI; NCI CGAP Subs is a subtracted library derived from NCI CGAP\_Sub4. The NCI\_CGAP\_Sub5 library had 3 million recombinants. A single-stranded DNA preparation of NCI\_CGAP\_Sub4 was used as a tracer in a subtractive hybridization with a driver comprising: the IMAGE pool (NCI\_CGAP\_Kid3 pool 1 LLAM

3334-3337, 3682-3683, 3798-3803 (IMAGE CloneIDs 1322376-1323911, 1456008-1456775, 1500552-1502855);  
 NCI\_CGAP\_Kid5 pool 1 LLAM 3338-3342, 3722-3725, 3776-3778 (IMAGE CloneIDs 1323912-1325831, 1471368-1472903, 1492104-1493255); NCI\_CGAP\_Lu5 pool 1 LLAM 3575-3582, 3851-3854 (IMAGE CloneIDs 1414920-1417991, 1520904-1522439); NCI\_CGAP\_GC4 pool 1 LLAM 3164-3167, 3716-3720, 3733-3735 (IMAGE CloneIDs 1257096-1258631, 1469064-1470983, 1475592-1476743);  
 NCI\_CGAP\_Pr22 pool 1 LLAM 2457-2459, 2758-2759, 3062-3068 (IMAGE CloneIDs 985608-986759, 1101192-1101959, 1217928-1220615); NCI\_CGAP\_Co10 pool 1 LLAM 2644-2653, 2871-2872 (IMAGE CloneIDs 1057416-1061255, 1144584-1145351). (10% of the driver population), plus a pool of 3,840 arrayed clones from NCI\_CGAP\_Sub1 (IMAGE CloneIDs 2708616-2710535) and NCI\_CGAP\_Sub2 (IMAGE CloneIDs 2710536-2712455) (10% of the driver population), plus a pool of 11,136 clones from NCI\_CGAP\_Sub3 (IMAGE CloneIDs 2712456-2723591) (10% of the driver population), plus a pool of 5,472 clones from NCI\_CGAP\_Sub4 (IMAGE CloneIDs 2723592-2728969) (70% of the driver population). Subtraction was performed as previously described [Bonaldo, Lennon & Soares (1996): Normalization and Subtraction: Two Approaches To Facilitate Gene Discovery. Genome Research 6, 791-806.  
 TAG TISSUE=germ cell  
 TAG\_LIB=NCI\_CGAP\_GC4  
 TAG\_SEQ=AAATC"

## ORIGIN

Query Match 100.0%; Score 25; DB 10; Length 443;  
 Best Local Similarity 100.0%; Pred. No. 0.0036;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GACTGTCCACAGCATTCGCTGACC 25

Db 356 GACTGTCCACAGCATTCGCTGACC 380

## RESULT 8

BG927169

LOCUS

DEFINITION

HNC18-1-D3.R.HC (Human Normal Cartilage) Homo sapiens

sequence.

ACCESSION BG927169

VERSION BG927169.1

KEYWORDS GI:14321692

SOURCE EST.

ORGANISM Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 531)

AUTHORS Kumar,S., Connor,J.R., Dodde,R.A., Halsey,W., Van Horn,M., Mao,J., Sathe,G., Mui,P., Agarwal,P., Badger,A.M., Lee,J.C., Gowen,M. and Lark,M.W.

TITLE Identification and initial characterization of 5000 expressed

sequenced tags (ESTs) each from adult human normal and

osteochondritic cartilage cDNA libraries

Osteochondr. Cartil. 9 (7), 641-653 (2001)

JOURNAL MEDLINE 21482651

PUBMED 11597177

COMMENT Contact: Sanjay Kumar

UW2109

GlaxoSmithKline

709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA

Tel: 610-270-7245

Fax: 610-270-5598

Email: sanjay.kumar-legsk.com

Seq primer: T7

Location/Qualifiers

1. .531

/organism="Homo sapiens"

/mol\_type="mRNA"

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/db_xref="taxon:9606"
/tissue_type="cartilage"
/lab_host="E.coli DH10 B"
/clone_lib="HNC (Human Normal Cartilage)"
/note="Vector: pSPORT I; Site_1: SalI; Site_2: NotI; Directional"

ORIGIN
Query Match      100.0%; Score 25; DB 12; Length 531;
Best Local Similarity 100.0%; Pred. No. 0.0036;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GACTGTCCACAGCATTCGCGTGACC 25
    |||||
Db 439 GACTGTCCACAGCATTCGCGTGACC 477

RESULT 10
BF094682
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)

REFERENCE
AUTHORS
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
JOURNAL
MEDLINE
PUBMED
20202663
10737800
COMMENT
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?t1=MR3&t2=MR3-UT0050-130
900-003-g03&t3=2000-09-13&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 586.
Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="UT0050"
/note="Organ: uterus tumor; Vector: puc18; Site_1: SmaI;
Site_2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the puc 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

ORIGIN
Query Match      100.0%; Score 25; DB 10; Length 588;
Best Local Similarity 100.0%; Pred. No. 0.0037;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GACTGTCCACAGCATTCGCGTGACC 25
    |||||
Db 453 GACTGTCCACAGCATTCGCGTGACC 477

RESULT 11
BF953848
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)

REFERENCE
AUTHORS
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
JOURNAL
MEDLINE
PUBMED
20202663
10737800
COMMENT
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?t1=MR3&t2=MR3-UT0050-
250900-003-g03&t3=2000-09-25&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 586.
Location/Qualifiers
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
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/note="Organ: uterus tumor; Vector: puc18; Site_1: SmaI;
Site_2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the puc 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

ORIGIN
Query Match      100.0%; Score 25; DB 10; Length 588;
Best Local Similarity 100.0%; Pred. No. 0.0037;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GACTGTCCACAGCATTCGCGTGACC 25
    |||||
Db 439 GACTGTCCACAGCATTCGCGTGACC 463

RESULT 9
BF380221
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)

REFERENCE
AUTHORS
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
JOURNAL
MEDLINE
PUBMED
20202663
10737800
COMMENT
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?t1=MR3&t2=MR3-UT0050-
250900-003-g03&t3=2000-09-25&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 586.
Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
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/note="Organ: uterus tumor; Vector: puc18; Site_1: SmaI;
Site_2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the puc 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

ORIGIN
Query Match      100.0%; Score 25; DB 10; Length 588;
Best Local Similarity 100.0%; Pred. No. 0.0037;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GACTGTCCACAGCATTCGCGTGACC 25
    |||||
Db 439 GACTGTCCACAGCATTCGCGTGACC 463

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VERSION      BF953848.1  GI:12371149
KEYWORDS     EST.
SOURCE       Homo sapiens (human)
ORGANISM     Homo sapiens

REFERENCE    1 (bases 1 to 590)
AUTHORS      Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
              Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
              Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
              Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
              O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
              Simpson,A.J.
TITLE        Shotgun sequencing of the human transcriptome with ORF expressed
              sequence tags
JOURNAL      Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE      20022663
PUBMED       10737800
COMMENT      Contact: Simpson A.J.G.
              Laboratory of Cancer Genetics
              Ludwig Institute for Cancer Research
              Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
              Brazil
              Tel: +55-11-2704922
              Fax: +55-11-2707001
              Email: asimpson@ludwig.org.br
              This sequence was derived from the FAPESP/LICR Human Cancer Genome
              Project. This entry can be seen in the following URL
              (http://www.ludwig.org.br/scripts/gethtml2.pl?ti=MR0&t2=MR0-NN1170-
              131100-302-f01&t3=2000-11-13&t4=1)
              Seq primer: puc 18 forward
              High quality sequence start: 31
              High quality sequence stop: 569.

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                /lab_host="DH10B (phage-resistant)"
                /clone_lib="NIH MGC 8"
                /note="Organ: lymph; Vector: pOTB7; Site 1: XhoI; Site 2:
                EcoRI; cDNA made by oligo-dT priming. Directionally
                cloned into EcoRI/XhoI sites using the following 5'
                adaptor: GGCACGAG(G). Size-selected >500bp for average
                insert size 1.8kb. Library constructed by Ling Hong in
                the laboratory of Gerald M. Rubin (University of
                California, Berkeley) using ZAP-cDNA synthesis kit
                (Stratagene) and Superscript II RT (Life technologies)."
```

---

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JOURNAL      Unpublished (1999)
COMMENT      Contact: Robert Strausberg, Ph.D.
              Email: cgabbs-r@mail.nih.gov
              Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
              cDNA Library Preparation: Ling Hong/Rubin Laboratory
              CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
              DNA Sequencing by: Incyte Genomics, Inc.
              Clone distribution: MGC clone distribution information can be
              found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
              Plate: LLCM294 row: 9 column: 13
              High quality sequence stop: 597.

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                /lab_host="DH10B (phage-resistant)"
                /clone_lib="NIH MGC 8"
                /note="Organ: lymph; Vector: pOTB7; Site 1: XhoI; Site 2:
                EcoRI; cDNA made by oligo-dT priming. Directionally
                cloned into EcoRI/XhoI sites using the following 5'
                adaptor: GGCACGAG(G). Size-selected >500bp for average
                insert size 1.8kb. Library constructed by Ling Hong in
                the laboratory of Gerald M. Rubin (University of
                California, Berkeley) using ZAP-cDNA synthesis kit
                (Stratagene) and Superscript II RT (Life technologies)."
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ORIGIN
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Best Local Similarity 100.0%; Pred. No. 0.0037;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GACTGTCCACAGCATTCCGCTGACC 25
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DB 569 GACTGTCCACAGCATTCCGCTGACC 593

RESULT 13
AW961897      605 bp mRNA linear EST 01-JUN-2000
LOCUS         EST373970 MAGE resequences, MAGG Homo sapiens cDNA, mRNA sequence.
DEFINITION    AW961897
ACCESSION     AW961897
VERSION       AW961897.1 GI:8151583
KEYWORDS      EST.
SOURCE        Homo sapiens (human)
ORGANISM      Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE     1 (bases 1 to 605)
AUTHORS       Hegde,P., Qi,R., Abernathy,K., Dharap,S., Gaspard,R., Gay,C.,
              Holt,I.E., Saeed,A.I., Sharov,V., Lee,N.H., Yeatman,T.J. and
              Quackenbush,J.
TITLE         Assessment of gene expression patterns in a model of colon tumor
              metastasis using a 19,200 element cDNA microarray
JOURNAL       Unpublished (2000)
COMMENT       Contact: John Quackenbush
              The Institute for Genomic Research
              9712 Medical Center Dr., Rockville, MD 20850, USA
              Tel: 301 838 3528
              Fax: 301 838 0208
              Email: johnq@tigr.org
              Plate: 167
              Seq primer: Reverse.
              Location/Qualifiers
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                  /organism="Homo sapiens"
                  /mol_type="mRNA"
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FEATURES     source
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                /db_xref="taxon:9606"
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                /note="Vector: pBluescriptSkM"
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Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 188 GACTGTCCACAGCATTCCGCTGACC 212

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LOCUS         601290652F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3621156 5',
DEFINITION    mRNA sequence.
ACCESSION     BE396942
VERSION       BE396942.1 GI:9342307
KEYWORDS      EST.
SOURCE        Homo sapiens (human)
ORGANISM      Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE     1 (bases 1 to 597)
AUTHORS       NIH-MGC http://imgc.ncbi.nih.gov/.
              National Institutes of Health, Mammalian Gene Collection (MGC)
              TITLE
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Query Match      100.0%; Score 25; DB 10; Length 605;
Best Local Similarity 100.0%; Pred. NO. 0.0037;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GACTGTCCACAGCATTCGCGTGACC 25
DB 413 GACTGTCCACAGCATTCGCGTGACC 437

RESULT 14
LOCUS BE267891
DEFINITION 601125452F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3345084 5',
mRNA sequence.
ACCESSION BE267891
VERSION BE267891.1 GI:9141488
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 621)
AUTHORS NIH-MGC http://mgs.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCW132 row: h column: 13
High quality sequence stop: 619.
FEATURES             location/Qualifiers
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     /tissue_type="Burkitt lymphoma"
     /lab_host="DH10B (phage-resistant)"
     /clone_lib="NIH MGC 8"
     /note="Organ: lymph; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."

ORIGIN
Query Match      100.0%; Score 25; DB 10; Length 621;
Best Local Similarity 100.0%; Pred. NO. 0.0037;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GACTGTCCACAGCATTCGCGTGACC 25
DB 184 GACTGTCCACAGCATTCGCGTGACC 208

RESULT 15
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DEFINITION 1006091 Human Fat Cell 5'-Stretch Plus cDNA Library Homo sapiens
cDNA 5', mRNA sequence.
ACCESSION CB267185
VERSION CB267185.1 GI:28441771
KEYWORDS EST.
SOURCE Homo sapiens (human)

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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 637)
AUTHORS Yang, R.-Z., Shuldiner, A. and Gong, D.-W.
TITLE EST analysis of human adipose gene expression
JOURNAL Unpublished (2002)
COMMENT Contact: Gong Da-Wei
Division of Endocrinology, Diabetes and Nutrition
University of Maryland
660 Redwood St, HH497, Baltimore, MD 21201, USA
Tel: 410 706 1672
Fax: 410 706 1622
Email: dgong@medicine.umaryland.edu
PCR Primers
FORWARD: CTCGGGAAGCGCGCATTGTGTGGT
BACKWARD: AATACGACTCATTATAGGGGAATTGG
Seq primer: GTTGGTACCGGAATTC.
FEATURES             location/Qualifiers
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     /sex="Male and Female"
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     /clone_lib="Human Fat Cell 5'-Stretch Plus cDNA Library"
     /note="Vector: lambdaTriplex"

ORIGIN
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Best Local Similarity 100.0%; Pred. NO. 0.0037;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GACTGTCCACAGCATTCGCGTGACC 25
DB 404 GACTGTCCACAGCATTCGCGTGACC 428

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Job time : 883.692 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 26, 2004, 16:00:31 ; Search time 532.065 Seconds  
(without alignments)  
2036.547 Million cell updates/sec

Title: US-09-121-239-10

Perfect score: 25  
Sequence: 1 GATGUGCCACAGCAUCCGUGACC 25

Scoring table: OLIGO NUC  
Gapop 60.0 , Gapext 60.0

Searched: 3470272 seqs, 21671516995 residues

Word size : 0  
Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

GenEmbl.\*

1: gb\_ba.\*

2: gb\_hg.\*

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16: em\_fun.\*

17: em\_hum.\*

18: em\_in.\*

19: em\_mu.\*

20: em\_om.\*

21: em\_or.\*

22: em\_ov.\*

23: em\_pat.\*

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34: em\_hg\_pln.\*

35: em\_hg\_rtd.\*

36: em\_hg\_mam.\*

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39: em\_hgo\_hum.\*

40: em\_hgo\_mus.\*

41: em\_hgo\_other.\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	25	100.0	25	6	BD222531	BD222531 Methods f
2	25	100.0	25	6	BD222532	BD222532 Methods f
3	25	100.0	25	6	BD222533	BD222533 Methods f
4	25	100.0	25	6	BD222534	BD222534 Methods f
5	25	100.0	56	6	I12447	I12447 Sequence 17
6	25	100.0	56	6	I14509	I14509 Sequence 17
7	25	100.0	210	6	AY043457	AY043457 Homo sapi
8	25	100.0	250	9	AF321981	AF321981 Homo sapi
9	25	100.0	305	9	AF192533	AF192533 Homo sapi
10	25	100.0	350	6	BD222546	BD222546 Methods f
11	25	100.0	561	9	HUMMK562B	M19695 Human myelo
12	25	100.0	679	9	HUMABLB	M30832 Human bcr/a
13	25	100.0	854	9	HUMABLD	M30829 Human bcr/a
14	25	100.0	922	9	HSAL131467	AJ131467 Homo sapi
15	25	100.0	997	9	HSAL131466	AJ131466 Homo sapi
16	25	100.0	1078	6	A92081	A92081 Sequence 5
17	25	100.0	1078	6	AR230888	AR230888 Sequence
18	25	100.0	1157	6	BD177069	BD177069 Standard
19	25	100.0	2255	6	E00984	E00984 Probe detec
20	25	100.0	2255	6	I04527	I04527 Sequence 1
21	25	100.0	2541	9	HUMBCRX	M55395 Human break
22	25	100.0	2811	6	AX780333	AX780333 Sequence
23	25	100.0	3481	9	AK128501	AK128501 Homo sapi
24	25	100.0	4714	9	HSBCR	Y00661 Human bcr m
25	25	100.0	4739	6	AX331144	AX331144 Sequence
26	25	100.0	4739	9	HSBCRR	X02596 Human mRNA
27	25	100.0	5000	9	HUMBCRE	L02935 Human major
28	25	100.0	111249	9	AP000343	AP000343 Homo sapi
29	25	100.0	152141	9	HSU07000	U07000 Human break
30	24	96.0	26	6	I83632	I83632 Sequence 6
31	24	96.0	40	6	E16986	E16986 Sense prime
32	21	84.0	468	9	HUMMK562A	M25946 Human chron
33	21	84.0	219210	2	AC145066	M13096 Human chine
34	21	84.0	240115	2	AC138021	AC145066 Pan trogl
35	21	84.0	240115	2	AC138021	AC138021 Pan trogl
36	18	72.0	22	6	I58643	I58643 Sequence 11
37	18	72.0	62	6	AR100681	AR100681 Sequence
38	18	72.0	81	6	AR100682	AR100682 Sequence
39	18	72.0	205	6	I02402	I02402 Sequence 1
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ALIGNMENTS

RESULT 1  
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LOCUS BD222531 25 bp DNA linear PAT 17-JUL-2003  
DEFINITION Methods for detecting and measuring spliced nucleic acids.  
ACCESSION BD222531  
VERSION BD222531.1 GI:33032301  
KEYWORDS JP 2002521037-A/9,  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1 (bases 1 to 25)  
AUTHORS Harvey,R.C. and Eastman,P.S.  
TITLE Methods for detecting and measuring spliced nucleic acids  
JOURNAL Patent: JP 2002521037-A 9 16-JUL-2002;  
GEN PROBE INC



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Query Match      100.0%; Score 25; DB 6; Length 25;
Best Local Similarity 80.0%; Pred. No. 3.9e-05;
Matches 20; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 GACUGUCCACAGCAUUCGCGUGACC 25
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RESULT 5
LOCUS 112447 56 bp DNA linear PAT 26-JUL-1995
DEFINITION Sequence 17 from patent US 5424413.
ACCESSION 112447
VERSION 112447.1 GI:909831
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 56)
AUTHORS Hogan, J.J., Arnold, L.J. Jr., Nelson, N.C. and Bezverkov, R.
TITLE Branched nucleic acid probes
JOURNAL Patent: US 5424413-A 17 13-JUN-1995;
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DEFINITION Sequence 17 from patent US 5451503.
ACCESSION 114509
VERSION 114509.1 GI:996992
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 56)
AUTHORS Hogan, J.J., Arnold, L.J. Jr., Nelson, N.C. and Bezverkov, R.
TITLE Method for use of branched nucleic acid probes
JOURNAL Patent: US 5451503-A 17 19-SEP-1995;
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Db 3 GACTGTCCACAGCATTCGCTGACC 27

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DEFINITION Homo sapiens BCR-ABL fusion protein (BCR-ABL fusion) mRNA, partial cds.
ACCESSION AY043457

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VERSION AY043457.1 GI:22073966
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 210)
AUTHORS Otazu, I.B., Helen Rivero, M., Olicio, R., Pinto, A., Zalberg, I. and
Seuanez, H.N.
TITLE A rare, in-frame BCR-ABL fusion (e13a3) in a patient with an
aggressive chronic myeloid leukaemia
JOURNAL Acta Haematol. 108 (3), 150-153 (2002)
MEDLINE 22259050
PUBMED 12373087
REFERENCE 2 (bases 1 to 210)
AUTHORS Otazu, I.B., Rivero, M.B. and Olicio, R.
TITLE Direct Submission
JOURNAL Submitted (03-JUL-2001) Genetics Division, Instituto Nacional de
Cancer, Praca da Cruz Vermelha, 23, sexto andar, Rio de Janeiro, RJ
21230-130, Brazil
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Matches 20; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 GACUGUCCACAGCAUUCGCGUGACC 25
Db 67 GACTGTCCACAGCATTCGCTGACC 91

RESULT 8
LOCUS AF321981 250 bp mRNA linear PRI 21-FEB-2001
DEFINITION Homo sapiens BCR-ABL fusion transcript e15a2 mRNA sequence.
ACCESSION AF321981
VERSION AF321981.1 GI:13021894
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 250)
AUTHORS Moreno, M.P., Cortinas, M.N., Bonomi, R., Cardeza, A. and Uriarte, M.R.
TITLE A novel BCR-ABL fusion transcript (e15a2) in two patients with
atypical Chronic Myeloproliferative Syndrome
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 250)
AUTHORS Moreno, M.P., Cortinas, M.N., Bonomi, R., Cardeza, A. and Uriarte, M.R.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2000) Biologia Molecular, Asociacion Espanola,
Bulevar Artigas 1465, Montevideo 11200, Uruguay
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22; t(9;22)"

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Db 41 GACTGTCCACAGCATTCGCGTGACC 65

RESULT 9
AF192533 305 bp mRNA linear PRI 04-APR-2000
LOCUS Homo sapiens BCR-ABL fusion protein (BCR-ABL fusion) mRNA, partial
DEFINITION cds.
ACCESSION AF192533.1 GI:7406986
VERSION AF192533.1
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 305)
AUTHORS Cortinas,M.N., Uriarte,M.R. and Moreno,M.P.
TITLE Identification of a novel BCR ABL fusion transcript in two patients
JOURNAL with persistent neutrophilia in absence of Philadelphia chromosome
REFERENCE 2 (bases 1 to 305)
AUTHORS Cortinas,M.N., Uriarte,M.R. and Moreno,M.P.
TITLE Direct Submission
JOURNAL Submitted (06-OCT-1999) Biologia Molecular, Asociacion Espanola
Primera de Socorroos Mutuos, Bvar. Artigas 1465, Montevideo 11200,
Uruguay

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Db 88 GACTGTCCACAGCATTCGCGTGACC 112

RESULT 10
BD222546 350 bp DNA linear PAT 17-JUL-2003
LOCUS Methods for detecting and measuring spliced nucleic acids.
DEFINITION
ACCESSION BD222546
VERSION BD222546.1 GI:33032316
KEYWORDS JP 2002521037-A/24.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 350)
AUTHORS Harvey,K.C. and Eastman,P.S.
TITLE Methods for detecting and measuring spliced nucleic acids
JOURNAL Patent: JP 2002521037-A 24 16-JUL-2002;
GEN PROBE INC
COMMENT OS Homo sapiens (human)
PN JP 2002521037-A/24
PD 16-JUL-2002
PF 23-JUL-1999 JP 2000561364
PR 23-JUL-1998 US 09/121239
PI RICHARD C HARVEY,PAUL S EASTMAN
PC C1201/68,C12N15/09,C12N15/00
CC Methods for detecting and measuring spliced nucleic acids FH
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Matches 20; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

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Db 89 GACTGTCCACAGCATTCGCGTGACC 113

RESULT 11
HUMMK562B 561 bp mRNA linear PRI 27-APR-1993
LOCUS Human myelocytic chimeric bcr and chromosome 9 fusion gene, exons
DEFINITION 1-4.
ACCESSION M19695
VERSION M19695.1 GI:188567
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 561)
AUTHORS Grosveid,G., Verwoerd,T., van Aghoven,T., de Klein,A.,
TITLE The chronic myelocytic cell line K562 contains a breakpoint in bcr
JOURNAL and produces a chimeric bcr/c-abl transcript
MEDLINE Mol. Cell. Biol. 6 (2), 607-616 (1986)
PUBMED 87064346
COMMENT 3023859
Original source text: Human myelocytic Ph(1)-positive CML K562 cell

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line, cDNA to mRNA, clone 8E.  
The bcr region of the fusion protein is located on chromosome 22q11; the abl region was translocated from chromosome 9q34.

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**RESULT 12**  
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**LOCUS** HUMABLB 679 bp. mRNA linear PRI 13-FEB-1996  
**DEFINITION** Human bcr/abl fusion protein, partial cds, clone E3.  
**ACCESSION** M30832  
**VERSION** M30832.1 GI:177944  
**KEYWORDS** Philadelphia chromosome; abl proto-oncogene; translocation.  
**SOURCE** Homo sapiens (human)  
**ORGANISM** Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
**REFERENCE** 1 (bases 1 to 679)  
**AUTHORS** Shitvelman, E., Lifshitz, B., Gale, R.P. and Canaani, E.  
**TITLE** Fused transcript of abl and bcr genes in chronic myelogenous leukaemia  
**JOURNAL** Nature 315 (6020), 550-554 (1985)  
**MEDLINE** 85240529  
**PUBMED** 2989692  
**COMMENT** Original source text: Homo sapiens (clone: E3.) cDNA to mRNA.  
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**RESULT 13**  
**HUMABLD**  
**LOCUS** HUMABLD 854 bp. mRNA linear PRI 14-FEB-1996  
**DEFINITION** Human bcr/abl fusion protein mRNA, partial cds, clone K28.

**ACCESSION** M30829  
**VERSION** M30829.1 GI:177953  
**KEYWORDS** Philadelphia chromosome; abl proto-oncogene; translocation.  
**SOURCE** Homo sapiens (human)  
**ORGANISM** Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
**REFERENCE** 1 (bases 1 to 854)  
**AUTHORS** Shitvelman, E., Lifshitz, B., Gale, R.P. and Canaani, E.  
**TITLE** Fused transcript of abl and bcr genes in chronic myelogenous leukaemia  
**JOURNAL** Nature 315 (6020), 550-554 (1985)  
**MEDLINE** 85240529  
**PUBMED** 2989692  
**COMMENT** Original source text: Homo sapiens (clone: K28.) cDNA to mRNA.  
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**Db** 477 GACTGTCCACAGCATTCGCTGACC 501  
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**RESULT 14**  
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**LOCUS** HSA131467 922 bp. mRNA linear PRI 11-OCT-2000  
**DEFINITION** Homo sapiens mRNA for BCR/ABL chimeric fusion peptide, partial.  
**ACCESSION** AJ131467  
**VERSION** AJ131467.1 GI:4033556  
**KEYWORDS** BCR/ABL chimeric fusion peptide; bcr/abl gene.  
**SOURCE** Homo sapiens (human)  
**ORGANISM** Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
**REFERENCE** 1  
**AUTHORS** Burmeister, T., Maurer, J., Aivado, M., Elmaagaccli, A.H., Grunebach, F., Held, K.R., Hess, G., Hochhaus, A., Hoppner, W., Lenters, K.U., Lubbert, M., Schafer, K.L., Schafhausen, P., Schmidt, C.A., Schuler, F., Seeger, K., Seeliger, R., Thiede, C., Viehmann, S., Weber, C., Wilhelm, S., Christmann, A., Clement, J.H., Ebener, U., Enczmann, J., Leo, R., Schleuning, M., Schoch, R. and Thiel, E.  
**TITLE** Quality assurance in RT-PCR-based BCR/ABL diagnostics--results of an interlaboratory test and a standardization approach  
**JOURNAL** Leukemia 14 (10), 1850-1856 (2000)  
**MEDLINE** 20471781  
**PUBMED** 11021760  
**REFERENCE** 2 (bases 1 to 922)  
**AUTHORS** Burmeister, T.  
**TITLE** Direct Submission  
**JOURNAL** Submitted (04-DEC-1998) Burmeister T., Medizinische Klinik III, FU Berlin, Hindenburgdamm 30, Berlin, Germany 12200, Germany





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exon /gene="abl"  
844. .>997 /number=4  
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Matches 20; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GACUGUCCACAGCAUUCGCGUACC 25  
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OM nucleic - nucleic search, using sw model

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Title: US-09-121-239-10

Perfect score: 25  
Sequence: 1 GACUGUCCACAGCAUCCGUGACC 25

Scoring table: OLIGO NUC  
Gapop 60.0 , Gapext 60.0

Searched: 3373863 seqs, 2124099041 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : N\_Geneseq\_29Jan04.\*

- 1: Geneseqn1980s.\*
- 2: Geneseqn1990s.\*
- 3: Geneseqn2000s.\*
- 4: Geneseqn2001as.\*
- 5: Geneseqn2001bs.\*
- 6: Geneseqn2002as.\*
- 7: Geneseqn2003as.\*
- 8: Geneseqn2003bs.\*
- 9: Geneseqn2003cs.\*
- 10: Geneseqn2004s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	25	100.0	25	3 AA260850	Oligonucleotide used to detect bcr b3-abl fusion transcripts.
2	25	100.0	25	3 AA260849	Fusion transcript; translocation; bcr b3 region; abl gene;
3	25	100.0	25	3 AA260851	amplification assay; detection assay; medical diagnosis;
4	25	100.0	25	3 AA260848	clinical monitoring; chimeric RNA; fusion RNA; condition marker;
5	25	100.0	45	9 ADC38532	disease marker; cancer; leukemia; ss.
6	25	100.0	56	2 AAQ46951	Synthetic.
7	25	100.0	200	2 AAT88785	WO200005418-A1.
8	25	100.0	250	6 ABS73175	03-FEB-2000.
9	25	100.0	305	6 ABS73174	23-JUL-1999; 99WO-US016832.
10	25	100.0	350	3 AA260863	23-JUL-1998; 98US-00121239.
11	25	100.0	504	5 AAS85023	(GENP-) GEN-PROBE INC.
12	25	100.0	504	8 ACH38242	Harvey RC, Eastman PS;
13	25	100.0	561	6 ABS73169	WPI; 2000-182730/16.
14	25	100.0	679	6 ABS73172	Novel methods for preparing RNA from biological samples, used for the
15	25	100.0	766	5 ABV29306	detection and measurement of nucleic acids and fusion nucleic acids.
16	25	100.0	766	5 ABV23449	Claim 19; Page 41; 49pp; English.
17	25	100.0	854	6 ABS73170	Oligonucleotides AA260840-62 and AA260865-66 are used in the method of
18	25	100.0	921	5 AAS85025	the invention to detect fusion transcripts produced from a translocation
19	25	100.0	922	6 ABS73180	between the bcr b3 region and the abl gene. The specification describes a
20	25	100.0	997	6 ABS73173	method for detecting a fusion nucleic acid (particularly chimeric mRNA
21	25	100.0	1097	2 AAT91764	species), in a biological sample. The method comprises contacting a
22	25	100.0	1157	9 ADC64640	sample of fusion nucleic acid with primers, amplifying the hybridized
23	25	100.0	1212	5 AAS85028	fusion nucleic acid, and detecting the target hybrid. The method is used

24	25	100.0	2255	1 AAN60228	Aan60228 Sequence
25	25	100.0	4725	5 AAS76375	Aas76375 DNA encod
26	25	100.0	4739	6 ABL63316	Ab163316 Breast ca
27	25	100.0	4739	7 ACC00031	Acc00031 Human bcr
28	25	100.0	4756	5 AAS85030	Aas85030 DNA encod
29	25	100.0	4775	5 AAS76377	Aas76377 DNA encod
30	25	100.0	5795	5 AAS85031	Aas85031 DNA encod
31	25	100.0	152141	7 ACA64961	Aca64961 Human bcr
32	24	96.0	26	2 AAQ51830	AaQ51830 bcr mRNA
33	24	96.0	40	2 AAV58775	Aav58775 Forward p
34	21	84.0	468	6 ABS73171	Ab573171 Human tra
35	20	80.0	20	2 AAT91761	Aat91761 Primer DE
36	19	76.0	45	2 AAT91782	Aat91782 Primer BB
37	18	72.0	22	2 AAQ34635	AaQ34635 Human bcr
38	18	72.0	62	2 AAQ66774	AaQ66774 L6(1)31 r
39	18	72.0	81	2 AAQ66775	AaQ66775 L6(1)31 r
40	18	72.0	205	1 AAN91666	An91666 Bcr-abl f
41	18	72.0	257	2 AAQ34625	AaQ34625 Human bcr
42	18	72.0	257	2 AAV20458	Aav20458 Human bcr
43	17	68.0	20	3 AAZ91685	Aaz91685 PCR prime
44	17	68.0	20	8 ADB68429	Adb68429 PCR prime
45	17	68.0	20	9 ADD06158	Add06158 Bcr-abl f

## ALIGNMENTS

RESULT 1	
AAZ60850/c	
ID	AAZ60850 standard; DNA; 25 BP.
XX	
AC	AAZ60850;
XX	
DT	16-MAY-2000 (first entry)
XX	
DE	Oligonucleotide used to detect bcr b3-abl fusion transcripts.
XX	
KW	Fusion transcript; translocation; bcr b3 region; abl gene;
KW	amplification assay; detection assay; medical diagnosis;
KW	clinical monitoring; chimeric RNA; fusion RNA; condition marker;
KW	disease marker; cancer; leukemia; ss.
XX	
OS	Synthetic.
XX	
PN	WO200005418-A1.
XX	
PD	03-FEB-2000.
XX	
PF	23-JUL-1999; 99WO-US016832.
XX	
PR	23-JUL-1998; 98US-00121239.
XX	
PA	(GENP-) GEN-PROBE INC.
XX	
PI	Harvey RC, Eastman PS;
XX	
DR	WPI; 2000-182730/16.
XX	
PT	Novel methods for preparing RNA from biological samples, used for the
PT	detection and measurement of nucleic acids and fusion nucleic acids.
XX	
PS	Claim 19; Page 41; 49pp; English.
XX	
CC	Oligonucleotides AA260840-62 and AA260865-66 are used in the method of
CC	the invention to detect fusion transcripts produced from a translocation
CC	between the bcr b3 region and the abl gene. The specification describes a
CC	method for detecting a fusion nucleic acid (particularly chimeric mRNA
CC	species), in a biological sample. The method comprises contacting a
CC	sample of fusion nucleic acid with primers, amplifying the hybridized
CC	fusion nucleic acid, and detecting the target hybrid. The method is used
CC	for the sample and rapid preparation of RNA from a biological sample,
CC	particularly from the cytoplasm of eukaryotic cells, which is suitable
CC	for use in an amplification and detection assay. The methods are used for

CC the analysis and detection of nucleic acids in biological samples. The  
 CC methods are useful in the human medical and veterinary fields, for  
 CC medical diagnoses and clinical monitoring of a patient's response to  
 CC therapy where a disease or medical condition is associated with a  
 CC particular type and/or level of mRNA present in the sample. The methods  
 CC are also useful for detecting or quantifying fusion or chimeric RNA  
 CC species, and for detecting a translocation as a marker for a given  
 CC condition or disease, e.g. translocations associate with cancers,  
 CC particularly forms of leukemia

XX Sequence 25 BP; 5 A; 5 C; 10 G; 5 T; 0 U; 0 Other;  
 SQ Query Match 100.0%; Score 25; DB 3; Length 25;  
 Best Local Similarity 80.0%; Pred. No. 0.00021;  
 Matches 20; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 GACUGUCCACAGCAUUCGCGUACC 25  
 DB |||:|||||:|||||:|||||:|||||

25 GACTGTCCACAGCATTCGCGTACC 1

RESULT 2  
 AAZ60849  
 ID AAZ60849 standard; RNA; 25 BP.  
 XX  
 AC AAZ60849;  
 XX  
 DT 16-MAY-2000 (first entry)  
 XX  
 DE Oligonucleotide used to detect bcr b3-abl fusion transcripts.  
 XX  
 KW Fusion transcript; translocation; bcr b3 region; abl gene;  
 KW amplification assay; detection assay; medical diagnosis;  
 KW clinical monitoring; chimeric RNA; fusion RNA; condition marker;  
 KW disease marker; cancer; leukemia; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200005418-A1.  
 XX  
 PD 03-FEB-2000.  
 XX  
 PF 23-JUL-1999; 99WO-US016832.  
 XX  
 PR 23-JUL-1998; 98US-00121239.  
 XX  
 PA (GENP-) GEN-PROBE INC.  
 XX  
 PI Harvey RC, Eastman PS;  
 XX  
 DR WPI; 2000-182730/16.  
 XX  
 PT Novel methods for preparing RNA from biological samples, used for the  
 PT detection and measurement of nucleic acids and fusion nucleic acids.  
 XX  
 PS Claim 19; Page 41; 49pp; English.  
 XX  
 CC Oligonucleotides AAZ60840-62 and AAZ60865-66 are used in the method of  
 CC the invention to detect fusion transcripts produced from a translocation  
 CC between the bcr b3 region and the abl gene. The specification describes a  
 CC method for detecting a fusion nucleic acid (particularly chimeric mRNA  
 CC species), in a biological sample. The method comprises contacting a  
 CC sample of fusion nucleic acid with primers, amplifying the hybridized  
 CC fusion nucleic acid, and detecting the target hybrid. The method is used  
 CC for the simple and rapid preparation of RNA from a biological sample,  
 CC particularly from the cytoplasm of eukaryotic cells, which is suitable  
 CC for use in an amplification and detection assay. The methods are used for  
 CC the analysis and detection of nucleic acids in biological samples. The  
 CC methods are useful in the human medical and veterinary fields, for  
 CC medical diagnoses and clinical monitoring of a patient's response to  
 CC therapy where a disease or medical condition is associated with a  
 CC particular type and/or level of mRNA present in the sample. The methods  
 CC are also useful for detecting or quantifying fusion or chimeric RNA  
 CC species, and for detecting a translocation as a marker for a given  
 CC condition or disease, e.g. translocations associate with cancers,  
 CC particularly forms of leukemia

CC species, and for detecting a translocation as a marker for a given  
 CC condition or disease, e.g. translocations associate with cancers,  
 CC particularly forms of leukemia

XX Sequence 25 BP; 5 A; 10 C; 5 G; 0 T; 5 U; 0 Other;  
 SQ Query Match 100.0%; Score 25; DB 3; Length 25;  
 Best Local Similarity 100.0%; Pred. No. 0.00021;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GACUGUCCACAGCAUUCGCGUACC 25  
 DB |||:|||||:|||||:|||||:|||||

1 GACUGUCCACAGCAUUCGCGUACC 25

RESULT 3  
 AAZ60851/c  
 ID AAZ60851 standard; RNA; 25 BP.  
 XX  
 AC AAZ60851;  
 XX  
 DT 16-MAY-2000 (first entry)  
 XX  
 DE Oligonucleotide used to detect bcr b3-abl fusion transcripts.  
 XX  
 KW Fusion transcript; translocation; bcr b3 region; abl gene;  
 KW amplification assay; detection assay; medical diagnosis;  
 KW clinical monitoring; chimeric RNA; fusion RNA; condition marker;  
 KW disease marker; cancer; leukemia; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200005418-A1.  
 XX  
 PD 03-FEB-2000.  
 XX  
 PF 23-JUL-1999; 99WO-US016832.  
 XX  
 PR 23-JUL-1998; 98US-00121239.  
 XX  
 PA (GENP-) GEN-PROBE INC.  
 XX  
 PI Harvey RC, Eastman PS;  
 XX  
 DR WPI; 2000-182730/16.  
 XX  
 PT Novel methods for preparing RNA from biological samples, used for the  
 PT detection and measurement of nucleic acids and fusion nucleic acids.  
 XX  
 PS Claim 19; Page 41; 49pp; English.  
 XX  
 CC Oligonucleotides AAZ60840-62 and AAZ60865-66 are used in the method of  
 CC the invention to detect fusion transcripts produced from a translocation  
 CC between the bcr b3 region and the abl gene. The specification describes a  
 CC method for detecting a fusion nucleic acid (particularly chimeric mRNA  
 CC species), in a biological sample. The method comprises contacting a  
 CC sample of fusion nucleic acid with primers, amplifying the hybridized  
 CC fusion nucleic acid, and detecting the target hybrid. The method is used  
 CC for the simple and rapid preparation of RNA from a biological sample,  
 CC particularly from the cytoplasm of eukaryotic cells, which is suitable  
 CC for use in an amplification and detection assay. The methods are used for  
 CC the analysis and detection of nucleic acids in biological samples. The  
 CC methods are useful in the human medical and veterinary fields, for  
 CC medical diagnoses and clinical monitoring of a patient's response to  
 CC therapy where a disease or medical condition is associated with a  
 CC particular type and/or level of mRNA present in the sample. The methods  
 CC are also useful for detecting or quantifying fusion or chimeric RNA  
 CC species, and for detecting a translocation as a marker for a given  
 CC condition or disease, e.g. translocations associate with cancers,  
 CC particularly forms of leukemia

XX Sequence 25 BP; 5 A; 5 C; 10 G; 0 T; 5 U; 0 Other;  
 SQ

Query Match 100.0%; Score 25; DB 3; Length 25;  
Best Local Similarity 80.0%; Pred. No. 0.00021;  
Matches 20; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 GACUGUCCACAGCAUUCGCGUACC 25  
25 GACTGTCCACAGCATTCGCTGACC 1

RESULT 4  
AAZ60848  
ID AAZ60848 standard; DNA; 25 BP.  
XX  
AC AAZ60848;  
XX  
DT 16-MAY-2000 (first entry)  
XX  
DE Oligonucleotide used to detect bcr b3-abl fusion transcripts.  
XX  
KW Fusion transcript; translocation; bcr b3 region; abl gene;  
KW amplification assay; detection assay; medical diagnosis;  
KW clinical monitoring; chimeric RNA; fusion RNA; condition marker;  
KW disease marker; cancer; leukemia; ss.  
XX  
OS Synthetic.  
XX  
PN WO200005418-A1.  
XX  
PD 03-FEB-2000.  
XX  
PF 23-JUL-1999; 99WO-US016832.  
XX  
PR 23-JUL-1998; 98US-00121239.  
XX  
PA (GENP-) GEN-PROBE INC.  
XX  
PI Harvey RC, Eastman PS;  
XX  
DR WPI; 2000-182730/16.  
XX  
PT Novel methods for preparing RNA from biological samples, used for the  
PT detection and measurement of nucleic acids and fusion nucleic acids.

Claim 19; Page 41; 49pp; English.  
XX  
CC Oligonucleotides AAZ60840-62 and AAZ60865-66 are used in the method of  
CC the invention to detect fusion transcripts produced from a translocation  
CC between the bcr b3 region and the abl gene. The specification describes a  
CC method for detecting a fusion nucleic acid (particularly chimeric mRNA  
CC species), in a biological sample. The method comprises contacting a  
CC sample of fusion nucleic acid with primers, amplifying the hybridized  
CC fusion nucleic acid, and detecting the target hybrid. The method is used  
CC for the simple and rapid preparation of RNA from a biological sample,  
CC particularly from the cytoplasm of eukaryotic cells, which is suitable  
CC for use in an amplification and detection assay. The methods are used for  
CC the analysis and detection of nucleic acids in biological samples. The  
CC methods are useful in the human medical and veterinary fields, for  
CC medical diagnoses and clinical monitoring of a patient's response to  
CC therapy where a disease or medical condition is associated with a  
CC particular type and/or level of mRNA present in the sample. The methods  
CC are also useful for detecting or quantifying fusion or chimeric RNA  
CC species, and for detecting a translocation as a marker for a given  
CC condition or disease, e.g. translocations associate with cancers,  
CC particularly forms of leukemia  
XX  
SQ Sequence 25 BP; 5 A; 10 C; 5 G; 5 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 3; Length 25;  
Best Local Similarity 80.0%; Pred. No. 0.00021;  
Matches 20; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 GACUGUCCACAGCAUUCGCGUACC 25  
||||:|||||:|||||:|||||:|||||

Db 1 GACTGTCCACAGCATTCGCTGACC 25

RESULT 5  
ADC38532  
ID ADC38532 standard; DNA; 45 BP.  
XX  
AC ADC38532;  
XX  
DT 18-DEC-2003 (first entry)  
XX  
DE Template translocation oligonucleotide SEQ ID 9.  
XX  
KW Chromosome translocation; cancer; leukaemia; lymphoma; ss.  
XX  
OS Synthetic.  
XX  
PN WO2003044486-A2.  
XX  
PD 30-MAY-2003.  
XX  
PF 20-NOV-2002; 2002WO-US037507.  
XX  
PR 20-NOV-2001; 2001US-0335716P.  
XX  
PA (REGC ) UNIV CALIFORNIA.  
XX  
PI Nolan JP, Zhou F;  
XX  
DR WPI; 2003-468806/44.  
XX  
PT Detecting chromosome translocations in a target nucleic acid sequence for  
PT diagnosing cancers associated with chromosome translocations, by using  
PT microsphere arrays.  
XX  
PS Claim 52; Fig 7; 57pp; English.

The present invention relates to a method (M) for detecting chromosome  
translocation. The method comprises amplifying a target nucleic acid  
sequence from a sample, hybridizing oligonucleotides (ONTs) specific for  
regions of the translocation to the amplified target, where the ONTs  
comprise capture tags, extending the ONTs to produce labelled and extended  
ONTs, hybridizing the ONTs to address tags on solid support. (M) is  
the presence of labelled extended ONTs on the solid support. (M) is  
useful for detecting a chromosomal translocation in a target nucleic acid  
sequence, preferably a cDNA from a biological sample from a human. The  
chromosome translocation is associated with cancer (e.g. leukaemia) and  
this method is especially useful for diagnosing cancer, especially  
leukaemia, and also lymphoma. The present sequence is a template  
translocation oligonucleotide used to illustrate the invention.

Query Match 100.0%; Score 25; DB 9; Length 45;  
Best Local Similarity 80.0%; Pred. No. 0.00021;  
Matches 20; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 GACUGUCCACAGCAUUCGCGUACC 25  
||||:|||||:|||||:|||||:|||||

Db 7 GACTGTCCACAGCATTCGCTGACC 31  
||||:|||||:|||||:|||||:|||||

RESULT 6  
AAQ46951  
ID AAQ46951 standard; DNA; 56 BP.  
XX  
AC AAQ46951;  
XX  
DT 25-MAR-2003 (revised)  
DT 21-JAN-1994 (first entry)  
XX  
DE Branched probe to CMLb translocation region of chromosome 22.  
XX

KW Chronic myelogenous leukaemia; CMLb; abl region;  
 KW acute lymphocytic leukaemia; ALL; genetic translocation: chromosome 22;  
 KW target sequence; universal detection oligomer; branched probe;  
 KW chemiluminescent acridinium ester; ss.  
 XX  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT misc\_feature 1..40 /tag= a  
 FT /note= "Complementary to region of chromosome 22  
 FT associated with CMLb translocation"  
 FT 41..56  
 FT misc\_feature /tag= b  
 FT /note= "Complementary to nucleotides 16-1 of universal  
 FT detection probe AAQ46949"  
 FT  
 XX  
 PN EP552931-A1.  
 XX  
 XX  
 PD 28-JUL-1993.  
 XX  
 XX  
 PF 20-JAN-1993; 93EP-00300377.  
 XX  
 XX 22-JAN-1992; 92US-00827021.  
 XX (GENP-) GEN PROBE INC.  
 PA  
 PI Hogan JJ, Arnold LJ, Nelson NC, Bezverkov R;  
 XX  
 XX WPI; 1993-236606/30.  
 XX  
 XX Nucleic acid molecules which hybridise in presence of target nucleic acid  
 PT - are used as probes in hybridisation assays or as therapeutic agents for  
 PT diseases.  
 PT  
 XX  
 PS Example 6; Fig 12B; 58pp; English.  
 XX  
 XX Chimeric targets were synthesised homologous to 3 different genetic  
 CC translocations between a constant abl region of chromosome 9 and various  
 CC regions of chromosome 22; two are the most common translocations  
 CC associated with chronic myelogenous leukaemia (CMLa and CMLb) and the  
 CC other is associated with acute lymphocytic leukaemia (ALL). An AB-  
 CC labelled universal detection oligomer (AAQ46949) specific for the abl  
 CC region was synthesised. Three different strands were designed to contain  
 CC a probe region specific for one of the translocated chromosome 22 regions  
 CC as well as an arm region complementary to part of the universal probe  
 CC (AAQ46950-2). The probe mixes were found to detect only the correct  
 CC chimeric targets and did not cross-react significantly with the other  
 CC targets. (Updated on 25-MAR-2003 to correct PN field.) (Updated on 25-MAR  
 CC -2003 to correct PA field.)  
 XX  
 XX Sequence 56 BP; 18 A; 18 C; 9 G; 11 T; 0 U; 0 Other;  
 SQ  
 Query Match 100.0%; Score 25; DB 2; Length 56;  
 Best Local Similarity 80.0%; Pred. No. 0.00021;  
 Matches 20; Conservative 5; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GACUGUCCACAGCAUUCGCGUACC 25  
 |||:|||||:|||||:  
 DB 3 GACTGTCCACAGCATTCGCTGACC 27  
 RESULT 7  
 AAT88785  
 ID AAT88785 standard; DNA; 200 BP.  
 XX  
 AC AAT88785;  
 XX  
 DT 23-MAR-1998 (first entry)  
 XX  
 DE Leukaemic cell BCR-ABL mRNA PCR product target sequence.  
 XX  
 KW Leukaemia; BCR-ABL; cell line K562; target; immunoassay; probe;

KW hybridisation; diagnostic; luciferase; genetic disease; ss.  
 XX  
 OS Unidentified.  
 XX  
 PN CA2186998-A.  
 XX  
 PD 31-MAY-1997.  
 XX  
 PF 02-OCT-1996; 96CA-02186998.  
 XX  
 PR 30-NOV-1995; 95US-00565055.  
 XX  
 PA (UYWI-) UNIV WINDSOR.  
 XX  
 PI Christopoulos TK;  
 XX  
 DR WPI; 1997-415964/39.  
 XX  
 XX Immunoassays and nucleic acid hybridisation assays - using protein-  
 PT encoding nucleic acid fragments as labels.  
 PT  
 XX  
 PS Disclosure; Page 26; 39pp; English.  
 XX  
 CC A novel assay has been developed for determining an analyte. The assay  
 CC comprises labelling the analyte with a nucleic acid fragment that encodes  
 CC a protein, expressing the nucleic acid, and detecting the protein. The  
 CC present sequence represents a target sequence from a leukaemic cell (cell  
 CC line K562), used in an example of the present assay. The assay is used  
 CC for the determination of antigens or nucleic acids for diagnostic or  
 CC research purposes, e.g. detecting low levels of tumour markers, analysing  
 CC nucleic acid mutations associated with genetic diseases, diagnosing and  
 CC monitoring pathogen infections, or searching for new disease markers. The  
 CC immunoassay when using a luciferase for detection is more sensitive than  
 CC an enzyme-amplified, time-resolved fluorometric immunoassay and does not  
 CC require preparation of a luciferase-antibody conjugate  
 XX  
 XX Sequence 200 BP; 49 A; 52 C; 51 G; 48 T; 0 U; 0 Other;  
 SQ  
 Query Match 100.0%; Score 25; DB 2; Length 200;  
 Best Local Similarity 80.0%; Pred. No. 0.0002; Mismatches 0; Indels 0; Gaps 0;  
 Matches 20; Conservative 5; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GACUGUCCACAGCAUUCGCGUACC 25  
 |||:|||||:|||||:  
 DB 40 GACTGTCCACAGCATTCGCTGACC 64  
 RESULT 8  
 ABS73175  
 ID ABS73175 standard; DNA; 250 BP.  
 XX  
 AC ABS73175;  
 XX  
 DT 04-DEC-2002 (first entry)  
 XX  
 DE Human translocation (9: 22) (q34: q11) #3.  
 XX  
 XX Chromosome aberration; oncogenic fusion protein; cancer;  
 KW proliferative disease; cellular protein isoform; heat shock protein 90;  
 KW HSP-90; rheumatoid arthritis; cancer; haematopoietic disorder;  
 KW T cell lymphoma; B cell lymphoma; chronic myeloid leukaemia; CML;  
 KW acute myeloid leukaemia; AML; chronic myelomonocytic leukaemia; CMML;  
 KW acute lymphoblastic leukaemia; ALL; APL; NHL; solid tumour;  
 KW papillary thyroid carcinoma; Ewing's sarcoma; melanoma; liposarcoma;  
 KW rhabdomyosarcoma; synovial sarcoma; viral infection; gene; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO200269900-A2.  
 PN  
 XX  
 PD 12-SEP-2002.  
 XX  
 XX 01-MAR-2002; 2002WO-US006518.

```

XX 01-MAR-2001; 2001US-0272751P.
XX (CONF-) CONFORMA THERAPEUTICS CORP.
XX Fritz LC, Burrows FJ;
XX WPI; 2002-698710/75.
XX
XX Treating genetically-defined disease associated with chromosomal
XX aberrations yielding oncogenic fusion proteins, e.g. cell proliferative
XX diseases, involves administering an inhibitor of heat shock protein 90.
XX
XX Disclosure; Page 97; 389pp; English.
XX
XX The invention describes a method of treating genetically-defined disease
XX associated with chromosomal aberrations yielding oncogenic fusion
XX proteins (I), treating cancerous cells containing (I) in a heterogeneous
XX cell population, treating proliferative diseases associated with mutant
XX protein or cellular protein isoforms (II) dependent on heat shock protein
XX (HSP)-90, or selectively treating cells expressing (II) involving
XX administering HSP90-inhibitor. The method is useful for treating
XX genetically-defined disease with chromosomal aberration yielding
XX oncogenic fusion protein, treating cancerous cells containing fusion
XX protein in heterogeneous cell population, treating proliferative disease
XX (e.g. rheumatoid arthritis or cancer) associated with mutant protein or
XX cellular protein isoform dependent on heat shock protein (HSP)-90 (e.g.
XX p53), or selectively treating cells expressing mutant protein or cellular
XX protein isoform in a patient heterozygous for (II). The method is useful
XX for treating a disease e.g. haematopoietic disorder such as T or B cell
XX lymphoma, chronic myeloid leukaemia (CML), APL, ALL, NHL and CMMML,
XX or a disease characterised by a solid tumour such as papillary thyroid
XX carcinoma, Ewing's sarcoma, melanoma, liposarcoma, rhabdomyosarcoma and
XX synovial sarcoma. The method is also useful for treating viral
XX infections. This represents the DNA sequence of a chromosome aberration
XX
XX Sequence 250 BP; 65 A; 62 C; 63 G; 60 T; 0 U; 0 Other;
XX
Query Match 100.0%; Score 25; DB 6; Length 250;
Best Local Similarity 80.0%; Pred. No. 0.0002;
Matches 20; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
OY 1 GACUGUCCACAGCAUUCGCTGACC 25
DB 41 GACTGTCCACAGCATTCGCTGACC 65
||||:|||||:|||||:|||||
||||:|||||:|||||:|||||

RESULT 9
ABS73174
ID ABS73174 standard; DNA; 305 BP.
XX
XX AC ABS73174;
XX
XX DT 04-DEC-2002 (first entry)
XX
XX DE DNA encoding human translocation (9: 22) (q34: q11) protein #5.
XX
XX Chromosome aberration; oncogenic fusion protein; cancer;
XX proliferative disease; cellular protein isoform; heat shock protein 90;
XX HSP-90; rheumatoid arthritis; cancer; haematopoietic disorder;
XX T cell lymphoma; B cell lymphoma; chronic myeloid leukaemia; CML;
XX acute myeloid leukaemia; AML; chronic myelomonocytic leukaemia; CMMML;
XX acute lymphoblastic leukaemia; ALL; APL; NHL; solid tumour;
XX papillary thyroid carcinoma; Ewing's sarcoma; melanoma; liposarcoma;
XX rhabdomyosarcoma; synovial sarcoma, viral infection; gene; ds.
XX
XX OS Homo sapiens.
XX
XX PN WO200269900-A2.
XX
XX PD 12-SEP-2002.
XX
XX PF 01-MAR-2002; 2002WO-US006518.

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XX 01-MAR-2001; 2001US-0272751P.
XX (CONF-) CONFORMA THERAPEUTICS CORP.
XX Fritz LC, Burrows FJ;
XX WPI; 2002-698710/75.
XX P-PSDB; ABG95013.
XX
XX Treating genetically-defined disease associated with chromosomal
XX aberrations yielding oncogenic fusion proteins, e.g. cell proliferative
XX diseases, involves administering an inhibitor of heat shock protein 90.
XX
XX Disclosure; Page 97; 389pp; English.
XX
XX The invention describes a method of treating genetically-defined disease
XX associated with chromosomal aberrations yielding oncogenic fusion
XX proteins (I), treating cancerous cells containing (I) in a heterogeneous
XX cell population, treating proliferative diseases associated with mutant
XX protein or cellular protein isoforms (II) dependent on heat shock protein
XX (HSP)-90, or selectively treating cells expressing (II) involving
XX administering HSP90-inhibitor. The method is useful for treating
XX genetically-defined disease with chromosomal aberration yielding
XX oncogenic fusion protein, treating cancerous cells containing fusion
XX protein in heterogeneous cell population, treating proliferative disease
XX (e.g. rheumatoid arthritis or cancer) associated with mutant protein or
XX cellular protein isoform dependent on heat shock protein (HSP)-90 (e.g.
XX p53), or selectively treating cells expressing mutant protein or cellular
XX protein isoform in a patient heterozygous for (II). The method is useful
XX for treating a disease e.g. haematopoietic disorder such as T or B cell
XX lymphoma, chronic myeloid leukaemia (CML), APL, ALL, NHL and CMMML,
XX or a disease characterised by a solid tumour such as papillary thyroid
XX carcinoma, Ewing's sarcoma, melanoma, liposarcoma, rhabdomyosarcoma and
XX synovial sarcoma. The method is also useful for treating viral
XX infections. This represents the DNA sequence of a chromosome aberration
XX
XX Sequence 305 BP; 77 A; 79 C; 77 G; 72 T; 0 U; 0 Other;
XX
Query Match 100.0%; Score 25; DB 6; Length 305;
Best Local Similarity 80.0%; Pred. No. 0.0002;
Matches 20; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
OY 1 GACUGUCCACAGCAUUCGCTGACC 25
DB 88 GACTGTCCACAGCATTCGCTGACC 112
||||:|||||:|||||:|||||
||||:|||||:|||||:|||||

RESULT 10
AAZ60863
ID AAZ60863 standard; DNA; 350 BP.
XX
XX AC AAZ60863;
XX
XX DT 16-MAY-2000 (first entry)
XX
XX DE Region surrounding a bcr-able splice junction.
XX
XX Fusion transcript; translocation; bcr b3 region; abl gene;
XX amplification assay; detection assay; medical diagnosis;
XX clinical monitoring; chimeric RNA; fusion RNA; condition marker;
XX disease marker; cancer; leukemia; ss.
XX
XX OS Unidentified.
XX
XX PN WO200005418-A1.
XX
XX PD 03-FEB-2000.
XX
XX PF 23-JUL-1999; 99WO-US016832.
XX
XX PR 23-JUL-1998; 98US-00121239.
XX

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PT New polynucleotide sequences obtained from various cDNA libraries, useful  
PT as hybridization probes, as oligomers for PCR, for chromosome and gene  
PT mapping, in the recombinant production of protein, or in generating  
PT antisense DNA or RNA.

XX Claim 1; SEQ ID NO 25454; 44pp; English.

XX The invention relates to an isolated polynucleotide comprising any one of  
CC 38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence was  
CC determined by the technique of SBH (sequencing by hybridisation). Also  
CC included is a purified polypeptide comprising a sequence corresponding to  
CC a reading frame of the novel polynucleotide. The nucleic acid sequences  
CC are useful in diagnostics as expressed sequence tags (EST) for  
CC identifying expressed genes or for physical mapping of the human genome,  
CC in forensics, in assessing biodiversity, or in identifying mutations  
CC responsible for genetic disorders and other traits. The nucleotide  
CC sequences are also useful as hybridisation probes, as oligomers for PCR,  
CC for chromosome and gene mapping, in the recombinant production of  
CC protein, or in generating antisense DNA or RNA. The purified polypeptide  
CC is useful for generating antibodies specific for it. The present sequence  
CC is one of the 38043 isolated cDNA/EST sequences. Note: The sequence data  
CC for this patent did not form part of the printed specification, but was  
CC obtained in electronic format directly from USPTO at  
CC seqdata.uspto.gov/sequence.html?DocID=20030073623

XX SQ Sequence 504 BP; 119 A; 122 C; 144 G; 117 T; 0 U; 2 Other;

Query Match 100.0%; Score 25; DB 8; Length 504;  
Best Local Similarity 80.0%; Pred. No. 0.0002; Mismatches 0; Indels 0; Gaps 0;  
Matches 20; Conservative 5;

QY 1 GACGUCCACAGCAUUCGCGUACC 25  
DB 239 GACTGTCCACAGCATTCGCTGACC 263  
|||:|||||:|||||:|||||

RESULT 13

ABS73169  
ID ABS73169 standard; DNA; 561 BP.

AC ABS73169;

XX 04-DEC-2002 (first entry)

XX Human translocation (9: 22) (q34: q11) #1.

XX Chromosome aberration; oncogenic fusion protein; cancer;  
KW Proliferative disease; cellular protein isoform; heat shock protein 90;  
KW HSP-90; rheumatoid arthritis; cancer; haematopoietic disorder;  
KW T cell lymphoma; B cell lymphoma; chronic myeloid leukaemia; CML;  
KW acute myeloid leukaemia; AML; chronic myelomonocytic leukaemia; CMML;  
KW acute lymphoblastic leukaemia; ALL; APL; NHL; solid tumour;  
KW papillary thyroid carcinoma; Ewing's sarcoma; melanoma; liposarcoma;  
KW rhabdomyosarcoma; synovial sarcoma; viral infection; gene; ds.

XX Homo sapiens.

OS WO200269900-A2.

XX 12-SEP-2002.

PF 01-MAR-2002; 2002WO-US006518.

XX 01-MAR-2001; 2001US-0272751P.

XX (CONF-) CONFORMA THERAPEUTICS CORP.

XX Fritz LC, Burrows FJ;

XX WPI; 2002-698710/75.

XX Treating genetically-defined disease associated with chromosomal

PT aberrations yielding oncogenic fusion proteins, e.g. cell proliferative

PT diseases, involves administering an inhibitor of heat shock protein 90.  
XX Disclosure; Page 91-92; 389pp; English.

XX The invention describes a method of treating genetically-defined disease  
CC associated with chromosomal aberrations yielding oncogenic fusion  
CC proteins (I), treating cancerous cells containing (I) in a heterogeneous  
CC cell population, treating proliferative diseases associated with mutant  
CC protein or cellular protein isoforms (II) dependent on heat shock protein  
CC (HSP)-90, or selectively treating cells expressing (II) involving  
CC administering HSP90-inhibitor. The method is useful for treating  
CC genetically-defined disease with chromosomal aberration yielding  
CC oncogenic fusion protein, treating cancerous cells containing fusion  
CC protein in heterogeneous cell population, treating proliferative disease  
CC (e.g. rheumatoid arthritis or cancer) associated with mutant protein or  
CC cellular protein isoform dependent on heat shock protein (HSP)-90 (e.g.  
CC p53), or selectively treating cells expressing mutant protein or cellular  
CC protein isoform in a patient heterozygous for (II). The method is useful  
CC for treating a disease e.g. haematopoietic disorder such as T or B cell  
CC lymphoma, chronic myeloid leukaemia (CML), APL, ALL, NHL and CMML,  
CC or a disease characterised by a solid tumour such as papillary thyroid  
CC carcinoma, Ewing's sarcoma, melanoma, liposarcoma, rhabdomyosarcoma and  
CC synovial sarcoma. The method is also useful for treating viral  
CC infections. This represents the DNA sequence of a chromosome aberration

XX SQ Sequence 561 BP; 134 A; 134 C; 136 G; 157 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 6; Length 561;  
Best Local Similarity 80.0%; Pred. No. 0.0002; Mismatches 0; Indels 0; Gaps 0;  
Matches 20; Conservative 5;

QY 1 GACGUCCACAGCAUUCGCGUACC 25  
DB 84 GACTGTCCACAGCATTCGCTGACC 108  
|||:|||||:|||||:|||||

RESULT 14

ABS73172  
ID ABS73172 standard; DNA; 679 BP.

AC ABS73172;

XX 04-DEC-2002 (first entry)

XX DNA encoding human translocation (9: 22) (q34: q11) protein #3.

XX Chromosome aberration; oncogenic fusion protein; cancer;  
KW Proliferative disease; cellular protein isoform; heat shock protein 90;  
KW HSP-90; rheumatoid arthritis; cancer; haematopoietic disorder;  
KW T cell lymphoma; B cell lymphoma; chronic myeloid leukaemia; CML;  
KW acute myeloid leukaemia; AML; chronic myelomonocytic leukaemia; CMML;  
KW acute lymphoblastic leukaemia; ALL; APL; NHL; solid tumour;  
KW papillary thyroid carcinoma; Ewing's sarcoma; melanoma; liposarcoma;  
KW rhabdomyosarcoma; synovial sarcoma; viral infection; gene; ds.

XX Homo sapiens.

OS WO200269900-A2.

XX 12-SEP-2002.

PF 01-MAR-2002; 2002WO-US006518.

XX 01-MAR-2001; 2001US-0272751P.

XX (CONF-) CONFORMA THERAPEUTICS CORP.

XX Fritz LC, Burrows FJ;

XX WPI; 2002-698710/75.

XX P-PSDB; ABG95011.

XX Treating genetically-defined disease associated with chromosomal

PT aberrations yielding oncogenic fusion proteins, e.g. cell proliferative  
 PT diseases, involves administering an inhibitor of heat shock protein 90.  
 PS  
 XX Disclosure; Page 94-95; 389pp; English.  
 CC The invention describes a method of treating genetically-defined disease  
 CC associated with chromosomal aberrations yielding oncogenic fusion  
 CC proteins (I), treating cancerous cells containing (I) in a heterogeneous  
 CC cell population, treating proliferative diseases associated with mutant  
 CC protein or cellular protein isoforms (II) dependent on heat shock protein  
 CC (HSP)-90, or selectively treating cells expressing (II) involving  
 CC administering HSP90-inhibitor. The method is useful for treating  
 CC genetically-defined disease with chromosomal aberration yielding  
 CC oncogenic fusion protein, treating cancerous cells containing fusion  
 CC protein in heterogeneous cell population, treating proliferative disease  
 CC (e.g. rheumatoid arthritis or cancer) associated with mutant protein or  
 CC cellular protein isoform dependent on heat shock protein (HSP)-90 (e.g.  
 CC p53), or selectively treating cells expressing mutant protein or cellular  
 CC protein isoform in a patient heterozygous for (II). The method is useful  
 CC for treating a disease e.g. haematopoietic disorder such as T or B cell  
 CC lymphoma, chronic myeloid leukaemia (CML), APL, ALL, NHL and CML,  
 CC or a disease characterised by a solid tumour such as papillary thyroid  
 CC carcinoma, Ewing's sarcoma, melanoma, liposarcoma, rhabdomyosarcoma and  
 CC synovial sarcoma. The method is also useful for treating viral  
 CC infections. This represents the DNA sequence of a chromosome aberration  
 XX  
 SQ Sequence 679 BP; 186 A; 165 C; 184 G; 144 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 6; Length 679;  
 Best Local Similarity 80.0%; Pred. No. 0.0002;  
 Matches 20; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 GACUGUCCACAGCAUUCGUGACC 25  
 DB 302 GACTGTCCACAGCATTCGCTGACC 326

RESULT 15  
 ABV29306/c  
 ID ABV29306 standard; cDNA; 766 BP.  
 XX  
 AC ABV29306;  
 XX  
 DT 16-SEP-2002 (first entry)  
 XX  
 DE Human prostate expression marker cDNA 29297.  
 XX  
 KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;  
 KW pharmacogenomic marker; gene; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200160860-A2.  
 XX  
 PD 23-AUG-2001.  
 XX  
 PF 20-FEB-2001; 2001WO-US005171.  
 XX  
 PR 17-FEB-2000; 2000US-0183319P.  
 PR 16-MAR-2000; 2000US-0189862P.  
 PR 25-MAY-2000; 2000US-0207454P.  
 PR 09-JUN-2000; 2000US-0211314P.  
 PR 18-JUL-2000; 2000US-0219007P.  
 PR 13-DEC-2000; 2000US-0255281P.  
 XX  
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
 XX  
 PI Schlegel R, Endege WO, Monahan JE;  
 XX  
 DR WPI; 2001-662795/76.  
 XX  
 PT Novel isolated nucleic acid molecule associated with cancerous state of  
 PT prostate cells and correlating with presence of prostate cancer, useful

PT for detecting presence of prostate cancer, stage of prostate cancer.  
 XX  
 PS Claim 1; Page 6267; 11750pp; English.  
 XX  
 CC The invention relates to an isolated nucleic acid molecule (I) comprising  
 CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the  
 CC specification or its complement. (I) is useful for: (a) assessing whether  
 CC a patient is afflicted with prostate cancer; (b) monitoring the  
 CC progression of prostate cancer in a patient; (c) assessing the efficacy  
 CC of a test compound to inhibit prostate cancer in a patient; (d) assessing  
 CC the efficacy of a therapy for inhibiting prostate cancer in a patient;  
 CC (e) selecting a composition for inhibiting prostate cancer in a patient;  
 CC (f) assessing the prostate cell carcinogenic potential of a compound; (g)  
 CC determining whether prostate cancer has metastasized in a patient; (h)  
 CC assessing the aggressiveness or indolence of prostate cancer in a patient  
 CC ; (I) is also useful as a pharmacodynamic or pharmacogenomic marker  
 XX  
 SQ Sequence 766 BP; 166 A; 237 C; 193 G; 170 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 25; DB 5; Length 766;  
 Best Local Similarity 80.0%; Pred. No. 0.0002;  
 Matches 20; Conservative 5; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GACUGUCCACAGCAUUCGUGACC 25  
 DB 553 GACTGTCCACAGCATTCGCTGACC 529

Search completed: May 26, 2004, 16:52:17  
 Job time : 111.497 secs



```
RESULT 2
US-08-255-553-17
; Sequence 17, Application US/08255553
; Patent No. 5451503
; GENERAL INFORMATION:
; APPLICANT: James J. Hogan et al.
; TITLE OF INVENTION: BRANCHED NUCLEIC ACID PROBES
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 611 West Sixth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90017
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
; OPERATING SYSTEM: IBM P.C. DOS Version 3.30
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/255,553
; FILING DATE: 07-JUN-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/940,652
; FILING DATE: 04-SEP-1992
; APPLICATION NUMBER: US/07/827,021
; FILING DATE: 22-JAN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 199/201
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 56
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-255-553-17
Query Match 100.0%; Score 25; DB 1; Length 56;
Best Local Similarity 80.0%; Pred. No. 6.5e-06;
Matches 20; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 GACUGUCCACAGCAUUCGCGACC 25
Db 3 GACTGTCCACAGCATTCGCTGACC 27

RESULT 3
US-09-310-842-1
; Sequence 1, Application US/09310842A
; Patent No. 6451593
; GENERAL INFORMATION:
; APPLICANT: Wittig, Prof. Burghardt
; APPLICANT: Jungmans, Claas
; TITLE OF INVENTION: Design Principle for Constructing Expression Constructs for Gene
; FILE REFERENCE: XI 597/99
; CURRENT APPLICATION NUMBER: US/09/310,842A
; CURRENT FILING DATE: 1999-05-12
; EARLIER APPLICATION NUMBER: DE 196 48 625.4
; EARLIER FILING DATE: 1996-11-13
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
```

```
; LENGTH: 1078
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: gene
; LOCATION: (1)..(1078)
; OTHER INFORMATION: bcr3=abl2; Oligo DNA Dumbbell
; FEATURE:
; NAME/KEY: misc binding
; LOCATION: (1)_(2)
; OTHER INFORMATION: intramolecular binding site; the T-nucleotides at position 1 to
; OTHER INFORMATION: 2 can be modified with amino or caroxy features
; FEATURE:
; NAME/KEY: misc binding
; LOCATION: (1077)..(1078)
; OTHER INFORMATION: intramolecular binding site; the T-nucleotides at position 1077
; OTHER INFORMATION: to 1078 can be modified with amino or caroxy features
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Strandness: both; nucleic
; OTHER INFORMATION: acid (linear), hypothetical: No. 6451593 anti-sense: No
US-09-310-842-1
Query Match 100.0%; Score 25; DB 4; Length 1078;
Best Local Similarity 80.0%; Pred. No. 6.5e-06;
Matches 20; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 GACUGUCCACAGCAUUCGCGACC 25
Db 662 GACTGTCCACAGCATTCGCTGACC 686

RESULT 4
US-08-363-233B-6
; Sequence 6, Application US/08363233B
; Patent No. 5714383
; GENERAL INFORMATION:
; APPLICANT: Thompson, James D.
; TITLE OF INVENTION: METHOD AND REAGENT FOR TREATING CHRONIC
; TITLE OF INVENTION: MYELOGENOUS LEUKEMIA
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/363,233B
; FILING DATE: December 23, 1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION DATA: including application
; PRIOR APPLICATION DATA: described below:
; APPLICATION NUMBER: 07/882,822
; FILING DATE: May 14, 1992
; APPLICATION NUMBER: 08/193,922
; FILING DATE: February 7, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 209/165
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
```

INFORMATION FOR SEQ ID NO: 6:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 26 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 US-08-363-233B-6

Query Match  
 Best Local Similarity 96.0%; Score 24; DB 1; Length 26;  
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GACUGCCACAGCAUCCGCGAC 24  
 |||||  
 DB 3 GACUGCCACAGCAUCCGCGAC 26

RESULT 5  
 US-08-152-621-11  
 ; Sequence 11, Application US/08152621  
 ; Patent No. 5652222  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Calabretta, Bruno  
 ; APPLICANT: Gewirtz, Alan M.  
 ; TITLE OF INVENTION: Selective Inhibition of  
 ; TITLE OF INVENTION: Leukemic Cell Proliferation by bcr-abl  
 ; TITLE OF INVENTION: Antisense Oligonucleotides  
 ; NUMBER OF SEQUENCES: 34  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: SEIDEL, GONDA, LAVORGNA  
 ; ADDRESSEE: & MONACO, P.C.  
 ; STREET: 1800 Two Penn Center  
 ; CITY: Philadelphia  
 ; STATE: Pennsylvania  
 ; COUNTRY: U.S.A.  
 ; ZIP: 19102

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb  
 COMPUTER: IBM PS/2  
 OPERATING SYSTEM: MS-DOS  
 SOFTWARE: WordPerfect 5.1  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/152,621  
 FILING DATE: NO. 5652222ember 15, 1993  
 CLASSIFICATION: 514  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 07/718,302  
 FILING DATE: June 18, 1991  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Monaco, Daniel A.  
 REGISTRATION NUMBER: 30,480  
 REFERENCE/DOCKET NUMBER: 6056-120 (CT.) 1  
 TELEPHONE: (215) 568-8383  
 TELEFAX: (215) 568-5549  
 TELEX: No. 5652222e  
 INFORMATION FOR SEQ ID NO: 11:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 22 Nucleotides  
 TYPE: nucleic acid  
 STRANDEDNESS: double stranded  
 TOPOLOGY: linear  
 US-08-152-621-11

Query Match  
 Best Local Similarity 72.0%; Score 18; DB 1; Length 22;  
 Matches 15; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 8 CACAGCAUCCGCGAC 25  
 |||||  
 DB 1 CACAGCAUCCGCGAC 18

RESULT 6  
 PCT-US92-05035-11  
 ; Sequence 11, Application PC/TUS9205035  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Calabretta, Bruno  
 ; APPLICANT: Gewirtz, Alan M.  
 ; TITLE OF INVENTION: Selective Inhibition of  
 ; TITLE OF INVENTION: Leukemic Cell Proliferation by bcr-abl  
 ; TITLE OF INVENTION: Antisense Oligonucleotides  
 ; NUMBER OF SEQUENCES: 34  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Temple University - Of The Common-  
 ; ADDRESSEE: wealth System of Higher Education  
 ; STREET: 406 University Services Building  
 ; CITY: Philadelphia  
 ; STATE: Pennsylvania  
 ; COUNTRY: U.S.A.  
 ; ZIP: 19122

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb  
 COMPUTER: IBM PS/2  
 OPERATING SYSTEM: MS-DOS  
 SOFTWARE: WordPerfect 5.1  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: PCT/US92/05035  
 FILING DATE: 19920615  
 CLASSIFICATION: 514  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 07/718,302  
 FILING DATE: June 18, 1991  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 07/869,911  
 FILING DATE: April 14, 1991  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Monaco, Daniel A.  
 REGISTRATION NUMBER: 30,480  
 REFERENCE/DOCKET NUMBER: 6056-120 (CIP) 1  
 TELEPHONE: (215) 568-8383  
 TELEFAX: (215) 568-5549  
 TELEX: None  
 INFORMATION FOR SEQ ID NO: 11:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 22 Nucleotides  
 TYPE: NUCLEIC ACID  
 STRANDEDNESS: double stranded  
 TOPOLOGY: linear  
 PCT-US92-05035-11

Query Match  
 Best Local Similarity 72.0%; Score 18; DB 5; Length 22;  
 Matches 15; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 8 CACAGCAUCCGCGAC 25  
 |||||  
 DB 1 CACAGCAUCCGCGAC 18

RESULT 7  
 US-08-448-446B-1  
 ; Sequence 1, Application US/08448446B  
 ; Patent No. 6080851  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Pachuk et al.  
 ; TITLE OF INVENTION: Compounds and Methods for the Treatment  
 ; TITLE OF INVENTION: of Leukemias  
 ; NUMBER OF SEQUENCES: 23  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Woodcock Washburn  
 ; ADDRESSEE: Kurtz Mackiewicz & No. 6080851iris  
 ; STREET: One Liberty Place - 46th Floor  
 ; CITY: Philadelphia  
 ; STATE: PA

;/ COUNTRY: USA  
;/ ZIP: 19103  
;/ COMPUTER READABLE FORM:  
;/ MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE  
;/ COMPUTER: IBM PS/2  
;/ OPERATING SYSTEM: PC-DOS  
;/ SOFTWARE: WORDPERFECT 5.1  
;/ CURRENT APPLICATION DATA:  
;/ APPLICATION NUMBER: US/08/448,446B  
;/ FILING DATE: July 10, 1995  
;/ CLASSIFICATION: 435  
;/ PRIOR APPLICATION DATA:  
;/ APPLICATION NUMBER: 07/989,852  
;/ FILING DATE: December 4, 1992  
;/ ATTORNEY/AGENT INFORMATION:  
;/ NAME: Doreen Yanko Trujillo  
;/ REGISTRATION NUMBER: 35,719  
;/ REFERENCE/DOCKET NUMBER: APOL-0020  
;/ TELECOMMUNICATION INFORMATION: C  
;/ TELEPHONE: (215) 568-3100  
;/ TELEFAX: (215) 568-3439  
;/ INFORMATION FOR SEQ ID NO: 1:  
;/ SEQUENCE CHARACTERISTICS:  
;/ LENGTH: 62  
;/ TYPE: Nucleic Acid  
;/ STRANDEDNESS: Single  
;/ TOPOLOGY: Linear  
;/ ANTI-SENSE: No  
;/ US-08-448-446B-1

Query Match 72.0%; Score 18; DB 3; Length 62;  
Best Local Similarity 100.0%; Pred. No. 0.082;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CACAGCAUCCGUGACC 25  
Db 1 CACAGCAUCCGUGACC 18

RESULT 8  
US-08-448-446B-2/c  
; Sequence 2, Application US/08448446B  
; Patent No. 6080851  
; GENERAL INFORMATION:  
; APPLICANT: Pachuk et al.  
; TITLE OF INVENTION: Compounds and Methods for the Treatment  
; OF LEUKEMIA  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Woodcock Washburn  
; ADDRESSEE: Kurtz Mackiewicz & No. 6080851ris  
; STREET: One Liberty Place - 46th Floor  
; CITY: Philadelphia  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19103  
;/ COMPUTER READABLE FORM:  
;/ MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE  
;/ COMPUTER: IBM PS/2  
;/ OPERATING SYSTEM: PC-DOS  
;/ SOFTWARE: WORDPERFECT 5.1  
;/ CURRENT APPLICATION DATA:  
;/ APPLICATION NUMBER: US/08/448,446B  
;/ FILING DATE: July 10, 1995  
;/ CLASSIFICATION: 435  
;/ PRIOR APPLICATION DATA:  
;/ APPLICATION NUMBER: 07/989,852  
;/ FILING DATE: December 4, 1992  
;/ ATTORNEY/AGENT INFORMATION:  
;/ NAME: Doreen Yanko Trujillo  
;/ REGISTRATION NUMBER: 35,719  
;/ REFERENCE/DOCKET NUMBER: APOL-0020  
;/ TELECOMMUNICATION INFORMATION: C

;/ TELEPHONE: (215) 568-3100  
;/ TELEFAX: (215) 568-3439  
;/ INFORMATION FOR SEQ ID NO: 2:  
;/ SEQUENCE CHARACTERISTICS:  
;/ LENGTH: 81  
;/ TYPE: Nucleic Acid  
;/ STRANDEDNESS: Single  
;/ TOPOLOGY: Linear  
;/ ANTI-SENSE:  
;/ US-08-448-446B-2  
;/ Query Match 72.0%; Score 18; DB 3; Length 81;  
;/ Best Local Similarity 83.3%; Pred. No. 0.082;  
;/ Matches 15; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 8 CACAGCAUCCGUGACC 25  
Db 81 CACAGCAUCCGUGACC 64

RESULT 9  
US-08-152-621-1  
; Sequence 1, Application US/08152621  
; Patent No. 5652222  
; GENERAL INFORMATION:  
; APPLICANT: Calabretta, Bruno  
; APPLICANT: Gewirtz, Alan M.  
; TITLE OF INVENTION: Selective Inhibition of  
; OF LEUKEMIA CELL PROLIFERATION BY bcr-abl  
; TITLE OF INVENTION: Antisense Oligonucleotides  
; NUMBER OF SEQUENCES: 34  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SEIDEL CONDA, LAVORCNA  
; ADDRESSEE: & MONACO, P.C.  
; STREET: 1800 Two Penn Center  
; CITY: Philadelphia  
; STATE: Pennsylvania  
; COUNTRY: U.S.A.  
; ZIP: 19102  
;/ COMPUTER READABLE FORM:  
;/ MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb  
;/ COMPUTER: IBM PS/2  
;/ OPERATING SYSTEM: MS-DOS  
;/ SOFTWARE: WordPerfect 5.1  
;/ CURRENT APPLICATION DATA:  
;/ APPLICATION NUMBER: US/08/152,621  
;/ FILING DATE: No. 5652222ember 15, 1993  
;/ CLASSIFICATION: 514  
;/ PRIOR APPLICATION DATA:  
;/ APPLICATION NUMBER: 07/718,302  
;/ FILING DATE: June 18, 1991  
;/ ATTORNEY/AGENT INFORMATION:  
;/ NAME: Monaco, Daniel A.  
;/ REGISTRATION NUMBER: 30,480  
;/ REFERENCE/DOCKET NUMBER: 6056-120 (CT.) 1  
;/ TELECOMMUNICATION INFORMATION:  
;/ TELEPHONE: (215) 568-8383  
;/ TELEFAX: (215) 568-5549  
;/ TELEX: No. 5652222e  
;/ INFORMATION FOR SEQ ID NO: 1:  
;/ SEQUENCE CHARACTERISTICS:  
;/ LENGTH: 257 Nucleotides  
;/ TYPE: nucleic acid  
;/ STRANDEDNESS: single stranded  
;/ TOPOLOGY: linear  
;/ US-08-152-621-1

Query Match 72.0%; Score 18; DB 1; Length 257;  
Best Local Similarity 83.3%; Pred. No. 0.082;  
Matches 15; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 8 CACAGCAUCCGUGACC 25  
Db 81 CACAGCAUCCGUGACC 64

Db 1 CACAGCATTCGCTGACC 18

## RESULT 10

US-08-306-691B-36  
; Sequence 36, Application US/08306691B  
; Patent No. 5734039

; GENERAL INFORMATION:  
; APPLICANT: Calabretta, Bruno

; APPLICANT: Skorski, Tomasz  
; TITLE OF INVENTION: ANTISENSE

; TITLE OF INVENTION: OLIGONUCLEOTIDES TARGETING COOPERATING ONCOGENES  
; NUMBER OF SEQUENCES: 55

; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Seidel, Gonda, Lavoragna & Monaco, P.C.

; STREET: Two Penn Center, Suite 1800  
; CITY: Philadelphia

; STATE: Pennsylvania  
; COUNTRY: U.S.A.

; ZIP: 19102

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb

; COMPUTER: IBM PS/2  
; OPERATING SYSTEM: MS-DOS

; SOFTWARE: WordPerfect 5.1  
; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/306,691B  
; FILING DATE: September 15, 1994

; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:  
; FILING DATE:

; ATTORNEY/AGENT INFORMATION:  
; NAME: Monaco, Daniel A.

; REGISTRATION NUMBER: 30,480  
; REFERENCE/DOCKET NUMBER: 8321-8

; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (215) 568-8383

; TELEFAX: (215) 568-5549  
; TELEX: No. 5734039e

; INFORMATION FOR SEQ ID NO: 36:  
; SEQUENCE CHARACTERISTICS:

; LENGTH: 257 base pairs  
; TYPE: nucleic acid

; STRANDEDNESS: single  
; TOPOLOGY: linear

US-08-306-691B-36

Query Match 72.0%; Score 18; DB 1; Length 257;  
Best Local Similarity 83.3%; Pred. No. 0.082;

Matches 15; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 8 CACAGCAUUCGCGUACC 25

Db 1 CACAGCATTCGCTGACC 18

## RESULT 11

PCT-US92-05035-1

; Sequence 1, Application PC/TUS9205035  
; GENERAL INFORMATION:

; APPLICANT: Calabretta, Bruno  
; APPLICANT: Gewirtz, Alan M.

; TITLE OF INVENTION: Selective Inhibition of  
; TITLE OF INVENTION: Leukemic Cell Proliferation by bcr-abl

; TITLE OF INVENTION: Antisense Oligonucleotides  
; NUMBER OF SEQUENCES: 34

; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Temple University - Of The Common-

; ADDRESS: Wealth System of Higher Education  
; STREET: 406 University Services Building

; CITY: Philadelphia  
; STATE: Pennsylvania

; COUNTRY: U.S.A.

; ZIP: 19122

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb  
; COMPUTER: IBM PS/2

; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: WordPerfect 5.1

; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US92/05035

; FILING DATE: 19920615  
; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/718,302

; FILING DATE: June 18, 1991  
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/869,911  
; FILING DATE: April 14, 1991

; ATTORNEY/AGENT INFORMATION:  
; NAME: Monaco, Daniel A.

; REGISTRATION NUMBER: 30,480  
; REFERENCE/DOCKET NUMBER: 6056-120 (CIP) 1

; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (215) 568-8383

; TELEFAX: (215) 568-5549  
; TELEX: None

; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:

; LENGTH: 257 Nucleotides  
; TYPE: NUCLEIC ACID

; STRANDEDNESS: single stranded  
; TOPOLOGY: linear

PCT-US92-05035-1

Query Match 72.0%; Score 18; DB 5; Length 257;  
Best Local Similarity 83.3%; Pred. No. 0.082;

Matches 15; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 8 CACAGCAUUCGCGUACC 25

Db 1 CACAGCATTCGCTGACC 18

## RESULT 12

US-09-341-955-2/c

; Sequence 2, Application US/09341955  
; Patent No. 6251690

; GENERAL INFORMATION:  
; APPLICANT: Kulmala, Sakari

; APPLICANT: Ala-Kleme, Timo  
; APPLICANT: Eskola, Jarkko

; APPLICANT: Korpela, Timo  
; TITLE OF INVENTION: ELECTRICAL EXCITATION OF LABEL SUBSTANCES AT COATED

; TITLE OF INVENTION: ELECTRODES  
; FILE REFERENCE: TUR-080

; CURRENT APPLICATION NUMBER: US/09/341,955  
; CURRENT FILING DATE: 1999-07-21

; EARLIER APPLICATION NUMBER: PCT/FI98/00114  
; EARLIER FILING DATE: 1999-02-10

; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 2  
; LENGTH: 28

; TYPE: DNA  
; ORGANISM: Artificial Sequence

; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:

; OTHER INFORMATION: oligonucleotide containing an amino group  
US-09-341-955-2

Query Match

Best Local Similarity 64.0%; Score 16; DB 3; Length 28;  
Matches 13; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 10 CAGCAUUCGCGUACC 25  
||||:|||||  
Db 28 CAGCATTCCGCTGACC 13

## RESULT 13

US-09-779-881-2/c  
; Sequence 2, Application US/09779881  
; Patent No. 6645776  
; GENERAL INFORMATION:  
; APPLICANT: Kulmala, Sakari  
; APPLICANT: Ala-Kleme, Timo  
; APPLICANT: Eskola, Jarkko  
; APPLICANT: Korpela, Timo  
; TITLE OF INVENTION: ELECTRICAL EXCITATION OF LABEL SUBSTANCES AT COATED  
; TITLE OF INVENTION: ELECTRODES  
; FILE REFERENCE: TUR-080  
; CURRENT APPLICATION NUMBER: US/09/779,881  
; CURRENT FILING DATE: 2001-02-09  
; PRIOR APPLICATION NUMBER: 09/341,955  
; PRIOR FILING DATE: 1999-07-21  
; PRIOR APPLICATION NUMBER: PCT/FI98/00114  
; PRIOR FILING DATE: 1999-02-10  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 28  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:  
; OTHER INFORMATION: oligonucleotide containing an amino group  
US-09-779-881-2

Query Match 64.0%; Score 16; DB 4; Length 28;  
Best Local Similarity 81.2%; Pred. No. 1.2;  
Matches 13; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 10 CAGCAUUCGCGUACC 25  
||||:|||||  
Db 28 CAGCATTCCGCTGACC 13

## RESULT 14

US-09-489-039A-2414  
; Sequence 2414, Application US/09489039A  
; Patent No. 6610836  
; GENERAL INFORMATION:  
; APPLICANT: Gary Breton et. al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA  
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 2709.2004001  
; CURRENT APPLICATION NUMBER: US/09/489,039A  
; CURRENT FILING DATE: 2000-01-27  
; PRIOR APPLICATION NUMBER: US 60/117,747  
; PRIOR FILING DATE: 1999-01-29  
; NUMBER OF SEQ ID NOS: 14342  
; SEQ ID NO 2414  
; LENGTH: 864  
; TYPE: DNA  
; ORGANISM: Klebsiella pneumoniae  
US-09-489-039A-2414

Query Match 64.0%; Score 16; DB 4; Length 864;  
Best Local Similarity 81.2%; Pred. No. 1.2;  
Matches 13; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 8 CACAGCAUUCGCGUGA 23  
||||:|||||  
Db 679 CACAGCATTCCGCTGA 694

## RESULT 15

US-08-448-446B-19/c  
; Sequence 19, Application US/08448446B  
; Patent No. 6080851  
; GENERAL INFORMATION:  
; APPLICANT: Pachuk et al.  
; TITLE OF INVENTION: Compounds and Methods for the Treatment  
; TITLE OF INVENTION: of Leukemias  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSES: Woodcock Washburn  
; ADDRESSES: Kurtz Mackiewicz & No. 6080851iris  
; STREET: One Liberty Place - 46th Floor  
; CITY: Philadelphia  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19103  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE  
; COMPUTER: IBM PS/2  
; OPERATING SYSTEM: PC-DOS  
; SOFTWARE: WORDPERFECT 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/448,446B  
; FILING DATE: July 10, 1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/989,852  
; FILING DATE: December 4, 1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Doreen Yanko Trujillo  
; REGISTRATION NUMBER: 35,719  
; REFERENCE/DOCKET NUMBER: APOL-0020  
; TELECOMMUNICATION INFORMATION: C  
; TELEPHONE: (215) 568-3100  
; TELEFAX: (215) 568-3439  
; INFORMATION FOR SEQ ID NO: 19:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 61  
; TYPE: Nucleic Acid  
; STRANDEDNESS: Single  
; TOPOLOGY: Linear  
; ANTI-SENSE:  
US-08-448-446B-19

Query Match 56.0%; Score 14; DB 3; Length 61;  
Best Local Similarity 78.6%; Pred. No. 18;  
Matches 11; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 12 GCAUUCGCGUACC 25  
||||:|||||  
Db 61 GCATTCCGCTGACC 48

Search completed: May 27, 2004, 02:25:11  
Job time : 21.0702 secs



GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: May 27, 2004, 11:30:47 ; Search time 131.564 Seconds  
(without alignments)  
864.392 Million cell updates/sec

Title: US-09-121-239-10

Perfect score: 25

Sequence: 1 GACUCCACAGCAUCCGUGACC 25

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 2960401 seqs, 2274450654 residues

Word size : 0

Total number of hits satisfying chosen parameters: 5920802

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published Applications NA.\*

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4: /cgn2\_6/ptodata/2/pubpna/US06\_PUBCOMB.seq.\*  
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13: /cgn2\_6/ptodata/2/pubpna/US10A\_PUBCOMB.seq.\*  
14: /cgn2\_6/ptodata/2/pubpna/US10B\_PUBCOMB.seq.\*  
15: /cgn2\_6/ptodata/2/pubpna/US10C\_PUBCOMB.seq.\*  
16: /cgn2\_6/ptodata/2/pubpna/US10C\_PUBCOMB.seq.\*  
17: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq.\*  
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19: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	25	100.0	504	10	US-09-918-995-25454
2	25	100.0	542	9	US-09-796-692-8117
3	25	100.0	542	15	US-10-040-862-8117
4	25	100.0	542	16	US-10-057-475B-8117
5	25	100.0	542	16	US-10-154-884B-8117
6	25	100.0	596	9	US-09-796-692-8967
7	25	100.0	596	15	US-10-040-862-8967
8	25	100.0	596	16	US-10-057-475B-8967
9	25	100.0	596	16	US-10-154-884B-8967
10	25	100.0	1078	15	US-10-228-811-1
11	25	100.0	4739	9	US-09-954-531-586
12	25	100.0	4739	13	US-10-193-651-22
13	17	68.0	3664	15	US-10-128-714-206
14	17	68.0	3750	15	US-10-128-714-5206

c 15 64.0 28 9 US-09-779-881-2  
c 16 64.0 285 11 US-09-864-408A-4649  
c 17 60.0 383 9 US-09-960-352-9070  
c 18 60.0 483 9 US-09-974-300-8116  
c 19 60.0 501 9 US-09-974-300-8143  
c 20 60.0 765 16 US-10-369-493-39879  
c 21 60.0 804 16 US-10-369-493-39128  
c 22 60.0 804 16 US-10-369-493-39497  
c 23 60.0 828 16 US-10-388-934-133  
c 24 60.0 837 13 US-10-282-122A-25393  
c 25 60.0 933 9 US-09-974-300-2109  
c 26 60.0 3076 15 US-10-128-714-495  
c 27 60.0 3076 15 US-10-128-714-5495  
c 28 60.0 203264 13 US-10-087-192-988  
c 29 56.0 16 9 US-09-068-817-9  
c 30 56.0 21 10 US-09-864-636A-1953  
c 31 56.0 21 11 US-09-864-426A-1953  
c 32 56.0 21 15 US-10-084-839-1953  
c 33 56.0 28 9 US-09-747-165-7  
c 34 56.0 80 12 US-10-384-245-179  
c 35 56.0 134 15 US-10-029-386-26303  
c 36 56.0 268 13 US-10-052-283-149  
c 37 56.0 335 9 US-09-815-343-156  
c 38 56.0 335 13 US-10-097-105-156  
c 39 56.0 430 10 US-09-918-995-2118  
c 40 56.0 460 9 US-09-969-347-68  
c 41 56.0 461 10 US-09-918-995-14682  
c 42 56.0 462 10 US-09-918-995-9876  
c 43 56.0 474 15 US-10-369-493-38733  
c 44 56.0 493 13 US-10-052-283-38  
c 45 56.0 501 15 US-10-060-036-3547

#### ALIGNMENTS

#### RESULT 1

US-09-918-995-25454  
; Sequence 25454, Application US/09918995  
; Publication No. US20030073623A1  
; GENERAL INFORMATION:  
; APPLICANT: Hyseq, Inc.  
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED  
; FILE REFERENCE: 20411-756  
; CURRENT APPLICATION NUMBER: US/09/918,995  
; CURRENT FILING DATE: 2001-07-30  
; PRIOR APPLICATION NUMBER: US/09/235,076  
; PRIOR FILING DATE: 1999-01-20  
; NUMBER OF SEQ ID NOS: 38054  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 25454  
; LENGTH: 504  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1)..(504)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-918-995-25454

Query Match 100.0%; Score 25; DB 10; Length 504;  
Best Local Similarity 80.0%; Pred. No. 2.6e-05;  
Matches 20; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GACUCCACAGCAUCCGUGACC 25  
|||:|||||:|||||:|||||  
Db 239 GACTGCCACGATTCGCTGACC 263

#### RESULT 2

US-09-796-692-8117  
; Sequence 8117, Application US/09796692

```

; Publication No. US20020198362A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY
; TITLE OF INVENTION: HEMATOLOGICAL MALIGNANCIES
; FILE REFERENCE: 2077,001200
; CURRENT APPLICATION NUMBER: US/09/796,692
; CURRENT FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/222,903
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 60/223,416
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: 60/223,378
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: 60/223,416
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: 60/223,378
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: 60/223,378
; PRIOR FILING DATE: 2001-03-01
; NUMBER OF SEQ ID NOS: 10467
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8117
; LENGTH: 542
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-796-692-8117

Query Match 100.0%; Score 25; DB 9; Length 542;
Best Local Similarity 80.0%; Pred. No. 2.6e-05;
Matches 20; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 GACGUCCACAGCAUUCGCGACC 25
Db 433 GACTGTCCACAGCATTCGCTGACC 457

RESULT 3
US-10-040-862-8117
; Sequence 8117, Application US/10040862
; Publication No. US20030078396A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; TITLE OF INVENTION: Hematological Malignancies
; FILE REFERENCE: 014058-013520US
; CURRENT APPLICATION NUMBER: US/10/040,862
; CURRENT FILING DATE: 2001-11-06
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 60/223,416
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: 60/223,378
; PRIOR FILING DATE: 2000-08-07
; NUMBER OF SEQ ID NOS: 9597
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8117
; LENGTH: 542
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-796-692-8117

Query Match 100.0%; Score 25; DB 9; Length 542;
Best Local Similarity 80.0%; Pred. No. 2.6e-05;
Matches 20; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 GACGUCCACAGCAUUCGCGACC 25
Db 433 GACTGTCCACAGCATTCGCTGACC 457

RESULT 4
US-10-057-475B-8117
; Sequence 8117, Application US/10057475B
; Publication No. US20040002068A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Clapper, Jonathan David
; APPLICANT: Wang, Aijun
; APPLICANT: Ordonez, Nadia
; APPLICANT: Carter, Lauren
; APPLICANT: McNeill, Patricia Dianne
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; TITLE OF INVENTION: Hematological Malignancies
; FILE REFERENCE: 014058-014402US
; CURRENT APPLICATION NUMBER: US/10/057,475B
; CURRENT FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/222,903
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 60/223,416
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: 60/223,378
; PRIOR FILING DATE: 2001-03-01
; NUMBER OF SEQ ID NOS: 10467
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8117
; LENGTH: 542
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-040-862-8117

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; PRIOR APPLICATION NUMBER: US 60/222,903  
 ; PRIOR FILING DATE: 2000-08-03  
 ; Remaining Prior Application data removed - See File Wrapper or PALM.  
 ; NUMBER OF SEQ ID NOS: 10979  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 8117  
 ; LENGTH: 542  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-10-057-475B-8117

Query Match 100.0%; Score 25; DB 16; Length 542;  
 Best Local Similarity 80.0%; Pred. No. 2.6e-05;  
 Matches 20; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 GACUGUCCACAGCAUCCGUGACC 25  
 |||:|||||:|||||:|||||:|||||:  
 Db 433 GACTGTCCACAGCATTCGCTGACC 457

RESULT 5

US-10-154-884B-8117  
 ; Sequence 8117, Application US/10154884B  
 ; Publication No. US20040005561A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Gaiger, Alexander  
 ; APPLICANT: Algate, Paul A.  
 ; APPLICANT: Mannion, Jane  
 ; APPLICANT: Retter, Marc W.  
 ; APPLICANT: Corixa Corporation  
 ; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy  
 ; TITLE OF INVENTION: Hematological Malignancies  
 ; FILE REFERENCE: 014058-013521US  
 ; CURRENT APPLICATION NUMBER: US/10/154,884B  
 ; CURRENT FILING DATE: 2002-05-23  
 ; PRIOR APPLICATION NUMBER: US 60/186,126  
 ; PRIOR FILING DATE: 2000-03-01  
 ; PRIOR APPLICATION NUMBER: US 60/190,479  
 ; PRIOR FILING DATE: 2000-03-17  
 ; PRIOR APPLICATION NUMBER: US 60/200,545  
 ; PRIOR FILING DATE: 2000-04-27  
 ; PRIOR APPLICATION NUMBER: US 60/200,303  
 ; PRIOR FILING DATE: 2000-04-28  
 ; PRIOR APPLICATION NUMBER: US 60/200,779  
 ; PRIOR FILING DATE: 2000-04-28  
 ; PRIOR APPLICATION NUMBER: US 60/200,999  
 ; PRIOR FILING DATE: 2000-05-01  
 ; PRIOR APPLICATION NUMBER: US 60/202,084  
 ; PRIOR FILING DATE: 2000-05-04  
 ; PRIOR APPLICATION NUMBER: US 60/206,201  
 ; PRIOR FILING DATE: 2000-05-01  
 ; PRIOR APPLICATION NUMBER: US 60/202,084  
 ; PRIOR FILING DATE: 2000-05-04  
 ; PRIOR APPLICATION NUMBER: US 60/218,950  
 ; PRIOR FILING DATE: 2000-07-14  
 ; PRIOR APPLICATION NUMBER: US 60/222,903  
 ; PRIOR FILING DATE: 2000-08-03  
 ; PRIOR APPLICATION NUMBER: US 60/223,416  
 ; PRIOR FILING DATE: 2000-08-04  
 ; PRIOR APPLICATION NUMBER: 60/223,378  
 ; PRIOR FILING DATE: 2000-08-07  
 ; NUMBER OF SEQ ID NOS: 11290  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 8117  
 ; LENGTH: 542  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-10-154-884B-8117

Query Match 100.0%; Score 25; DB 16; Length 542;  
 Best Local Similarity 80.0%; Pred. No. 2.6e-05;  
 Matches 20; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 GACUGUCCACAGCAUCCGUGACC 25  
 |||:|||||:|||||:|||||:|||||:  
 Db 433 GACTGTCCACAGCATTCGCTGACC 457

RESULT 6  
 US-09-796-692-8967  
 ; Sequence 8967, Application US/09796692  
 ; Publication No. US20020198362A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Gaiger, Alexander  
 ; APPLICANT: Algate, Paul A.  
 ; APPLICANT: Mannion, Jane  
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY  
 ; TITLE OF INVENTION: HEMATOLOGICAL MALIGNANCIES  
 ; FILE REFERENCE: 2077.001200  
 ; CURRENT APPLICATION NUMBER: US/09/796,692  
 ; CURRENT FILING DATE: 2001-03-01  
 ; PRIOR APPLICATION NUMBER: 60/186,126  
 ; PRIOR FILING DATE: 2000-03-01  
 ; PRIOR APPLICATION NUMBER: 60/190,479  
 ; PRIOR FILING DATE: 2000-03-17  
 ; PRIOR APPLICATION NUMBER: 60/200,545  
 ; PRIOR FILING DATE: 2000-04-27  
 ; PRIOR APPLICATION NUMBER: 60/200,303  
 ; PRIOR FILING DATE: 2000-04-28  
 ; PRIOR APPLICATION NUMBER: 60/200,779  
 ; PRIOR FILING DATE: 2000-04-28  
 ; PRIOR APPLICATION NUMBER: 60/200,999  
 ; PRIOR FILING DATE: 2000-05-01  
 ; PRIOR APPLICATION NUMBER: 60/202,084  
 ; PRIOR FILING DATE: 2000-05-04  
 ; PRIOR APPLICATION NUMBER: 60/206,201  
 ; PRIOR FILING DATE: 2000-05-22  
 ; PRIOR APPLICATION NUMBER: 60/218,950  
 ; PRIOR FILING DATE: 2000-07-14  
 ; PRIOR APPLICATION NUMBER: 60/222,903  
 ; PRIOR FILING DATE: 2000-08-03  
 ; PRIOR APPLICATION NUMBER: 60/223,416  
 ; PRIOR FILING DATE: 2000-08-04  
 ; PRIOR APPLICATION NUMBER: 60/223,378  
 ; PRIOR FILING DATE: 2000-08-07  
 ; NUMBER OF SEQ ID NOS: 9597  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 8967  
 ; LENGTH: 596  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: unsure  
 ; LOCATION: (13)  
 ; OTHER INFORMATION: n=A,T,C or G  
 ; NAME/KEY: unsure  
 ; LOCATION: (47)  
 ; OTHER INFORMATION: n=A,T,C or G  
 ; NAME/KEY: unsure  
 ; LOCATION: (49)  
 ; OTHER INFORMATION: n=A,T,C or G  
 ; NAME/KEY: unsure  
 ; LOCATION: (58)  
 ; OTHER INFORMATION: n=A,T,C or G  
 ; NAME/KEY: unsure  
 ; LOCATION: (63)  
 ; OTHER INFORMATION: n=A,T,C or G  
 ; NAME/KEY: unsure  
 ; LOCATION: (81)  
 ; OTHER INFORMATION: n=A,T,C or G  
 ; NAME/KEY: unsure  
 ; LOCATION: (155)  
 ; OTHER INFORMATION: n=A,T,C or G  
 ; NAME/KEY: unsure  
 ; LOCATION: (196)  
 ; OTHER INFORMATION: n=A,T,C or G  
 ; NAME/KEY: unsure  
 ; LOCATION: (211)  
 ; OTHER INFORMATION: n=A,T,C or G  
 ; NAME/KEY: unsure  
 ; LOCATION: (267)

```

OTHER INFORMATION: n=A,T,C or G
NAME/KEY: unsure
LOCATION: (281)
OTHER INFORMATION: n=A,T,C or G
NAME/KEY: unsure
LOCATION: (282)
OTHER INFORMATION: n=A,T,C or G
NAME/KEY: unsure
LOCATION: (332)
OTHER INFORMATION: n=A,T,C or G
NAME/KEY: unsure
LOCATION: (372)
OTHER INFORMATION: n=A,T,C or G
NAME/KEY: unsure
LOCATION: (520)
OTHER INFORMATION: n=A,T,C or G
NAME/KEY: unsure
LOCATION: (521)
OTHER INFORMATION: n=A,T,C or G
NAME/KEY: unsure
LOCATION: (551)
OTHER INFORMATION: n=A,T,C or G
NAME/KEY: unsure
LOCATION: (579)
OTHER INFORMATION: n=A,T,C or G
NAME/KEY: unsure
LOCATION: (585)
OTHER INFORMATION: n=A,T,C or G
NAME/KEY: unsure
LOCATION: (586)
OTHER INFORMATION: n=A,T,C or G
US-09-796-692-8967

```

Query Match 100.0%; Score 25; DB 9; Length 596;  
 Best Local Similarity 80.0%; Pred. No. 2.6e-05;  
 Matches 20; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 GACGUCCACAGCAUUCGCGUACC 25
Db 433 GACTGTCCACAGCATTCGCGTACC 457

```

```

RESULT 7
US-10-040-862-8967
Sequence 8967, Application US/10040862
Publication No. US20030078396A1
GENERAL INFORMATION:
APPLICANT: Gaiger, Alexander
APPLICANT: Algate, Paul A.
APPLICANT: Mannion, Jane
APPLICANT: Retter, Marc
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
FILE REFERENCE: 014058-013520US
CURRENT APPLICATION NUMBER: US/10/040,862
CURRENT FILING DATE: 2001-11-06
PRIOR APPLICATION NUMBER: US 60/186,126
PRIOR FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: US 60/190,479
PRIOR FILING DATE: 2000-03-17
PRIOR APPLICATION NUMBER: US 60/200,545
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: US 60/200,303
PRIOR FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: US 60/200,779
PRIOR FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: US 60/200,999
PRIOR FILING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: US 60/202,084
PRIOR FILING DATE: 2000-05-04
PRIOR APPLICATION NUMBER: US 60/206,201
PRIOR FILING DATE: 2000-05-22

```

```

PRIOR APPLICATION NUMBER: US 60/218,950
PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 60/222,903
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: US 60/223,416
PRIOR FILING DATE: 2000-08-04
PRIOR APPLICATION NUMBER: US 60/223,378
PRIOR FILING DATE: 2000-08-07
PRIOR APPLICATION NUMBER: US 09/796,692
PRIOR FILING DATE: 2001-03-01
NUMBER OF SEQ ID NOS: 10467
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 8967
LENGTH: 596
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: unsure
LOCATION: (13)
OTHER INFORMATION: n=A,T,C or G
FEATURE:
NAME/KEY: unsure
LOCATION: (47)
OTHER INFORMATION: n=A,T,C or G
FEATURE:
NAME/KEY: unsure
LOCATION: (49)
OTHER INFORMATION: n=A,T,C or G
FEATURE:
NAME/KEY: unsure
LOCATION: (58)
OTHER INFORMATION: n=A,T,C or G
FEATURE:
NAME/KEY: unsure
LOCATION: (63)
OTHER INFORMATION: n=A,T,C or G
FEATURE:
NAME/KEY: unsure
LOCATION: (81)
OTHER INFORMATION: n=A,T,C or G
FEATURE:
NAME/KEY: unsure
LOCATION: (155)
OTHER INFORMATION: n=A,T,C or G
FEATURE:
NAME/KEY: unsure
LOCATION: (196)
OTHER INFORMATION: n=A,T,C or G
FEATURE:
NAME/KEY: unsure
LOCATION: (211)
OTHER INFORMATION: n=A,T,C or G
FEATURE:
NAME/KEY: unsure
LOCATION: (267)
OTHER INFORMATION: n=A,T,C or G
FEATURE:
NAME/KEY: unsure
LOCATION: (281)
OTHER INFORMATION: n=A,T,C or G
FEATURE:
NAME/KEY: unsure
LOCATION: (282)
OTHER INFORMATION: n=A,T,C or G
FEATURE:
NAME/KEY: unsure
LOCATION: (332)
OTHER INFORMATION: n=A,T,C or G
FEATURE:
NAME/KEY: unsure
LOCATION: (372)
OTHER INFORMATION: n=A,T,C or G
FEATURE:

```

```

; NAME/KEY: unsure
; LOCATION: (520)
; OTHER INFORMATION: n=A,T,C or G
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (521)
; OTHER INFORMATION: n=A,T,C or G
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (551)
; OTHER INFORMATION: n=A,T,C or G
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (579)
; OTHER INFORMATION: n=A,T,C or G
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (585)
; OTHER INFORMATION: n=A,T,C or G
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (586)
; OTHER INFORMATION: n=A,T,C or G
US-10-040-862-8967

```

```

Query Match      100.0%; Score 25; DB 15; Length 596;
Best Local Similarity 80.0%; Pred. No. 2.6e-05;
Matches 20; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 GACUGCCACAGCAUUCGCGUACC 25
      |||:|||||:|||||:|||||:|||||
DB      433 GACTGTCCACAGCATTCGCGTACC 457

```

# RESULT 8

```

; Sequence 8967, Application US/10057475B
; Publication No. US20040002068A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Mannion, Jane
; APPLICANT: Clapper, Jonathan David
; APPLICANT: Wang, Aijun
; APPLICANT: Ordonez, Nadia
; APPLICANT: Carter, Lauren
; APPLICANT: McNeill, Patricia Dianne
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; FILE REFERENCE: 014058-014402US
; CURRENT APPLICATION NUMBER: US/10/057,475B
; PRIOR FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 11290
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8967
; LENGTH: 596
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(596)
; OTHER INFORMATION: n = g, a, c or t
US-10-040-862-8967

```

```

Query Match      100.0%; Score 25; DB 15; Length 596;
Best Local Similarity 80.0%; Pred. No. 2.6e-05;
Matches 20; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

```

```

; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 10979
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8967
; LENGTH: 596
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(596)
; OTHER INFORMATION: n = g, a, c or t
US-10-057-475B-8967

```

```

Query Match      100.0%; Score 25; DB 16; Length 596;
Best Local Similarity 80.0%; Pred. No. 2.6e-05;
Matches 20; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 GACUGCCACAGCAUUCGCGUACC 25
      |||:|||||:|||||:|||||:|||||
DB      433 GACTGTCCACAGCATTCGCGTACC 457

```

# RESULT 9

```

; Sequence 8967, Application US/10154884B
; Publication No. US20040005561A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc W.
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; FILE REFERENCE: 014058-013521US
; CURRENT APPLICATION NUMBER: US/10/154,884B
; CURRENT FILING DATE: 2002-05-23
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 11290
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8967
; LENGTH: 596
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(596)
; OTHER INFORMATION: n = g, a, c or t
US-10-154-884B-8967

```

```

Query Match      100.0%; Score 25; DB 16; Length 596;
Best Local Similarity 80.0%; Pred. No. 2.6e-05;
Matches 20; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

```

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; PRIOR APPLICATION NUMBER: US/60/234,567
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 1392
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 586
; LENGTH: 4739
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-954-531-586

Query Match          100.0%; Score 25; DB 9; Length 4739;
Best Local Similarity 80.0%; Pred.No.2e-05;
Matches 20; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY      1      GACUGUCCACAGCAUUCGCGUACC 25
        |||:|:|||||:|||||:|||||:|||||
Db       3158  GACTGTCCACAGCATTCGCTGACC 3182

RESULT 12
US-10-193-651-22
; Sequence 22, Application US/10193651
; Publication No. US20030064061A1
; GENERAL INFORMATION:
; APPLICANT: Zhao, Xun
; APPLICANT: Ghaffari, Saghi
; APPLICANT: Lodish, Harvey F.
; APPLICANT: Malashkevich, Vladimir N.
; APPLICANT: Kim, Peter S.
; TITLE OF INVENTION: Bcr-Abl Oligomerization Domain
; TITLE OF INVENTION: Polypeptides and Uses Therefor
; FILE REFERENCE: 0399.2031-001
; CURRENT APPLICATION NUMBER: US/10/193,651
; CURRENT FILING DATE: 2002-11-19
; PRIOR APPLICATION NUMBER: US 60/303,857
; PRIOR FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 4739
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; OTHER INFORMATION: Bcr nucleic acid
US-10-193-651-22

Query Match          100.0%; Score 25; DB 13; Length 4739;
Best Local Similarity 80.0%; Pred.No.2e-05;
Matches 20; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY      1      GACUGUCCACAGCAUUCGCGUACC 25
        |||:|:|||||:|||||:|||||:|||||
Db       3158  GACTGTCCACAGCATTCGCTGACC 3182

RESULT 13
US-10-128-714-206
; Sequence 206, Application US/10128714
; Publication No. US20030119013A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Bo
; APPLICANT: Hu, Wengli
; APPLICANT: Tishkoff, Daniel
; APPLICANT: Zamudio, Carlos
; APPLICANT: Broshkin, Alexey M
; APPLICANT: Lemieux, Sebastien M
; TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and
; TITLE OF INVENTION: Methods of Use
; FILE REFERENCE: 10182-018-999
; CURRENT APPLICATION NUMBER: US/10/128,714
; CURRENT FILING DATE: 2002-04-23
; PRIOR APPLICATION NUMBER: US 60/285,697
; PRIOR FILING DATE: 2001-04-23

```

```

; PRIOR APPLICATION NUMBER: US 60/287,066
; PRIOR FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: US 60/295,890
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/303,899
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: US 60/316,362
; PRIOR FILING DATE: 2001-08-31
; NUMBER OF SEQ ID NOS: 8603
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 206
; LENGTH: 3664
; TYPE: DNA
; ORGANISM: Aspergillus fumigatus
US-10-128-714-206

```

```

Query Match      68.0%; Score 17; DB 15; Length 3664;
Best Local Similarity 76.5%; Pred. No. 1.2;
Matches 13; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      5 GUCCACAGCAUUCGCU 21
Db      3547 GTCCACAGCATTCGCT 3563

```

```

RESULT 14
US-10-128-714-5206
; Sequence 5206, Application US/10128714
; Publication No. US20030119013A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Bo
; APPLICANT: Hu, Wengqi
; APPLICANT: Tishkoff, Daniel
; APPLICANT: Zamudio, Carlos
; APPLICANT: Eroshkin, Alexey M
; APPLICANT: Lemieux, Sebastien M
; TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and
; TITLE OF INVENTION: Methods of Use
; FILE REFERENCE: 10182-018-999
; CURRENT APPLICATION NUMBER: US/10/128,714
; CURRENT FILING DATE: 2002-04-23
; PRIOR APPLICATION NUMBER: US 60/285,697
; PRIOR FILING DATE: 2001-04-23
; PRIOR APPLICATION NUMBER: US 60/287,066
; PRIOR FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: US 60/295,890
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/303,899
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: US 60/316,362
; PRIOR FILING DATE: 2001-08-31
; NUMBER OF SEQ ID NOS: 8603
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5206
; LENGTH: 3750
; TYPE: DNA
; ORGANISM: Aspergillus fumigatus
US-10-128-714-5206

```

```

Query Match      68.0%; Score 17; DB 15; Length 3750;
Best Local Similarity 76.5%; Pred. No. 1.2;
Matches 13; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      5 GUCCACAGCAUUCGCU 21
Db      3636 GTCCACAGCATTCGCT 3652

```

```

RESULT 15
US-09-779-881-2/c
; Sequence 2, Application US/09779881
; Patent No. US20020081749A1
; GENERAL INFORMATION:

```

```

; APPLICANT: Kulmala, Sakari
; APPLICANT: Ala-Kieme, Timo
; APPLICANT: Eskola, Jarkko
; APPLICANT: Korpela, Timo
; TITLE OF INVENTION: ELECTRICAL EXCITATION OF LABEL SUBSTANCES AT COATED
; TITLE OF INVENTION: ELECTRODES
; FILE REFERENCE: TUR-080
; CURRENT APPLICATION NUMBER: US/09/779,881
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 09/341,955
; PRIOR FILING DATE: 1999-07-21
; PRIOR APPLICATION NUMBER: PCT/FI98/00114
; PRIOR FILING DATE: 1999-02-10
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 28
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: oligonucleotide containing an amino group
US-09-779-881-2

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Query Match      64.0%; Score 16; DB 9; Length 28;
Best Local Similarity 81.2%; Pred. No. 8.6;
Matches 13; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

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QY      10 CAGCAUCCGCGUACC 25
Db      28 CAGCATTCGCTGACC 13

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Search completed: May 27, 2004, 14:58:27
Job time : 131.564 secs

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        /organism="Homo sapiens"
        /mol_type="mRNA"
        /db_xref="taxon:9606"
        /clone="C22.652"
        /lab_host="E. coli DH5a"
        /notes="Vector: pBluescriptIIKS+; Site_1: Sal I; Site_2: Bam HI (destroyed); Exons were isolated from human chromosome 22 specific cosmids using a modification of the method of exon amplification (Proc. Natl. Acad. Sci. USA 88:4005-4009, 1991). Amplified exons were digested with Sal I and Bgl II and subsequently cloned into pBluescriptIIKS+ at the Sal I and Bam HI sites."

ORIGIN
  Query Match      100.0%; Score 25; DB 14; Length 181;
  Best Local Similarity 80.0%; Pred. No. 0.0033;
  Matches 20; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGUGCCACAGCAUUCGCGUACC 25
    |||:|||||:|||||:|||||:
Db 144 GACTGTCCACAGCATTCGCTGACC 168

RESULT 2
D79153
LOCUS HUM532H11B Human placenta polyA+ (TFujiwara) Homo sapiens cDNA
DEFINITION clone GEN=532H11 5', mRNA sequence.
ACCESSION D79153
VERSION D79153.1 GI:1181026
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 314)
AUTHORS Fujiwara, T., Hirano, H., Katagiri, T., Kawai, A., Kuga, Y., Nagata, M., Okuno, S., Ozaki, K., Shimizu, F., Shimada, Y., Shinomiya, H., Takachi, A., Takeda, S., Watanabe, T., Takahashi, E., Hirai, Y., Maekawa, H., Shin, S. and Nakamura, Y.
TITLE Fujiwara et al. (1995)
JOURNAL Unpublished (1995)
COMMENT Contact: Tsutomu Fujiwara
Otsuka GEN Research Institute
Otsuka Pharmaceutical Co., Ltd
463-10 Kagasuno Kawauchi-cho, Tokushima, Tokushima, 771-01 Japan
Tel: 0886-65-2888
Fax: 0886-37-1035.

FEATURES
  source
    Location/Qualifiers
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        /organism="Homo sapiens"
        /mol_type="mRNA"
        /db_xref="taxon:9606"
        /clone="GEN=532H11"
        /tissue_type="placenta"
        /clone_lib="Human placenta polyA+ (TFujiwara)"

ORIGIN
  Query Match      100.0%; Score 25; DB 14; Length 314;
  Best Local Similarity 80.0%; Pred. No. 0.0035;
  Matches 20; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGUGCCACAGCAUUCGCGUACC 25
    |||:|||||:|||||:|||||:
Db 53 GACTGTCCACAGCATTCGCTGACC 77

RESULT 3
BE168421/c
LOCUS BE168421 360 bp mRNA linear EST 21-JUN-2000

FEATURES
  source
    Location/Qualifiers
      1..360
        /organism="Homo sapiens"
        /mol_type="mRNA"
        /db_xref="taxon:9606"
        /dev_stage="Adult"
        /clone_lib="HT0513"
        /note="Organ: head neck; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN
  Query Match      100.0%; Score 25; DB 10; Length 360;
  Best Local Similarity 80.0%; Pred. No. 0.0035;
  Matches 20; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGUGCCACAGCAUUCGCGUACC 25
    |||:|||||:|||||:|||||:
Db 328 GACTGTCCACAGCATTCGCTGACC 304

RESULT 4
BF800308
LOCUS CM4-CI0062-181000-370-b10 CI0062 Homo sapiens cDNA, mRNA sequence.
DEFINITION BF800308
ACCESSION BF800308.1 GI:12129297
VERSION BF800308.1
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 377)
AUTHORS Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

FEATURES
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        /mol_type="mRNA"
        /db_xref="taxon:9606"
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        /clone_lib="HT0513"
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ORIGIN
  Query Match      100.0%; Score 25; DB 10; Length 360;
  Best Local Similarity 80.0%; Pred. No. 0.0035;
  Matches 20; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGUGCCACAGCAUUCGCGUACC 25
    |||:|||||:|||||:|||||:
Db 328 GACTGTCCACAGCATTCGCTGACC 304

RESULT 4
BF800308
LOCUS CM4-CI0062-181000-370-b10 CI0062 Homo sapiens cDNA, mRNA sequence.
DEFINITION BF800308
ACCESSION BF800308.1 GI:12129297
VERSION BF800308.1
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 377)
AUTHORS Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

```

Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.

Shotgun sequencing of the human transcriptome with ORF expressed

sequence tags

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

20202663

10737800

PUBMED

COMMENT

Contact: Simpson A.J.G.

Laboratory of Cancer Genetics

Ludwig Institute for Cancer Research

Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,

Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome

Project. This entry can be seen in the following URL

(<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CM4&t2=CM4-CI0062-181000-370-b10&t3=2000-10-18&t4=1>)

Seq primer: puc 18 forward

High quality sequence start: 18

High quality sequence stop: 377.

#### FEATURES

source

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/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/dev\_stage="Adult"

/clone\_lib="CI0062"

/note="Organ: colon; ins; Vector: puc18; Site 1: SmaI;

Site 2: SmaI; A mini-library was made by cloning products

derived from ORESTES PCR (U.S. Letters Patent application

No. 196,716 - Ludwig Institute for Cancer Research)

profiles into the puc 18 vector. Reverse transcription of

tissue mRNA and cDNA amplification were performed under

low stringency conditions."

#### ORIGIN

Query Match 100.0%; Score 25; DB 10; Length 377;

Best Local Similarity 80.0%; Pred. No. 0.0035; Indels 0; Gaps 0;

Matches 20; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 GACUGUCCACAGCAUUCGCGUACC 25

||||:|||||:|||||:|||||

Db 250 GACTGTCCACAGCATTCGCTGACC 274

#### RESULT 5

R54267

LOCUS

DEFINITION

YG74h05.r1 Soares infant brain IN1B Homo sapiens cDNA clone

IMAGE:9270 5. similar to gb:U01147 BREAKPOINT CLUSTER REGION

PROTEIN (HUMAN); mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished (1995)

Contact: Wilson RK

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

Insert Size: 1872

High quality sequence stops: 342 Source: IMAGE Consortium, LNL

This clone is available royalty-free through LNL; contact the

IMAGE Consortium ([info@image.lnl.gov](mailto:info@image.lnl.gov)) for further information.

Insert Length: 1872 Std Error: 0.00

Seq primer: M13RP1

High quality sequence stop: 342.

Location/Qualifiers

#### FEATURES

source

1..401

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="GDB:411811"

/db\_xref="taxon:9606"

/clone="IMAGE:39270"

/sex="female"

/dev\_stage="73 days post natal"

/lab\_host="DH10B (ampicillin resistant)"

/clone\_lib="Soares infant brain IN1B"

/note="Organ: whole brain; Vector: Lafmid BA; Site 1: Not

I; Site 2: Hind III; 1st strand cDNA was primed with a Not

I - oligo(dT) primer [5'

AACTGGAAGAATTCGGCCGACGAAATTTTTTTTTTTT 3'];

double-stranded cDNA was ligated to Hind III adaptors

(Pharmacia), digested with Not I and directionally cloned

into the Not I and Hind III sites of the Lafmid BA vector.

Library went through one round of normalization. Library

constructed by Bento Soares and M.Fatima Bonaldo."

#### ORIGIN

Query Match 100.0%; Score 25; DB 14; Length 401;

Best Local Similarity 80.0%; Pred. No. 0.0035;

Matches 20; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 GACUGUCCACAGCAUUCGCGUACC 25

||||:|||||:|||||:|||||

Db 226 GACTGTCCACAGCATTCGCTGACC 250

#### RESULT 6

BF873838/c

LOCUS

DEFINITION

BF873838

ACCESSION

BF873838.1

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

20202663

PUBMED

COMMENT

Contact: Simpson A.J.G.

Laboratory of Cancer Genetics

Ludwig Institute for Cancer Research

Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,

Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL:  
 (http://www.ludwig.org.br/scripts/gethtml2.pl?ti=IL3&t=IL3-ET0114-071100-338-C02&t3=2000-11-07&t4=1)  
 Seq primer: puc 18 forward  
 High quality sequence stop: 390.

## FEATURES

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 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /dev\_stage="Adult"  
 /clone\_lib="ET0114"

/note="Organ: lung tumor; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

## ORIGIN

Query Match 100.0%; Score 25; DB 10; Length 437;  
 Best Local Similarity 80.0%; Pred. No. 0.0036;  
 Matches 20; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 GACUGUCCACAGAUUCCGUGACC 25  
 |||:|||||:|||||:|||||  
 Db 318 GACTGTCCACAGCATTCGCGTACC 294

## RESULT 7

AW452440

## LOCUS

UI-H-BI3-als-c-04-0-UI.s1 NCI\_CGAP\_Sub5 Homo sapiens cDNA clone  
 IMAGE:3068526 3', mRNA sequence.

## ACCESSION

AW452440

## VERSION

AW452440.1

## KEYWORDS

EST.

## SOURCE

Homo sapiens (human)

## ORGANISM

Homo sapiens

## REFERENCE

1 (bases 1 to 443)

## AUTHORS

NCI-CGAP

## TITLE

National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

## JOURNAL

Unpublished (1997)

## COMMENT

Contact: Robert Strausberg, Ph.D.  
 Email: cgabs-r@mail.nih.gov  
 Oligo-dT track not found, Not 1 site shown in beginning of sequence  
 is likely internal to the message. cDNA library preparation: M.B.  
 Soares Lab Clone distribution: NCI-CGAP clone distribution  
 Information can be found through the I.M.A.G.E. Consortium/LLNL at:  
 www-bio.llnl.gov/bbrp/image/image.html The following repetitive  
 elements were found in this cDNA sequence: 147-207, >HSR1T  
 Seq primer: M13 Forward  
 POLYA=No.

## FEATURES

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 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:3068526"  
 /clone\_lib="NCI\_CGAP\_Sub5"  
 /lab\_host="DH10B (Life Technologies)"  
 /notes="Vector: pT73D-Pac (Pharmacia) with a modified  
 polylinker; Site 1: Not 1; Site 2: Eco RI; NCI\_CGAP Sub5  
 is a subcloned library derived from NCI\_CGAP\_Sub4. The  
 NCI\_CGAP\_Sub5 library had 3 million recombinants. A  
 single-stranded DNA preparation of NCI\_CGAP\_Sub4 was used  
 as a tracer in a subtractive hybridization with a driver  
 comprising: the IMAGE pool (NCI\_CGAP\_Kid3 pool 1 LLAM

3334-3337, 3682-3683, 3798-3803 (IMAGE CloneIDs  
 1322376-1323911, 1456008-1456775, 1500552-1502855);  
 NCI\_CGAP\_Kid5 pool 1 LLAM 3338-3342, 3722-3725, 3776-3778  
 (IMAGE CloneIDs 1323912-1325831, 1471368-1472903,  
 1492104-1493255); NCI\_CGAP\_Lu5 pool 1 LLAM 3575-3582,  
 3851-3854 (IMAGE CloneIDs  
 1414920-1417991, 1520904-1522439); NCI\_CGAP\_GC4 pool 1 LLAM  
 3164-3167, 3716-3720, 3733-3735 (IMAGE CloneIDs  
 1257096-1258631, 1469064-1470983, 1475592-1476743);  
 NCI\_CGAP\_Pr22 pool 1 LLAM 2457-2459, 2758-2759, 3062-3068  
 (IMAGE CloneIDs 985608-986759, 1101192-1101959,  
 1217928-1220615); NCI\_CGAP\_Co10 pool 1 LLAM 2644-2653,  
 2871-2872 (IMAGE CloneIDs  
 1057416-1061255, 1144584-1145351). (10% of the driver  
 population), plus a pool of 3,840 arrayed clones from  
 NCI\_CGAP\_Sub1 (IMAGE CloneIDs 2708616-2710535) and  
 NCI\_CGAP\_Sub2 (IMAGE CloneIDs 2710536-2712455) (10% of  
 the driver population), plus a pool of 11,136 clones from  
 NCI\_CGAP\_Sub3 (IMAGE CloneIDs 2712456-2723591) (10% of the  
 driver population), plus a pool of 5,472 clones from  
 NCI\_CGAP\_Sub4 (IMAGE CloneIDs 2723592-2728969) (70% of the  
 driver population). Subtraction was performed as  
 previously described (Bonaldi, Lennon & Soares (1996):  
 Normalization and Subtraction: Two Approaches To  
 Facilitate Gene Discovery. Genome Research 6, 791-806.  
 TAG TISSUE=germ cell  
 TAG\_LIB=NCI\_CGAP\_GC4  
 TAG\_SEQ=AAATC"

## ORIGIN

Query Match 100.0%; Score 25; DB 10; Length 443;  
 Best Local Similarity 80.0%; Pred. No. 0.0036;  
 Matches 20; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 GACUGUCCACAGAUUCCGUGACC 25  
 |||:|||||:|||||:|||||  
 Db 356 GACTGTCCACAGCATTCGCGTACC 380

## RESULT 8

BG927169

## LOCUS

HNC18-1-D3.R.HC (Human Normal Cartilage) Homo sapiens cDNA, mRNA  
 sequence.

## ACCESSION

BG927169

## VERSION

BG927169.1

## KEYWORDS

EST.

## SOURCE

Homo sapiens (human)

## ORGANISM

Homo sapiens

## REFERENCE

1 (bases 1 to 531)

## AUTHORS

Kumar, S., Connor, J.R., Dodds, R.A., Halsey, W., Van Horn, M., Mao, J.,  
 Sathe, G., Mui, P., Agarwal, P., Badger, A.M., Lee, J.C., Gowen, M. and  
 Lark, M.W.

## TITLE

Identification and initial characterization of 5000 expressed  
 sequenced tags (ESTs) each from adult human normal and  
 osteoarthritic cartilage cDNA libraries

## JOURNAL

Osteoarthritis. Cartil. 9 (7), 641-653 (2001)

## MEDLINE

21482651

## PUBMED

11597177

## COMMENT

Contact: Sanjay Kumar  
 UW2109

## GlaxoSmithKline

709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA  
 Tel: 610-270-7245  
 Fax: 610-270-5598  
 Email: sanjay.kumar-l@gsk.com  
 Seq primer: T7

## FEATURES

Location/Qualifiers

1. .531  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"

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/db_xref="taxon:9606"
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/lab_host="E.coli DH10 B"
/clone_lib="HNC (Human Normal Cartilage)"
/notes="Vector: pSPORT I; Site_1: SalI; Site_2: NotI;
Directional"

ORIGIN
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Best Local Similarity 80.0%; Pred. NO. 0.0036;
Matches 20; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 GACUGUCCACAGCAUUCGCGUACC 25
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Db 439 GACTGTCCACAGCATTCGCGTACC 463

RESULT 9
BF380221
LOCUS
DEFINITION
MR3-UT0050-250900-003-g03 UT0050 Homo sapiens cDNA, mRNA sequence.
ACCESSION
BF380221
VERSION
BF380221.1 GI:11369346
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
REFERENCE
1 (bases 1 to 588)
AUTHORS
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jorgeneel,C.V.,
O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
TITLE
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
JOURNAL
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE
20202663
PUBMED
10737800
COMMENT
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?t1=MR3&t2=MR3-UT0050-
250900-003-g03&t3=2000-09-25&t4=1)
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High quality sequence stop: 586.
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            /clone_lib="UT0050"
            /note="Organ: uterus_tumor; Vector: puc18; Site_1: SmaI;
            Site_2: SmaI; A mini-library was made by cloning products
            derived from ORESTES PCR (U.S. Letters Patent application
            No. 196,716 - Ludwig Institute for Cancer Research)
            profiles into the pUC 18 vector. Reverse transcription of
            tissue mRNA and cDNA amplification were performed under
            low stringency conditions."

ORIGIN
Query Match      100.0%; Score 25; DB 10; Length 588;
Best Local Similarity 80.0%; Pred. NO. 0.0037;
Matches 20; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

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QY 1 GACUGUCCACAGCAUUCGCGUACC 25
    |||:|||||:|||||:|||||:|||||
Db 453 GACTGTCCACAGCATTCGCGTACC 477

RESULT 10
BF094682
LOCUS
DEFINITION
MR3-UT0050-130900-003-g03 UT0050 Homo sapiens cDNA, mRNA sequence.
ACCESSION
BF094682
VERSION
BF094682.1 GI:10900392
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
REFERENCE
1 (bases 1 to 588)
AUTHORS
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jorgeneel,C.V.,
O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
TITLE
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
JOURNAL
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE
20202663
PUBMED
10737800
COMMENT
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?t1=MR3&t2=MR3-UT0050-130
900-003-g03&t3=2000-09-13&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 586.
FEATURES
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            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /dev_stage="Adult"
            /clone_lib="UT0050"
            /note="Organ: uterus_tumor; Vector: puc18; Site_1: SmaI;
            Site_2: SmaI; A mini-library was made by cloning products
            derived from ORESTES PCR (U.S. Letters Patent application
            No. 196,716 - Ludwig Institute for Cancer Research)
            profiles into the pUC 18 vector. Reverse transcription of
            tissue mRNA and cDNA amplification were performed under
            low stringency conditions."

ORIGIN
Query Match      100.0%; Score 25; DB 10; Length 588;
Best Local Similarity 80.0%; Pred. NO. 0.0037;
Matches 20; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 GACUGUCCACAGCAUUCGCGUACC 25
    |||:|||||:|||||:|||||:|||||
Db 453 GACTGTCCACAGCATTCGCGTACC 477

RESULT 11
BF953848
LOCUS
DEFINITION
MR0-NN1170-131100-302-f01 NN1170 Homo sapiens cDNA, mRNA sequence.
ACCESSION
BF953848

```

```

VERSION BF953848.1 GI:12371149
SOURCE EST.
ORGANISM Homo sapiens (human)

REFERENCE
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W.Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldan,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.

TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
PUBMED 10737800
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?ti=MR0&t2=MR0-NN1170-131100-302-f01&t3=2000-11-13&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 31
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DEFINITION mRNA sequence.
ACCESSION BE396942 GI:9342307
VERSION BE396942.1
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
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1 (bases 1 to 597)
/note="NCBI http://imgc.nci.nih.gov/National Institutes of Health, Mammalian Gene Collection (MGC)"

REFERENCE
AUTHORS NIH-MGC
TITLE NIH-MGC http://imgc.nci.nih.gov/

JOURNAL JOURNAL
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA library Preparation: Ling Hong/Rubin Laboratory
cDNA library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCW294 row: 9 column: 13
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ACCESSION BE267891
VERSION BE267891.1 GI:9141488
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 621)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM132 row: h column: 13
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            insert size 1.8kb. Library constructed by Ling Hong in
            the laboratory of Gerald M. Rubin (University of
            California, Berkeley) using ZAP-cDNA synthesis kit
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ACCESSION CB267185  
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KEYWORDS EST.  
SOURCE Homo sapiens (human)

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Matches 20; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

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Job time : 882.692 secs

ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 637)  
AUTHORS Yang, R.-Z., Shuldiner, A. and Gong, D.-W.  
TITLE EST analysis of human adipose gene expression  
JOURNAL Unpublished (2002)  
COMMENT Contact: Gong Da-Wei  
Division of Endocrinology, Diabetes and Nutrition  
University of Maryland  
660 Redwood St, HH497, Baltimore, MD 21201, USA  
Tel: 410 706 1672  
Fax: 410 706 1622  
Email: dgong@medicine.umaryland.edu  
PCR Primers  
FORWARD: CTCGGGAAGCGCGCCATTGTGTGGT  
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Db 404 GACTGTCCACAGCATTCGCGTGACC 428

Search completed: May 26, 2004, 22:44:24  
Job time : 882.692 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 26, 2004, 16:00:31 ; Search time 532.065 Seconds  
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Sequence: 1 GGTACGGGATGCTGTGACAGTC 25

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 3470272 seqs, 21671516995 residues

Word size : 0  
Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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32: em\_hgt\_other.\*

33: em\_hgt\_mus.\*

34: em\_hgt\_pln.\*

35: em\_hgt\_rod.\*

36: em\_hgt\_mam.\*

37: em\_hgt\_vrt.\*

38: em\_sy.\*

39: em\_hgo\_hum.\*

40: em\_hgo\_mus.\*

41: em\_hgo\_other.\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

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C 2	25	100.0	25	6	BD222532	BD222532 Methods f
C 3	25	100.0	25	6	BD222533	BD222533 Methods f
C 4	25	100.0	25	6	BD222534	BD222534 Methods f
C 5	25	100.0	56	6	I12447	I12447 Sequence 17
C 6	25	100.0	56	6	I14509	I14509 Sequence 17
C 7	25	100.0	210	9	AY043457	AY043457 Homo sapi
C 8	25	100.0	250	9	AF321981	AF321981 Homo sapi
C 9	25	100.0	305	9	AF192533	AF192533 Homo sapi
C 10	25	100.0	350	6	BD222546	BD222546 Methods f
C 11	25	100.0	561	9	HUMMK562B	M19695 Human myelo
C 12	25	100.0	679	9	HUMABLB	M30832 Human bcr/a
C 13	25	100.0	854	9	HUMABLD	M30829 Human bcr/a
C 14	25	100.0	922	9	HSA131467	AJ131467 Homo sapi
C 15	25	100.0	997	9	HSA131466	AJ131466 Homo sapi
C 16	25	100.0	1078	6	A92081	A92081 Sequence 5
C 17	25	100.0	1078	6	AR230888	AR230888 Sequence
C 18	25	100.0	1157	6	BD177069	BD177069 Standard
C 19	25	100.0	2255	6	E00984	E00984 Probe detec
C 20	25	100.0	2255	6	I04527	I04527 Sequence 1
C 21	25	100.0	2541	9	HUMBCRX	M55195 Human break
C 22	25	100.0	2811	6	AX780333	AX780333 Sequence
C 23	25	100.0	3481	9	AK128501	AK128501 Homo sapi
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C 28	25	100.0	111249	9	AP000343	AP000343 Homo sapi
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C 30	24	96.0	26	6	I83632	I83632 Sequence 6
C 31	24	96.0	40	6	E16986	E16986 Sense prime
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C 33	21	84.0	219210	2	AC145066	M13096 Human chro
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C 35	18	72.0	22	6	I58643	AC138021 Pan trogl
C 36	18	72.0	62	6	AR100681	I58643 Sequence 11
C 37	18	72.0	81	6	AR100682	AR100681 Sequence
C 38	18	72.0	205	6	I02402	AR100682 Sequence
C 39	18	72.0	257	6	I58633	I02402 Sequence 1
C 40	18	72.0	257	6	I58633	I58633 Sequence 1
C 41	18	72.0	60	6	A50293	I96199 Sequence 36
C 42	17	68.0	13980	1	AE001036	A50293 Sequence 13
C 43	17	68.0	80526	2	AC145976	AE001036 Archaeogl
C 44	17	68.0	110000	2	AC107201_3	AC145976 Gallus ga
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DEFINITION Methods for detecting and measuring spliced nucleic acids.  
ACCESSION BD222531  
VERSION BD222531.1 GI:33032301  
KEYWORDS JP 2002521037-A/9.  
SOURCE synthetic construct  
ORGANISM artificial sequences.  
REFERENCE 1 (bases 1 to 25)  
AUTHORS Harvey,R.C. and Eastman,P.S.  
TITLES Methods for detecting and measuring spliced nucleic acids  
JOURNAL Patent: JP 2002521037-A 9 16-JUL-2002;  
GEN PROBE INC

COMMENT OS Artificial Sequence  
 PN JP 2002521037-A/9  
 PD 16-JUL-2002  
 PF 23-JUL-1999 JP 2000561364  
 PR 23-JUL-1998 US 09/121239  
 PI RICHARD C HARVEY, PAUL S EASTMAN  
 PC C12Q1/68, C12N15/09, C12N15/00  
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 ACCESSION BD222532  
 VERSION BD222532.1 GI:33032302  
 KEYWORDS JP 2002521037-A/10.  
 SOURCE synthetic construct  
 ORGANISM artificial sequences.  
 REFERENCE 1 (bases 1 to 25)  
 AUTHORS Harvey, R.C. and Eastman, P.S.  
 TITLE Methods for detecting and measuring spliced nucleic acids  
 JOURNAL Patent: JP 2002521037-A 10 16-JUL-2002;  
 GEN PROBE INC  
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 ACCESSION BD222533  
 VERSION BD222533.1 GI:33032303  
 KEYWORDS JP 2002521037-A/11.  
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 ORGANISM artificial sequences.  
 REFERENCE 1 (bases 1 to 25)  
 AUTHORS Harvey, R.C. and Eastman, P.S.  
 TITLE Methods for detecting and measuring spliced nucleic acids  
 JOURNAL Patent: JP 2002521037-A 11 16-JUL-2002;  
 GEN PROBE INC  
 COMMENT OS Artificial Sequence  
 PN JP 2002521037-A/11  
 PD 16-JUL-2002  
 PF 23-JUL-1999 JP 2000561364  
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 AUTHORS Harvey, R.C. and Eastman, P.S.  
 TITLE Methods for detecting and measuring spliced nucleic acids  
 JOURNAL Patent: JP 2002521037-A 11 16-JUL-2002;  
 GEN PROBE INC  
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 PN JP 2002521037-A/11  
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 PF 23-JUL-1999 JP 2000561364  
 PR 23-JUL-1998 US 09/121239  
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 LOCUS  
 DEFINITION Methods for detecting and measuring spliced nucleic acids.  
 ACCESSION BD222534  
 VERSION BD222534.1 GI:33032304  
 KEYWORDS JP 2002521037-A/12.  
 SOURCE synthetic construct  
 ORGANISM artificial sequences.  
 REFERENCE 1 (bases 1 to 25)  
 AUTHORS Harvey, R.C. and Eastman, P.S.  
 TITLE Methods for detecting and measuring spliced nucleic acids  
 JOURNAL Patent: JP 2002521037-A 12 16-JUL-2002;  
 GEN PROBE INC  
 COMMENT OS Artificial Sequence  
 PN JP 2002521037-A/12  
 PD 16-JUL-2002  
 PF 23-JUL-1999 JP 2000561364  
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 PC C12Q1/68, C12N15/09, C12N15/00  
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RESULT 5
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DEFINITION Sequence 17 from patent US 5424413.
ACCESSION I12447
VERSION I12447.1 GI:909831
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 56)
AUTHORS Hogan,J.J., Arnold,L.J. Jr., Nelson,N.C. and Bezverkov,R.
TITLE Branched nucleic acid probes
JOURNAL Patent: US 5424413-A 17 13-JUN-1995;
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DEFINITION Sequence 17 from patent US 5451503.
ACCESSION I14509
VERSION I14509.1 GI:996992
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 56)
AUTHORS Hogan,J.J., Arnold,L.J. Jr., Nelson,N.C. and Bezverkov,R.
TITLE Method for use of branched nucleic acid probes
JOURNAL Patent: US 5451503-A 17 19-SEP-1995;
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RESULT 7
LOCUS AY043457/c 210 bp mRNA linear PRI 27-JUN-2003
DEFINITION Homo sapiens BCR-ABL fusion protein (BCR-ABL fusion) mRNA, partial cds.
ACCESSION AY043457

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VERSION AY043457.1 GI:22073966
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 210)
AUTHORS Otazu,I.B., Belen Rivero,M., Olcico,R., Pinto,A., Zalcborg,I. and Seunanez,H.N.
TITLE A rare, in-frame BCR-ABL fusion (e13a3) in a patient with an aggressive chronic myeloid leukaemia
JOURNAL Acta Haematol. 108 (3), 150-153 (2002)
MEDLINE 22259050
PUBMED 12373087
REFERENCE 2 (bases 1 to 210)
AUTHORS Otazu,I.B., Rivero,M.B. and Olcico,R.
TITLE Direct Submission
JOURNAL Submitted (03-JUL-2001) Genetics Division, Instituto Nacional de Cancer, Praca da Cruz Vermelha, 23, sexto andar, Rio de Janeiro, RJ 21230-130, Brazil
FEATURES Location/Qualifiers
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            /note="chronic myeloid leukaemia patient with e13a3 BCR-ABL rearrangement"
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                    /protein_id="AAL05889.1"
                    /db_xref="GI:22073967"
                    /translation="FRSFSLSVLEQLMTNSCVKLQTVHSIPLTINKEGEKLRLVLYN HNGEWCBAQTNGQGWVPSNYITPV"

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Best Local Similarity 100.0%; Pred. No. 4.1e-05;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTACGCGGAATGCTGTGGACAGTC 25
    |||||
Db 91 GGTACGCGGAATGCTGTGGACAGTC 67

RESULT 8
LOCUS AF321981/c 250 bp mRNA linear PRI 21-FEB-2001
DEFINITION Homo sapiens BCR-ABL fusion transcript e15a2 mRNA sequence.
ACCESSION AF321981
VERSION AF321981.1 GI:13021894
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 250)
AUTHORS Moreno,M.P., Cortinas,M.N., Bonomi,R., Cardeza,A. and Uriarte,M.R.
TITLE A novel BCR-ABL fusion transcript (e15a2) in two patients with atypical Chronic Myeloproliferative Syndrome
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 250)
AUTHORS Moreno,M.P., Cortinas,M.N., Bonomi,R., Cardeza,A. and Uriarte,M.R.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2000) Biologia Molecular, Asociacion Espanola, Bulevar Artigas 1465, Montevideo 11200, Uruguay
FEATURES Location/Qualifiers
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translocation between the 3' portion of the c-ABL oncogene
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22; t(9;22)"

ORIGIN
Query Match      100.0%; Score 25; DB 9; Length 250;
Best Local Similarity 100.0%; Pred. No. 4.1e-05;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTACGCGGAATGCTGTGGACAGTC 25
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Db 65 GGTACGCGGAATGCTGTGGACAGTC 41

RESULT 9
AF192533/c
LOCUS      AF192533.1 GI:7406986
DEFINITION Homo sapiens BCR-ABL fusion protein (BCR-ABL fusion) mRNA, partial
cds.
ACCESSION  AF192533
VERSION     AF192533.1
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
ORGANISM   Homo sapiens
REFERENCE  1 (bases 1 to 305)
AUTHORS   Cortinas,M.N., Uriarte,M.R. and Moreno,M.P.
TITLE     Identification of a novel BCR ABL fusion transcript in two patients
          with persistent neutrophilia in absence of Philadelphia chromosome
          Unpublished
JOURNAL
REFERENCE  2 (bases 1 to 305)
AUTHORS   Cortinas,M.N., Uriarte,M.R. and Moreno,M.P.
TITLE     Direct Submission
JOURNAL   Submitted (06-OCT-1999) Biologia Molecular, Asociacion Espanola
          Primera de Socorros Mutuos, Bvar. Artigas 1465, Montevideo 11200,
          Uruguay

FEATURES             Location/Qualifiers
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ORIGIN

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Query Match      100.0%; Score 25; DB 9; Length 305;
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Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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    |||
Db 112 GGTACGCGGAATGCTGTGGACAGTC 88

RESULT 10
BD222546/c
LOCUS      BD222546
DEFINITION Methods for detecting and measuring spliced nucleic acids.
ACCESSION  BD222546
VERSION     BD222546.1 GI:33032316
KEYWORDS   JP 2002521037-A/24.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
REFERENCE  1 (bases 1 to 350)
AUTHORS   Harvey,R.C. and Eastman,P.S.
TITLE     Methods for detecting and measuring spliced nucleic acids
JOURNAL   Patent: JP 2002521037-A 24 16-JUL-2002;
          GEN PROBE INC
COMMENT    OS Homo sapiens (human)
          PN JP 2002521037-A/24
          PD 16-JUL-2002
          PF 23-JUL-1999 JP 2000561364
          PR 23-JUL-1998 US 09/121239
          PI RICHARD C HARVEY, PAUL S EASTMAN
          PC C12Q1/68,C12N15/09,C12N15/00
          CC Methods for detecting and measuring spliced nucleic acids FH
          Key source location/Qualifiers
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ORIGIN

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Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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    |||
Db 113 GGTACGCGGAATGCTGTGGACAGTC 89

RESULT 11
HUMMK562B/c
LOCUS      HUMMK562B
DEFINITION Human myelocytic chimeric bcr and chromosome 9 fusion gene, exons
1-4.
ACCESSION  M19695
VERSION     M19695.1 GI:188567
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
ORGANISM   Homo sapiens
REFERENCE  1 (bases 1 to 561)
AUTHORS   Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
          Grosveid,G., Verwoerd,T., van Agthoven,T., de Klein,A.,
          Ramachandran,K.L., Heisterkamp,N., Stam,K. and Groffen,J.
          The chronic myelocytic cell line K562 contains a breakpoint in bcr
          and produces a chimeric bcr/c-abl transcript
          Mol Cell. Biol. 6 (2), 607-616 (1986)
          87064346
          3023859
          Original source text: Human myelocytic Ph(1)-positive CML K562 cell

COMMENT

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line, cDNA to mRNA, clone 8E.  
The bcr region of the fusion protein is located on chromosome 22q11; the abl region was translocated from chromosome 9q34.

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ORIGIN  
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Query Match 100.0%; Score 25; DB 9; Length 561;  
Best Local Similarity 100.0%; Pred. No. 4.1e-05;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTACGCGGAATGCTGTGCAGATC 25  
|||||  
Db 108 GGTACGCGGAATGCTGTGCAGATC 84  
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RESULT 12  
HUMABLB/c  
LOCUS  
DEFINITION Human bcr/abl fusion protein, partial cds, clone E3. PRI 13-FEB-1996  
ACCESSION M30832  
VERSION 30832.1 GI:177944  
KEYWORDS Philadelphia chromosome; abl proto-oncogene; translocation.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 679)  
AUTHORS Shtivelman, E., Lifshitz, B., Gale, R.P. and Canaani, E.  
TITLE Fused transcript of abl and bcr genes in chronic myelogenous leukaemia  
JOURNAL Nature 315 (6020), 550-554 (1985)  
MEDLINE 85240529  
PUBMED 2989692  
COMMENT Original source text: Homo sapiens (clone: E3.) cDNA to mRNA.  
FEATURES  
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CDS  
LOCUS  
DEFINITION Homo sapiens mRNA for BCR/ABL chimeric fusion peptide, partial. PRI 11-OCT-2000  
ACCESSION AJ131467  
VERSION AJ131467.1 GI:4033556  
KEYWORDS BCR/ABL chimeric fusion peptide; bcr/abl gene.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1  
AUTHORS Burmeister, T., Maurer, J., Aivado, M., Elmaagacli, A.H., Grunebach, F., Held, K.R., Hees, G., Hochhaus, A., Hoppner, W., Lentze, K.U., Lubbert, M., Schafer, K.L., Schafhausen, P., Schmidt, C.A., Schuler, F., Seeger, K., Seelig, R., Thiede, C., Viehmann, S., Weber, C., Wilhelm, S., Christmann, A., Clement, J.H., Ebener, U., Enczmann, J., Leo, R., Schleuning, M., Schoch, R. and Thiel, E.  
TITLE Quality assurance in RT-PCR-based BCR/ABL diagnostics--results of an interlaboratory test and a standardization approach  
JOURNAL Leukemia 14 (10), 1850-1856 (2000)  
MEDLINE 20471781  
PUBMED 11021760  
REFERENCE 2 (bases 1 to 922)  
AUTHORS Burmeister, T.  
TITLE Direct Submission  
JOURNAL Submitted (04-DEC-1998) Burmeister T., Medizinische Klinik III, FU Berlin, Hindenburgdamm 30, Berlin, Germany 12200, Germany

Query Match 100.0%; Score 25; DB 9; Length 679;  
Best Local Similarity 100.0%; Pred. No. 4.2e-05;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTACGCGGAATGCTGTGCAGATC 25  
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Db 326 GGTACGCGGAATGCTGTGCAGATC 302  
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RESULT 13  
HUMABLD/c  
LOCUS  
DEFINITION Human bcr/abl fusion protein mRNA, partial cds, clone K28. PRI 14-FEB-1996

ACCESSION M30829  
VERSION M30829.1 GI:177953  
KEYWORDS Philadelphia chromosome; abl proto-oncogene; translocation.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 854)  
AUTHORS Shtivelman, E., Lifshitz, B., Gale, R.P. and Canaani, E.  
TITLE Fused transcript of abl and bcr genes in chronic myelogenous leukaemia  
JOURNAL Nature 315 (6020), 550-554 (1985)  
MEDLINE 85240529  
PUBMED 2989692  
COMMENT Original source text: Homo sapiens (clone: K28.) cDNA to mRNA.  
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Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTACGCGGAATGCTGTGCAGATC 25  
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Db 501 GGTACGCGGAATGCTGTGCAGATC 477  
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RESULT 14  
HSA131467/c  
LOCUS  
DEFINITION Homo sapiens mRNA for BCR/ABL chimeric fusion peptide, partial.  
ACCESSION AJ131467  
VERSION AJ131467.1 GI:4033556  
KEYWORDS BCR/ABL chimeric fusion peptide; bcr/abl gene.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1  
AUTHORS Burmeister, T., Maurer, J., Aivado, M., Elmaagacli, A.H., Grunebach, F., Held, K.R., Hees, G., Hochhaus, A., Hoppner, W., Lentze, K.U., Lubbert, M., Schafer, K.L., Schafhausen, P., Schmidt, C.A., Schuler, F., Seeger, K., Seelig, R., Thiede, C., Viehmann, S., Weber, C., Wilhelm, S., Christmann, A., Clement, J.H., Ebener, U., Enczmann, J., Leo, R., Schleuning, M., Schoch, R. and Thiel, E.  
TITLE Quality assurance in RT-PCR-based BCR/ABL diagnostics--results of an interlaboratory test and a standardization approach  
JOURNAL Leukemia 14 (10), 1850-1856 (2000)  
MEDLINE 20471781  
PUBMED 11021760  
REFERENCE 2 (bases 1 to 922)  
AUTHORS Burmeister, T.  
TITLE Direct Submission  
JOURNAL Submitted (04-DEC-1998) Burmeister T., Medizinische Klinik III, FU Berlin, Hindenburgdamm 30, Berlin, Germany 12200, Germany



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ORIGIN

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Best Local Similarity 100.0%; Pred. No. 4.2e-05;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy      1 GGTACGCGGAATGCTGTGGACAGTC 25
Db      285 GGTACGCGGAATGCTGTGGACAGTC 261

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GenCore version 5.1.1.6  
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OM nucleic - nucleic search, using sw model

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Scoring table: OLIGO NUC  
Gapop 60.0 , Gapext 60.0

Searched: 3373863 seqs, 2124099041 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

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Post-processing: Listing first 45 summaries

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- 2: Geneseqn1990s:\*
- 3: Geneseqn2000s:\*
- 4: Geneseqn2001as:\*
- 5: Geneseqn2001bs:\*
- 6: Geneseqn2002s:\*
- 7: Geneseqn2003as:\*
- 8: Geneseqn2003bs:\*
- 9: Geneseqn2003cs:\*
- 10: Geneseqn2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	25	100.0	25	3	Aaz60850	Aaz60850 Oligonucleotide
2	25	100.0	25	3	Aaz60849	Aaz60849 Oligonucleotide
3	25	100.0	25	3	Aaz60851	Aaz60851 Oligonucleotide
4	25	100.0	25	3	Aaz60848	Aaz60848 Oligonucleotide
5	25	100.0	45	9	Adc38532	Adc38532 Template
6	25	100.0	56	2	Aaq46951	Aaq46951 Branched
7	25	100.0	200	2	Aat88785	Aat88785 Leukaemic
8	25	100.0	250	6	Abs73175	Abs73175 Human tra
9	25	100.0	305	6	Abs73174	Abs73174 DNA encod
10	25	100.0	350	3	Aaz60863	Aaz60863 Region su
11	25	100.0	504	5	Aas85023	Aas85023 DNA encod
12	25	100.0	504	8	Ach38242	Ach38242 Human tra
13	25	100.0	561	6	Abs73169	Abs73169 Human tra
14	25	100.0	679	6	Abs73172	Abs73172 DNA encod
15	25	100.0	766	5	Abv29306	Abv29306 Human pro
16	25	100.0	766	5	Abv23449	Abv23449 Human pro
17	25	100.0	854	6	Abs73170	Abs73170 DNA encod
18	25	100.0	921	5	Aas85025	Aas85025 DNA encod
19	25	100.0	922	6	Abs73180	Abs73180 DNA encod
20	25	100.0	997	6	Abs73173	Abs73173 DNA encod
21	25	100.0	1097	2	Aat91764	Aat91764 Chimeric
22	25	100.0	1157	9	Adc4640	Adc4640 Hepatitis
23	25	100.0	1212	5	Aas85028	Aas85028 DNA encod

C 24	25	100.0	2255	1	AAN60228	AAN60228 Sequence
C 25	25	100.0	4725	5	AAS76375	AAS76375 DNA encod
C 26	25	100.0	4739	6	ABL63316	ABL63316 Breast ca
C 27	25	100.0	4739	7	ACC00031	ACC00031 Human Bcr
C 28	25	100.0	4756	5	AAS85030	AAS85030 DNA encod
C 29	25	100.0	4775	5	AAS76377	AAS76377 DNA encod
C 30	25	100.0	5795	5	AAS85031	AAS85031 DNA encod
C 31	25	100.0	152141	7	ACA64961	ACA64961 Human BCR
C 32	24	96.0	26	2	AAQ51830	AAQ51830 bcr mRNA
C 33	24	96.0	40	2	AAV58775	AAV58775 Forward p
C 34	21	84.0	468	6	ABS73171	ABS73171 Human tra
C 35	20	80.0	20	2	AAT91761	AAT91761 Primer DE
C 36	19	76.0	45	2	AAT91782	AAT91782 Primer BB
C 37	18	72.0	22	2	AAQ34635	AAQ34635 Human bcr
C 38	18	72.0	62	2	AAQ66774	AAQ66774 L6(1)31 r
C 39	18	72.0	81	2	AAQ66775	AAQ66775 L6(1)31 r
C 40	18	72.0	205	1	AAQ91666	AAQ91666 Bcr-abl f
C 41	18	72.0	257	2	AAQ34625	AAQ34625 Human bcr
C 42	18	72.0	257	2	AAV20458	AAV20458 Human bcr
C 43	17	68.0	20	3	AAZ91685	AAZ91685 PCR prime
C 44	17	68.0	20	8	ADB68429	ADB68429 PCR prime
C 45	17	68.0	20	9	ADD06158	ADD06158 Bcr-abl f

## ALIGNMENTS

RESULT 1  
AAZ60850  
ID AAZ60850 standard; DNA; 25 BP.  
XX  
AC AAZ60850;  
XX  
DT 16-MAY-2000 (first entry)  
XX  
DE Oligonucleotide used to detect bcr b3-abl fusion transcripts.  
XX  
KW Fusion transcript; translocation; bcr b3 region; abl gene;  
KW amplification assay; detection assay; medical diagnosis;  
KW clinical monitoring; chimeric RNA; fusion RNA; condition marker;  
KW disease marker; cancer; leukemia; ss.  
XX  
OS Synthetic.  
XX  
PN WO200005418-A1.  
XX  
PD 03-FEB-2000.  
XX  
PF 23-JUL-1999; 99WO-US016832.  
XX  
PR 23-JUL-1998; 98US-00121239.  
XX  
PA (GENP-) GEN-PROBE INC.  
XX  
PI Harvey RC, Eastman PS;  
XX  
DR WPI; 2000-182730/16.  
XX  
PT Novel methods for preparing RNA from biological samples, used for the  
PT detection and measurement of nucleic acids and fusion nucleic acids.  
XX  
Claim 19; Page 41; 49pp; English.  
XX  
CC Oligonucleotides AAZ60840-62 and AAZ60865-66 are used in the method of  
CC the invention to detect fusion transcripts produced from a translocation  
CC between the bcr b3 region and the abl gene. The specification describes a  
CC method for detecting a fusion nucleic acid (particularly chimeric mRNA  
CC species), in a biological sample. The method comprises contacting a  
CC sample of fusion nucleic acid with primers, amplifying the hybridized  
CC fusion nucleic acid, and detecting the target hybrid. The method is used  
CC for the simple and rapid preparation of RNA from a biological sample,  
CC particularly from the cytoplasm of eukaryotic cells, which is suitable  
CC for use in an amplification and detection assay. The methods are used for

CC the analysis and detection of nucleic acids in biological samples. The  
 CC methods are useful in the human medical and veterinary fields, for  
 CC medical diagnoses and clinical monitoring of a patient's response to  
 CC therapy where a disease or medical condition is associated with a  
 CC particular type and/or level of mRNA present in the sample. The methods  
 CC are also useful for detecting or quantifying fusion or chimeric RNA  
 CC species, and for detecting a translocation as a marker for a given  
 CC condition or disease, e.g. translocations associate with cancers,  
 CC particularly forms of leukemia

XX Sequence 25 BP; 5 A; 5 C; 10 G; 5 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 3; Length 25;

Best Local Similarity 100.0%; Pred. No. 0.00021;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTCAGCGGAATGCTGTGGACAGTC 25

Db 1 GGTCAGCGGAATGCTGTGGACAGTC 25

#### RESULT 2

AAZ60849/c

ID AAZ60849 standard; RNA; 25 BP.

XX AAZ60849;

XX 16-MAY-2000 (first entry)

DT Oligonucleotide used to detect bcr b3-abl fusion transcripts.

DE Fusion transcript; translocation; bcr b3 region; abl gene;

XX amplification assay; detection assay; medical diagnosis;

KW clinical monitoring; chimeric RNA; fusion RNA; condition marker;

KW disease marker; cancer; leukemia; ss.

XX Synthetic.

OS WO200005418-A1.

PN 03-FEB-2000.

XX 23-JUL-1999; 99WO-US016832.

XX 23-JUL-1998; 98US-00121239.

PR (GENP-) GEN-PROBE INC.

PA Harvey RC, Eastman PS;

XX WPI; 2000-182730/16.

XX Novel methods for preparing RNA from biological samples, used for the

PT detection and measurement of nucleic acids and fusion nucleic acids.

PS Claim 19; Page 41; 49pp; English.

XX Oligonucleotides AAZ60840-62 and AAZ60865-66 are used in the method of

CC the invention to detect fusion transcripts produced from a translocation

CC between the bcr b3 region and the abl gene. The specification describes a

CC method for detecting a fusion nucleic acid (particularly chimeric mRNA

CC species), in a biological sample. The method comprises contacting a

CC sample of fusion nucleic acid with primers, amplifying the hybridized

CC fusion nucleic acid, and detecting the target hybrid. The method is used

CC for the simple and rapid preparation of RNA from a biological sample,

CC particularly from the cytoplasm of eukaryotic cells, which is suitable

CC for use in an amplification and detection assay. The methods are used for

CC the analysis and detection of nucleic acids in biological samples. The

CC methods are useful in the human medical and veterinary fields, for

CC medical diagnoses and clinical monitoring of a patient's response to

CC therapy where a disease or medical condition is associated with a

CC particular type and/or level of mRNA present in the sample. The methods

CC are also useful for detecting or quantifying fusion or chimeric RNA

CC

CC species, and for detecting a translocation as a marker for a given  
 CC condition or disease, e.g. translocations associate with cancers,  
 CC particularly forms of leukemia

XX Sequence 25 BP; 5 A; 10 C; 5 G; 0 T; 5 U; 0 Other;

Query Match 100.0%; Score 25; DB 3; Length 25;

Best Local Similarity 100.0%; Pred. No. 0.00021;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTCAGCGGAATGCTGTGGACAGTC 25

Db 25 GGTCAGCGGAATGCTGTGGACAGTC 1

#### RESULT 3

AAZ60851

ID AAZ60851 standard; RNA; 25 BP.

XX AAZ60851;

XX 16-MAY-2000 (first entry)

DT Oligonucleotide used to detect bcr b3-abl fusion transcripts.

DE Fusion transcript; translocation; bcr b3 region; abl gene;

XX amplification assay; detection assay; medical diagnosis;

KW clinical monitoring; chimeric RNA; fusion RNA; condition marker;

KW disease marker; cancer; leukemia; ss.

XX Synthetic.

OS WO200005418-A1.

PN 03-FEB-2000.

XX 23-JUL-1999; 99WO-US016832.

XX 23-JUL-1998; 98US-00121239.

PR (GENP-) GEN-PROBE INC.

PA Harvey RC, Eastman PS;

XX WPI; 2000-182730/16.

XX Novel methods for preparing RNA from biological samples, used for the

PT detection and measurement of nucleic acids and fusion nucleic acids.

PS Claim 19; Page 41; 49pp; English.

XX Oligonucleotides AAZ60840-62 and AAZ60865-66 are used in the method of

CC the invention to detect fusion transcripts produced from a translocation

CC between the bcr b3 region and the abl gene. The specification describes a

CC method for detecting a fusion nucleic acid (particularly chimeric mRNA

CC species), in a biological sample. The method comprises contacting a

CC sample of fusion nucleic acid with primers, amplifying the hybridized

CC fusion nucleic acid, and detecting the target hybrid. The method is used

CC for the simple and rapid preparation of RNA from a biological sample,

CC particularly from the cytoplasm of eukaryotic cells, which is suitable

CC for use in an amplification and detection assay. The methods are used for

CC the analysis and detection of nucleic acids in biological samples. The

CC methods are useful in the human medical and veterinary fields, for

CC medical diagnoses and clinical monitoring of a patient's response to

CC therapy where a disease or medical condition is associated with a

CC particular type and/or level of mRNA present in the sample. The methods

CC are also useful for detecting or quantifying fusion or chimeric RNA

CC species, and for detecting a translocation as a marker for a given

CC condition or disease, e.g. translocations associate with cancers,

CC particularly forms of leukemia

XX Sequence 25 BP; 5 A; 5 C; 10 G; 0 T; 5 U; 0 Other;

DE Branched probe to CMLb translocation region of chromosome 22.

KW Chronic myelogenous leukaemia; CMLb; abl region;  
 KW acute lymphocytic leukaemia; ALL; genetic translocation; chromosome 22;  
 KW target sequence; universal detection oligomer; branched probe;  
 KW chemiluminescent acridinium ester; ss.  
 XX  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT misc\_feature 1..40  
 FT /\*tag= a  
 FT /note= "Complementary to region of chromosome 22  
 FT associated with CMLb translocation"  
 FT 41..56  
 FT misc\_feature  
 FT /\*tag= b  
 FT /note= "Complementary to nucleotides 16-1 of universal  
 FT detection probe AAQ46949"  
 XX  
 PN EP552931-A1.  
 XX  
 PD 28-JUL-1993.  
 XX  
 XX 20-JAN-1993; 93EP-00300377.  
 XX  
 PR 22-JAN-1992; 92US-00827021.  
 XX  
 PA (GENP-) GEN PROBE INC.  
 XX  
 PI Hogan JJ, Arnold LJ, Nelson NC, Bezverkov R;  
 XX  
 DR WPI; 1993-236606/30.  
 XX  
 PT Nucleic acid molecules which hybridise in presence of target nucleic acid  
 PT - are used as probes in hybridisation assays or as therapeutic agents for  
 PT diseases.  
 XX  
 PS Example 6; Fig 12B; 58pp; English.  
 XX  
 CC Chimeric targets were synthesised homologous to 3 different genetic  
 CC translocations between a constant abl region of chromosome 9 and various  
 CC regions of chromosome 22; two are the most common translocations  
 CC associated with chronic myelogenous leukaemia (CMLa and CMLb) and the  
 CC other is associated with acute lymphocytic leukaemia (ALL). An AB-  
 CC labelled universal detection oligomer (AAQ46949) specific for the abl  
 CC region was synthesised. Three different strands were designed to contain  
 CC a probe region specific for one of the translocated chromosome 22 regions  
 CC as well as an arm region complementary to part of the universal probe  
 CC (AAQ46950-2). The probe mixes were found to detect only the correct  
 CC chimeric targets and did not cross-react significantly with the other  
 CC targets. (Updated on 25-MAR-2003 to correct PN field.) (Updated on 25-MAR  
 CC -2003 to correct PA field.)  
 XX  
 SQ Sequence 56 BP; 18 A; 18 C; 9 G; 11 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 25; DB 2; Length 56;  
 Best Local Similarity 100.0%; Pred. No. 0.00021;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GGTACGCGGAATGCTGTGGACAGTC 25  
 DB 27 GGTACGCGGAATGCTGTGGACAGTC 3  
 RESULT 7  
 AAT8785/c  
 ID AAT8785 standard; DNA; 200 BP.  
 XX  
 AC AAT8785;  
 XX  
 DT 23-MAR-1998 (first entry)  
 XX  
 DE Leukaemic cell BCR-ABL mRNA PCR product target sequence.  
 XX  
 KW Leukaemia; BCR-ABL; cell line K562; target; immunoassay; probe;

KW hybridisation; diagnostic; luciferase; genetic disease; ss.  
 XX  
 OS Unidentified.  
 XX  
 PN CA2186998-A.  
 XX  
 PD 31-MAY-1997.  
 XX  
 XX 02-OCT-1996; 96CA-02186998.  
 PP  
 XX 30-NOV-1995; 95US-00565055.  
 PR  
 XX (UYWI-) UNIV WINDSOR.  
 PA  
 XX Christopoulos TK;  
 PI  
 XX WPI; 1997-415964/39.  
 DR  
 XX Immunoassays and nucleic acid hybridisation assays - using protein-  
 PT encoding nucleic acid fragments as labels.  
 PT  
 XX Disclosure; Page 26; 39pp; English.  
 PS  
 XX A novel assay has been developed for determining an analyte. The assay  
 CC comprises labelling the analyte with a nucleic acid fragment that encodes  
 CC a protein, expressing the nucleic acid, and detecting the protein. The  
 CC present sequence represents a target sequence from a leukaemic cell (cell  
 CC line K562), used in an example of the present assay. The assay is used  
 CC for the determination of antigens or nucleic acids for diagnostic or  
 CC research purposes, e.g. detecting low levels of tumour markers, analysing  
 CC nucleic acid mutations associated with genetic diseases, diagnosing and  
 CC monitoring pathogen infections, or searching for new disease markers. The  
 CC immunoassay when using a luciferase for detection is more sensitive than  
 CC an enzyme-amplified, time-resolved fluorometric immunoassay and does not  
 CC require preparation of a luciferase-antibody conjugate  
 XX  
 SQ Sequence 200 BP; 49 A; 52 C; 51 G; 48 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 25; DB 2; Length 200;  
 Best Local Similarity 100.0%; Pred. No. 0.0002;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GGTACGCGGAATGCTGTGGACAGTC 25  
 DB 64 GGTACGCGGAATGCTGTGGACAGTC 40  
 RESULT 8  
 ABS73175/c  
 ID ABS73175 standard; DNA; 250 BP.  
 XX  
 AC ABS73175;  
 XX  
 DT 04-DEC-2002 (first entry)  
 XX  
 DE Human translocation (9: 22)(q34: q11) #3.  
 XX  
 KW Chromosome aberration; oncogenic fusion protein; cancer;  
 KW proliferative disease; cellular protein isoform; heat shock protein 90;  
 KW HSP-90; rheumatoid arthritis; cancer; haematopoietic disorder;  
 KW T cell lymphoma; B cell lymphoma; chronic myeloid leukaemia; CML;  
 KW acute myeloid leukaemia; AML; chronic myelomonocytic leukaemia; CMML;  
 KW acute lymphoblastic leukaemia; ALL; APL; NHL; solid tumour;  
 KW papillary thyroid carcinoma; Ewing's sarcoma; melanoma; liposarcoma;  
 KW rhabdomyosarcoma; synovial sarcoma; viral infection; gene; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200269900-A2.  
 XX  
 PD 12-SEP-2002.  
 XX  
 PF 01-MAR-2002; 2002WO-US006518.

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XX 01-MAR-2001; 2001US-0272751P.
PR (CONF-) CONFORMA THERAPEUTICS CORP.
XX
XX Fritz LC, Burrows FU;
XX
XX WPI; 2002-698710/75.
DR P-PSDB; ABG95013.
XX
XX Treating genetically-defined disease associated with chromosomal
PT aberrations yielding oncogenic fusion proteins, e.g. cell proliferative
PT diseases, involves administering an inhibitor of heat shock protein 90.
XX
XX Disclosure; Page 97; 389pp; English.
XX
XX The invention describes a method of treating genetically-defined disease
CC associated with chromosomal aberrations yielding oncogenic fusion
CC proteins (I), treating cancerous cells containing (I) in a heterogeneous
CC cell population, treating proliferative diseases associated with mutant
CC protein or cellular protein isoforms (II) dependent on heat shock protein
CC (HSP)-90, or selectively treating cells expressing (II) involving
CC administering HSP90-inhibitor. The method is useful for treating
CC genetically-defined disease with chromosomal aberration yielding
CC oncogenic fusion protein, treating cancerous cells containing fusion
CC protein in heterogeneous cell population, treating proliferative disease
CC (e.g. rheumatoid arthritis or cancer) associated with mutant protein or
CC cellular protein isoform dependent on heat shock protein (HSP)-90 (e.g.
CC p53), or selectively treating cells expressing mutant protein or cellular
CC protein isoform in a patient heterozygous for (II). The method is useful
CC for treating a disease e.g. haematopoietic disorder such as T or B cell
CC lymphoma, chronic myeloid leukaemia (CML), APL, ALL, NHL and CMML,
CC or a disease characterised by a solid tumour such as papillary thyroid
CC carcinoma, Ewing's sarcoma, melanoma, liposarcoma, rhabdomyosarcoma and
CC synovial sarcoma. The method is also useful for treating viral
CC infections. This represents the DNA sequence of a chromosome aberration
XX
XX Sequence 250 BP; 65 A; 62 C; 63 G; 60 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 25; DB 6; Length 250;
Best Local Similarity 100.0%; Pred. No. 0.0002;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGTACGGGAATGCTGTGGACAGTC 25
Db 65 GGTACGGGAATGCTGTGGACAGTC 41
RESULT 9
AB573174/c
ID ABS73174 standard; DNA; 305 BP.
XX
XX ABS73174;
XX
XX 04-DEC-2002 (first entry)
XX
XX DNA encoding human translocation (9: 22) (q34: q11) protein #5.
XX
XX Chromosome aberration; oncogenic fusion protein; cancer;
XX proliferative disease; cellular protein isoform; heat shock protein 90;
XX HSP-90; rheumatoid arthritis; cancer; haematopoietic disorder;
XX T cell lymphoma; B cell lymphoma; chronic myeloid leukaemia; CML;
XX acute myeloid leukaemia; AML; chronic myelomonocytic leukaemia; CMML;
XX acute lymphoblastic leukaemia; ALL; APL; NHL; solid tumour;
XX papillary thyroid carcinoma; Ewing's sarcoma; melanoma; liposarcoma;
XX rhabdomyosarcoma; synovial sarcoma; viral infection; gene; ds.
XX
XX Homo sapiens.
XX
XX WO200269900-A2.
XX
XX 12-SEP-2002.
XX
XX 01-MAR-2002; 2002WO-US006518.
XX
XX 01-MAR-2001; 2001US-0272751P.
PR (CONF-) CONFORMA THERAPEUTICS CORP.
XX
XX Fritz LC, Burrows FU;
XX
XX WPI; 2002-698710/75.
DR P-PSDB; ABG95013.
XX
XX Treating genetically-defined disease associated with chromosomal
PT aberrations yielding oncogenic fusion proteins, e.g. cell proliferative
PT diseases, involves administering an inhibitor of heat shock protein 90.
XX
XX Disclosure; Page 97; 389pp; English.
XX
XX The invention describes a method of treating genetically-defined disease
CC associated with chromosomal aberrations yielding oncogenic fusion
CC proteins (I), treating cancerous cells containing (I) in a heterogeneous
CC cell population, treating proliferative diseases associated with mutant
CC protein or cellular protein isoforms (II) dependent on heat shock protein
CC (HSP)-90, or selectively treating cells expressing (II) involving
CC administering HSP90-inhibitor. The method is useful for treating
CC genetically-defined disease with chromosomal aberration yielding
CC oncogenic fusion protein, treating cancerous cells containing fusion
CC protein in heterogeneous cell population, treating proliferative disease
CC (e.g. rheumatoid arthritis or cancer) associated with mutant protein or
CC cellular protein isoform dependent on heat shock protein (HSP)-90 (e.g.
CC p53), or selectively treating cells expressing mutant protein or cellular
CC protein isoform in a patient heterozygous for (II). The method is useful
CC for treating a disease e.g. haematopoietic disorder such as T or B cell
CC lymphoma, chronic myeloid leukaemia (CML), APL, ALL, NHL and CMML,
CC or a disease characterised by a solid tumour such as papillary thyroid
CC carcinoma, Ewing's sarcoma, melanoma, liposarcoma, rhabdomyosarcoma and
CC synovial sarcoma. The method is also useful for treating viral
CC infections. This represents the DNA sequence of a chromosome aberration
XX
XX Sequence 305 BP; 77 A; 79 C; 77 G; 72 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 25; DB 6; Length 305;
Best Local Similarity 100.0%; Pred. No. 0.0002;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGTACGGGAATGCTGTGGACAGTC 25
Db 112 GGTACGGGAATGCTGTGGACAGTC 88
RESULT 10
AAZ60863/c
ID AAZ60863 standard; DNA; 350 BP.
XX
XX AAZ60863;
XX
XX 16-MAY-2000 (first entry)
XX
XX Region surrounding a bcr-able splice junction.
XX
XX Fusion transcript; translocation; bcr b3 region; abl gene;
XX amplification assay; detection assay; medical diagnosis;
XX clinical monitoring; chimeric RNA; fusion RNA; condition marker;
XX disease marker; cancer; leukemia; ss.
XX
XX Unidentified.
XX
XX WO200005418-A1.
XX
XX 03-FEB-2000.
XX
XX 23-JUL-1999; 99WO-US016832.
XX
XX 23-JUL-1998; 98US-00121239.
XX
XX

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PA (GENP-) GEN-PROBE INC.  
 XX Harvey RC, Eastman PS;  
 XX WPI; 2000-192730/16.  
 DR Novel methods for preparing RNA from biological samples, used for the  
 PT detection and measurement of nucleic acids and fusion nucleic acids.  
 XX Disclosure; Fig 2; 49pp; English.  
 CC The present sequence represents a region surrounding a bcr-able splice  
 CC junction. The specification describes oligonucleotides which are used to  
 CC detect fusion transcripts produced from a translocation between the bcr  
 CC b3 region and the abl gene. The specification also describes a method for  
 CC detecting a fusion nucleic acid (particularly chimeric mRNA species), in  
 CC a biological sample. The method comprises contacting a sample of fusion  
 CC nucleic acid with primers, amplifying the hybridized fusion nucleic acid,  
 CC and detecting the target hybrid. The method is used for the simple and  
 CC rapid preparation of RNA from a biological sample, particularly from the  
 CC cytoplasm of eukaryotic cells, which is suitable for use in an  
 CC amplification and detection assay. The methods are used for the analysis  
 CC and detection of nucleic acids in biological samples. The methods are  
 CC useful in the human medical and veterinary fields, for medical diagnoses  
 CC and clinical monitoring of a patient's response to therapy where a disease  
 CC or medical condition is associated with a particular type and/or level of  
 CC mRNA present in the sample. The methods are also useful for detecting or  
 CC quantifying fusion or chimeric RNA species, and for detecting a  
 CC translocation as a marker for a given condition or disease, e.g.  
 CC translocations associate with cancers, particularly forms of leukemia  
 XX  
 XX Sequence 350 BP; 85 A; 92 C; 89 G; 84 T; 0 U; 0 Other;  
 SQ  
 Query Match 100.0%; Score 25; DB 3; Length 350;  
 Best Local Similarity 100.0%; Pred. No. 0.0002;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GGTCAGCGGAATGCTGTGGACAGTC 25  
 DB 113 GGTCAGCGGAATGCTGTGGACAGTC 89  
 RESULT 11  
 AAS85023/c  
 ID AAS85023 standard; cDNA; 504 BP.  
 XX  
 AC AAS85023;  
 DT 13-FEB-2002 (first entry)  
 DE DNA encoding novel human diagnostic protein #20827.  
 XX Human; chromosome mapping; gene mapping; gene therapy; forensic;  
 KW food supplement; medical imaging; diagnostic; genetic disorder; ss.  
 XX Homo sapiens.  
 OS WO200175067-A2.  
 PN 11-OCT-2001.  
 PD 30-MAR-2001; 2001WO-US008631.  
 XX 31-MAR-2000; 2000US-00540217.  
 PR 23-AUG-2000; 2000US-00649167.  
 XX (HYSE-) HYSEQ INC.  
 PA Drmanac RT, Liu C, Tang YT;  
 XX WPI; 2001-639362/73.  
 DR P-PSDB; ABG20836.  
 XX

PT New isolated polynucleotide and encoded polypeptides, useful in  
 PT diagnostics, forensics, gene mapping, identification of mutations  
 PT responsible for genetic disorders or other traits and to assess  
 PT biodiversity.  
 XX Claim 1; SEQ ID NO 20827; 103pp; English.  
 PS  
 CC The invention relates to isolated polynucleotide (I) and polypeptide (II)  
 CC sequences. (I) is useful as hybridisation probes, polymerase chain  
 CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,  
 CC and in recombinant production of (II). The polynucleotides are also used  
 CC in diagnostics as expressed sequence tags for identifying expressed  
 CC genes. (I) is useful in gene therapy techniques to restore normal  
 CC activity of (II) or to treat disease states involving (II). (II) is  
 CC useful for generating antibodies against it, detecting or quantitating a  
 CC polypeptide in tissue, as molecular weight markers and as a food  
 CC supplement. (II) and its binding partners are useful in medical imaging  
 CC of sites expressing (II). (I) and (II) are useful for treating disorders  
 CC involving aberrant protein expression or biological activity. The  
 CC polypeptide and polynucleotide sequences have applications in  
 CC diagnostics, forensics, gene mapping, identification of mutations  
 CC responsible for genetic disorders or other traits to assess biodiversity  
 CC and to produce other types of data and products dependent on DNA and  
 CC amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic  
 CC coding sequences of the invention. Note: The sequence data for this  
 CC patent did not appear in the printed specification, but was obtained in  
 CC electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 504 BP; 119 A; 122 C; 144 G; 117 T; 0 U; 2 Other;  
 XX  
 Query Match 100.0%; Score 25; DB 5; Length 504;  
 Best Local Similarity 100.0%; Pred. No. 0.0002;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GGTCAGCGGAATGCTGTGGACAGTC 25  
 DB 263 GGTCAGCGGAATGCTGTGGACAGTC 239  
 RESULT 12  
 ACH38242/c  
 ID ACH38242 standard; cDNA; 504 BP.  
 XX  
 AC ACH38242;  
 XX  
 DT 13-OCT-2003 (first entry)  
 DE Human endothelial cell cDNA #6375.  
 XX Human; ss; sequencing by hybridisation; SBH; expressed sequence tag; EST;  
 KW genome mapping; biodiversity; genetic disorder.  
 XX Homo sapiens.  
 OS US2003073623-A1.  
 PN 17-APR-2003.  
 PD 30-JUL-2001; 2001US-00918995.  
 XX 30-JUL-2001; 2001US-00918995.  
 PR (DRMA/) DRMANAC R T.  
 PA (LABA/) LABAT I.  
 PA (STAC/) STACHE-CRAIN B.  
 PA (DICK/) DICKSON M C.  
 PA (JONE/) JONES L W.  
 XX Drmanac RT, Labat I, Stache-Crain B, Dickson MC, Jones LW;  
 XX WPI; 2003-615964/58.  
 XX

PT New polynucleotide sequences obtained from various cDNA libraries, useful  
PT as hybridization probes, as oligomers for PCR, for chromosome and gene  
PT mapping, in the recombinant production of protein, or in generating  
PT antisense DNA or RNA.

XX Claim 1; SEQ ID NO 25454; 44pp; English.

PS The invention relates to an isolated polynucleotide comprising any one of  
XX 38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence was  
CC determined by the technique of SBH (sequencing by hybridisation). Also  
CC included is a purified polypeptide comprising a sequence corresponding to  
CC a reading frame of the novel polynucleotide. The nucleic acid sequences  
CC are useful in diagnostics as expressed sequence tags (EST) for  
CC identifying expressed genes or for physical mapping of the human genome,  
CC in forensics, in assessing biodiversity, or in identifying mutations  
CC responsible for genetic disorders and other traits. The nucleotide  
CC sequences are also useful as hybridisation probes, as oligomers for PCR,  
CC for chromosome and gene mapping, in the recombinant production of  
CC protein, or in generating antisense DNA or RNA. The purified polypeptide  
CC is useful for generating antibodies specific for it. The present sequence  
CC is one of the 38043 isolated cDNA/EST sequences. Note: The sequence data  
CC for this patent did not form part of the printed specification, but was  
CC obtained in electronic format directly from USPTO at  
CC seqdata.uspto.gov/sequence.html?DocID=20030073623

XX Sequence 504 BP; 119 A; 122 C; 144 G; 117 T; 0 U; 2 Other;

Query Match 100.0%; Score 25; DB 8; Length 504;  
Best Local Similarity 100.0%; Pred. No. 0.0002;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTACGCGGAATGCTGTGGACAGTC 25

DB 263 GGTACGCGGAATGCTGTGGACAGTC 239

RESULT 13

ABS73169/c

ID ABS73169 standard; DNA; 561 BP.

AC ABS73169;

DT 04-DEC-2002 (first entry)

DE Human translocation (9: 22) (q34: q11) #1.

XX Chromosome aberration; oncogenic fusion protein; cancer;  
KW Proliferative disease; cellular protein isoform; heat shock protein 90;  
KW HSP-90; rheumatoid arthritis; cancer; haematopoietic disorder;  
KW T cell lymphoma; B cell lymphoma; chronic myeloid leukaemia; CML;  
KW acute myeloid leukaemia; AML; chronic myelomonocytic leukaemia; CMML;  
KW acute lymphoblastic leukaemia; ALL; APL; NHL; solid tumour;  
KW papillary thyroid carcinoma; Ewing's sarcoma; melanoma; liposarcoma;  
KW rhabdomyosarcoma; synovial sarcoma; viral infection; gene; ds.

OS Homo sapiens.

XX WO200269900-A2.

PD 12-SEP-2002.

PF 01-MAR-2002; 2002WO-US006518.

PR 01-MAR-2001; 2001US-0272751P.

XX (CONF-) CONFORMA THERAPEUTICS CORP.

XX Fritz LC, Burrows FJ;

XX WPI; 2002-698710/75.

XX Treating genetically-defined disease associated with chromosomal

PT aberrations yielding oncogenic fusion proteins, e.g. cell proliferative

PT diseases, involves administering an inhibitor of heat shock protein 90.  
XX Disclosure; Page 91-92; 389pp; English.

XX The invention describes a method of treating genetically-defined disease  
CC associated with chromosomal aberrations yielding oncogenic fusion  
CC proteins (I), treating cancerous cells containing (I) in a heterogeneous  
CC cell population, treating proliferative diseases associated with mutant  
CC protein or cellular protein isoforms (II) dependent on heat shock protein  
CC (HSP)-90, or selectively treating cells expressing (II) involving  
CC administering HSP90-inhibitor. The method is useful for treating  
CC genetically-defined disease with chromosomal aberration yielding  
CC oncogenic fusion protein, treating cancerous cells containing fusion  
CC protein in heterogeneous cell population, treating proliferative disease  
CC (e.g. rheumatoid arthritis or cancer) associated with mutant protein or  
CC cellular protein isoform dependent on heat shock protein (HSP)-90 (e.g.  
CC p53), or selectively treating cells expressing mutant protein or cellular  
CC protein isoform in a patient heterozygous for (II). The method is useful  
CC for treating a disease e.g. haematopoietic disorder such as T or B cell  
CC lymphoma, chronic myeloid leukaemia (CML), APL, ALL, NHL and CMML,  
CC or a disease characterised by a solid tumour such as papillary thyroid  
CC carcinoma, Ewing's sarcoma, melanoma, liposarcoma, rhabdomyosarcoma and  
CC synovial sarcoma. The method is also useful for treating viral  
CC infections. This represents the DNA sequence of a chromosome aberration

XX Sequence 561 BP; 134 A; 134 C; 136 G; 157 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 6; Length 561;  
Best Local Similarity 100.0%; Pred. No. 0.0002;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTACGCGGAATGCTGTGGACAGTC 25

DB 108 GGTACGCGGAATGCTGTGGACAGTC 84

RESULT 14

ABS73172/c

ID ABS73172 standard; DNA; 679 BP.

AC ABS73172;

DT 04-DEC-2002 (first entry)

DE DNA encoding human translocation (9: 22) (q34: q11) protein #3.

XX Chromosome aberration; oncogenic fusion protein; cancer;  
KW Proliferative disease; cellular protein isoform; heat shock protein 90;  
KW HSP-90; rheumatoid arthritis; cancer; haematopoietic disorder;  
KW T cell lymphoma; B cell lymphoma; chronic myeloid leukaemia; CML;  
KW acute myeloid leukaemia; AML; chronic myelomonocytic leukaemia; CMML;  
KW acute lymphoblastic leukaemia; ALL; APL; NHL; solid tumour;  
KW papillary thyroid carcinoma; Ewing's sarcoma; melanoma; liposarcoma;  
KW rhabdomyosarcoma; synovial sarcoma; viral infection; gene; ds.

OS Homo sapiens.

XX WO200269900-A2.

PD 12-SEP-2002.

PF 01-MAR-2002; 2002WO-US006518.

PR 01-MAR-2001; 2001US-0272751P.

XX (CONF-) CONFORMA THERAPEUTICS CORP.

XX Fritz LC, Burrows FJ;

XX WPI; 2002-698710/75.

XX P-PSDB; ABG95011.

XX Treating genetically-defined disease associated with chromosomal

PT aberrations yielding oncogenic fusion proteins, e.g. cell proliferative  
 PT diseases, involves administering an inhibitor of heat shock protein 90.  
 XX  
 PS Disclosure; Page 94-95; 389pp; English.  
 XX  
 CC The invention describes a method of treating genetically-defined disease  
 CC associated with chromosomal aberrations yielding oncogenic fusion  
 CC proteins (I), treating cancerous cells containing (I) in a heterogeneous  
 CC cell population, treating proliferative diseases associated with mutant  
 CC protein or cellular protein isoforms (II) dependent on heat shock protein  
 CC (HSP)-90, or selectively treating cells expressing (II) involving  
 CC administering HSP90-inhibitor. The method is useful for treating  
 CC genetically-defined disease with chromosomal aberration yielding  
 CC oncogenic fusion protein, treating cancerous cells containing fusion  
 CC protein in heterogeneous cell population, treating proliferative disease  
 CC (e.g. rheumatoid arthritis or cancer) associated with mutant protein or  
 CC cellular protein isoform dependent on heat shock protein (HSP)-90 (e.g.  
 CC p53), or selectively treating cells expressing mutant protein or cellular  
 CC protein isoform in a patient heterozygous for (II). The method is useful  
 CC for treating a disease e.g. haematopoietic disorder such as T or B cell  
 CC lymphoma, chronic myeloid leukaemia (CML), APL, ALL, NHL and CMWL,  
 CC or a disease characterised by a solid tumour such as papillary thyroid  
 CC carcinoma, Ewing's sarcoma, melanoma, liposarcoma, rhabdomyosarcoma and  
 CC synovial sarcoma. The method is also useful for treating viral  
 CC infections. This represents the DNA sequence of a chromosome aberration  
 XX  
 SQ Sequence 679 BP; 186 A; 165 C; 184 G; 144 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 6; Length 679;  
 Best Local Similarity 100.0%; Pred. No. 0.0002;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTCAGCGGAATGCTGTGGACAGTC 25  
 |||||  
 Db 326 GGTCAGCGGAATGCTGTGGACAGTC 302

RESULT 15  
 ABV29306  
 ID ABV29306 standard; cDNA; 766 BP.  
 XX  
 AC ABV29306;  
 XX  
 DT 16-SEP-2002 (first entry)  
 XX  
 DE Human prostate expression marker cDNA 29297.  
 XX  
 KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;  
 KW pharmacogenomic marker; gene; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200160860-A2.  
 XX  
 PD 23-AUG-2001.  
 XX  
 PF 20-FEB-2001; 2001WO-US005171.  
 XX  
 PR 17-FEB-2000; 2000US-0183319P.  
 PR 16-MAR-2000; 2000US-0189862P.  
 PR 25-MAY-2000; 2000US-0207454P.  
 PR 09-JUN-2000; 2000US-0211314P.  
 PR 18-JUL-2000; 2000US-0219007P.  
 PR 13-DEC-2000; 2000US-0255281P.  
 XX  
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
 XX  
 PI Schlegel R, Endege WO, Monahan JE;  
 XX  
 DR WPI; 2001-662795/76.  
 XX  
 PT Novel isolated nucleic acid molecule associated with cancerous state of  
 PT prostate cells and correlating with presence of prostate cancer, useful

PT for detecting presence of prostate cancer, stage of prostate cancer.  
 XX  
 PS Claim 1; Page 6267; 11750pp; English.  
 XX  
 CC The invention relates to an isolated nucleic acid molecule (I) comprising  
 CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the  
 CC specification or its complement. (I) is useful for: (a) assessing whether  
 CC a patient is afflicted with prostate cancer; (b) monitoring the  
 CC progression of prostate cancer in a patient; (c) assessing the efficacy  
 CC of a test compound to inhibit prostate cancer in a patient; (d) assessing  
 CC the efficacy of a therapy for inhibiting prostate cancer in a patient;  
 CC (e) selecting a composition for inhibiting prostate cancer in a patient;  
 CC (f) assessing the prostate cell carcinogenic potential of a compound; (g)  
 CC determining whether prostate cancer has metastasized in a patient; (h)  
 CC assessing the aggressiveness or indolence of prostate cancer in a patient  
 CC ; (I) is also useful as a pharmacodynamic or pharmacogenomic marker  
 XX  
 SQ Sequence 766 BP; 166 A; 237 C; 193 G; 170 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 5; Length 766;  
 Best Local Similarity 100.0%; Pred. No. 0.0002;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTCAGCGGAATGCTGTGGACAGTC 25  
 |||||  
 Db 529 GGTCAGCGGAATGCTGTGGACAGTC 553

Search completed: May 26, 2004, 16:52:17  
 Job time : 111.497 secs



GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: May 26, 2004, 16:02:51 ; Search time 21.0702 Seconds  
(without alignments)  
658.454 Million cell updates/sec

Title: US-09-121-239-11

Perfect score: 25  
Sequence: 1 GGTACGCGAATGCTGTGCACAGTC 25

Scoring table: OLIGO NUC  
Gapop 60.0 , Gapext 60.0

Searched: 682709 seqs, 277475446 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents NA.\*  
1: /cgn2\_6/prodata/2/ina/5A-COMB.seq.\*  
2: /cgn2\_6/prodata/2/ina/5B-COMB.seq.\*  
3: /cgn2\_6/prodata/2/ina/6A-COMB.seq.\*  
4: /cgn2\_6/prodata/2/ina/6B-COMB.seq.\*  
5: /cgn2\_6/prodata/2/ina/PCTUS-COMB.seq.\*  
6: /cgn2\_6/prodata/2/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	25	100.0	56	1	US-07-940-652-17
C 2	25	100.0	56	1	US-08-255-553-17
C 3	25	100.0	1078	1	US-09-310-842-1
C 4	24	96.0	26	1	US-08-363-233B-6
C 5	18	72.0	22	1	US-08-152-621-11
C 6	18	72.0	22	5	PCT-US92-05035-11
C 7	18	72.0	62	3	US-08-448-446B-1
C 8	18	72.0	81	3	US-08-448-446B-2
C 9	18	72.0	257	1	US-08-152-621-1
C 10	18	72.0	257	1	US-08-306-691B-36
C 11	18	72.0	257	5	PCT-US92-05035-1
C 12	16	64.0	28	3	US-09-341-955-2
C 13	16	64.0	28	4	US-09-779-881-2
C 14	16	64.0	864	4	US-09-489-039A-2414
C 15	14	56.0	61	3	US-08-448-446B-19
C 16	14	56.0	363	3	US-08-905-223-206
C 17	14	56.0	500	4	US-09-621-976-9874
C 18	14	56.0	930	4	US-09-252-991A-11373
C 19	14	56.0	981	4	US-09-252-991A-11296
C 20	14	56.0	1094	4	US-09-280-116-243
C 21	14	56.0	1197	4	US-09-252-991A-6737
C 22	14	56.0	1269	4	US-09-149-476-143
C 23	14	56.0	1272	4	US-09-252-991A-6952
C 24	14	56.0	1361	4	US-09-280-116-197
C 25	14	56.0	1427	4	US-09-907-794A-152
C 26	14	56.0	1427	4	US-09-905-125A-152
C 27	14	56.0	1427	4	US-09-902-775A-152

28	14	56.0	1620	1	US-07-616-022C-9	Sequence 9, Appli
29	14	56.0	1869	4	US-09-406-045-2	Sequence 2, Appli
C 30	14	56.0	2346	4	US-09-252-991A-6782	Sequence 6782, Ap
31	14	56.0	3041	4	US-09-339-159B-31	Sequence 31, Appli
32	14	56.0	36519	3	US-08-923-137-2	Sequence 2, Appli
C 33	14	56.0	786431	4	US-09-751-389-3	Sequence 3, Appli
34	13	52.0	277	4	US-09-313-294A-1791	Sequence 1791, Ap
35	13	52.0	288	4	US-09-134-000C-2182	Sequence 2182, Ap
C 36	13	52.0	396	4	US-09-621-976-16576	Sequence 16576, A
C 37	13	52.0	403	4	US-09-621-976-16577	Sequence 16577, A
C 38	13	52.0	437	4	US-09-221-017B-243	Sequence 243, App
39	13	52.0	444	4	US-09-252-991A-6828	Sequence 6828, Ap
C 40	13	52.0	458	4	US-09-621-976-16578	Sequence 16578, A
41	13	52.0	477	4	US-09-489-039A-1314	Sequence 1314, Ap
42	13	52.0	489	4	US-09-252-991A-12619	Sequence 12619, A
C 43	13	52.0	504	3	US-09-328-111-120	Sequence 120, App
C 44	13	52.0	792	4	US-09-489-039A-1358	Sequence 1358, Ap
45	13	52.0	857	4	US-09-660-176-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1  
US-07-940-652-17/c  
; Sequence 17, Application US/07940652  
; Patent No. 5424413  
; GENERAL INFORMATION:  
; APPLICANT: James J. Hogan et al.  
; TITLE OF INVENTION: BRANCHED NUCLEIC ACID PROBES  
; NUMBER OF SEQUENCES: 31  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 611 West Sixth Street  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: USA  
; ZIP: 90017  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: IBM P.C. DOS Version 3.30  
; SOFTWARE: WordPerfect (Version 5.1)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/940,652  
; FILING DATE: 19920904  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/07/827,021  
; FILING DATE: 22-JAN-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Warburg, Richard J.  
; REGISTRATION NUMBER: 32,327  
; REFERENCE/DOCKET NUMBER: 199/201  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (213) 489-1600  
; TELEFAX: (213) 955-0440  
; TELEX: 67-3510  
; INFORMATION FOR SEQ ID NO: 17:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 56  
; TYPE: NUCLEIC ACID  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-07-940-652-17  
Query Match 100.0%; Score 25; DB 1; Length 56;  
Best Local Similarity 100.0%; Pred. No. 6.5e-06;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGTACGCGAATGCTGTGCACAGTC 25  
DB 27 GGTACGCGAATGCTGTGCACAGTC 3

## RESULT 2

US-08-255-553-17/c  
; Sequence 17, Application US/08255553  
; Patent No. 5451503  
; GENERAL INFORMATION:  
; APPLICANT: James J. Hogan et al.  
; TITLE OF INVENTION: BRANCHED NUCLEIC ACID PROBES  
; NUMBER OF SEQUENCES: 31  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 611 West Sixth Street  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: USA  
; ZIP: 90017  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: IBM P.C. DOS Version 3.30  
; SOFTWARE: WordPerfect (Version 5.1)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/255,553  
; FILING DATE: 07-JUN-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/07/940,652  
; FILING DATE: 04-SEP-1992  
; APPLICATION NUMBER: US/07/827,021  
; FILING DATE: 22-JAN-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Warburg, Richard J.  
; REGISTRATION NUMBER: 32,327  
; REFERENCE/DOCKET NUMBER: 199/201  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (213) 489-1600  
; TELEFAX: (213) 955-0440  
; TELEX: 67-3510  
; INFORMATION FOR SEQ ID NO: 17:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 56  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-255-553-17

Query Match 100.0%; Score 25; DB 1; Length 56;  
Best Local Similarity 100.0%; Pred. No. 6.5e-06;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTCAGCGGAATGCTGTGGACATC 25  
Db 27 GGTCAGCGGAATGCTGTGGACATC 3

## RESULT 3

US-09-310-842-1/c  
; Sequence 1, Application US/09310842A  
; Patent No. 6451593  
; GENERAL INFORMATION:  
; APPLICANT: Wittig, Prof. Burghardt  
; APPLICANT: Junghans, Claas  
; TITLE OF INVENTION: Design Principle for Constructing Expression Constructs for Gene  
; FILE REFERENCE: XI 597/99  
; CURRENT APPLICATION NUMBER: US/09/310,842A  
; CURRENT FILING DATE: 1999-05-12  
; EARLIER APPLICATION NUMBER: DE 196 48 625.4  
; EARLIER FILING DATE: 1996-11-13  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 1

; LENGTH: 1078  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; NAME/KEY: gene  
; LOCATION: (1)..(1078)  
; OTHER INFORMATION: bcr3=abl2; Oligo DNA Dumbbell  
; FEATURE:  
; NAME/KEY: misc.binding  
; LOCATION: (1)..(2)  
; OTHER INFORMATION: intramolecular binding site; the T-nucleotides at position 1 to  
; OTHER INFORMATION: 2 can be modified with amino or caroxy features  
; FEATURE:  
; NAME/KEY: misc.binding  
; LOCATION: (1077)..(1078)  
; OTHER INFORMATION: intramolecular binding site; the T-nucleotides at position 1077  
; OTHER INFORMATION: to 1078 can be modified with amino or caroxy features  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Strandness: both; nucleic  
; OTHER INFORMATION: acid (linear), hypothetical: No. 6451593 anti-sense: No  
US-09-310-842-1

Query Match 100.0%; Score 25; DB 4; Length 1078;  
Best Local Similarity 100.0%; Pred. No. 6.5e-06;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTCAGCGGAATGCTGTGGACATC 25  
Db 686 GGTCAGCGGAATGCTGTGGACATC 662

## RESULT 4

US-08-363-233B-6/c  
; Sequence 6, Application US/08363233B  
; Patent No. 5714383  
; GENERAL INFORMATION:  
; APPLICANT: Thompson, James D.  
; TITLE OF INVENTION: METHOD AND REAGENT FOR TREATING CHRONIC  
; TITLE OF INVENTION: MYELOGENOUS LEUKEMIA  
; NUMBER OF SEQUENCES: 39  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 633 West Fifth Street  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 90071-2066  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; MEDIUM TYPE: storage  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: IBM P.C. DOS 5.0  
; SOFTWARE: FastSeq for Windows 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/363,233B  
; FILING DATE: December 23, 1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; PRIOR APPLICATION DATA: including application  
; PRIOR APPLICATION DATA: described below:  
; APPLICATION NUMBER: 07/882,822  
; FILING DATE: May 14, 1992  
; APPLICATION NUMBER: 08/193,922  
; FILING DATE: February 7, 1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Warburg, Richard J.  
; REGISTRATION NUMBER: 32,327  
; REFERENCE/DOCKET NUMBER: 209/165  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (213) 489-1600  
; TELEFAX: (213) 955-0440  
; TELEX: 67-3510

; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 26 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-363-233B-6

Query Match 96.0%; Score 24; DB 1; Length 26;  
Best Local Similarity 100.0%; Pred. No. 2.5e-05;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GTCACGGGAATGCTGTGACAGTC 25  
DB 26 GTCACGGGAATGCTGTGACAGTC 3

## RESULT 5

US-08-152-621-11/c  
; Sequence 11, Application US/08152621  
; Patent No. 5652222

## GENERAL INFORMATION:

; APPLICANT: Calabretta, Bruno  
; APPLICANT: Gewirtz, Alan M.  
; TITLE OF INVENTION: Selective Inhibition of  
; TITLE OF INVENTION: Leukemic Cell Proliferation by bcr-abl  
; TITLE OF INVENTION: Antisense Oligonucleotides  
; NUMBER OF SEQUENCES: 34  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SEIDEL, GONDA, LAVORGNA  
; ADDRESSEE: & MONACO, P.C.  
; STREET: 1900 Two Penn Center  
; CITY: Philadelphia  
; STATE: Pennsylvania  
; COUNTRY: U.S.A.  
; ZIP: 19102

## COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb  
; COMPUTER: IBM PS/2  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: WordPerfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/152,621  
; FILING DATE: No. 5652222ember 15, 1993  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/718,302  
; FILING DATE: June 18, 1991

## ATTORNEY/AGENT INFORMATION:

; NAME: Monaco, Daniel A.  
; REGISTRATION NUMBER: 30,480  
; REFERENCE/DOCKET NUMBER: 6056-120 (CT.) 1

## TELECOMMUNICATION INFORMATION:

; TELEPHONE: (215) 568-8383  
; TELEFAX: (215) 568-5549  
; TELEX: No. 5652222e

## INFORMATION FOR SEQ ID NO: 11:

; SEQUENCE CHARACTERISTICS:  
; LENGTH: 22 Nucleotides  
; TYPE: nucleic acid  
; STRANDEDNESS: double stranded  
; TOPOLOGY: linear  
US-08-152-621-11

Query Match 72.0%; Score 18; DB 1; Length 22;  
Best Local Similarity 100.0%; Pred. No. 0.082;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTACGGGAATGCTGTG 18  
DB 18 GGTACGGGAATGCTGTG 1

## RESULT 6

PCT-US92-05035-11/c  
; Sequence 11, Application PC/TUS9205035  
; GENERAL INFORMATION:

; APPLICANT: Calabretta, Bruno  
; APPLICANT: Gewirtz, Alan M.  
; TITLE OF INVENTION: Selective Inhibition of  
; TITLE OF INVENTION: Leukemic Cell Proliferation by bcr-abl  
; TITLE OF INVENTION: Antisense Oligonucleotides  
; NUMBER OF SEQUENCES: 34  
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Temple University - Of The Common-  
; ADDRESSEE: wealth System of Higher Education  
; STREET: 406 University Services Building  
; CITY: Philadelphia  
; STATE: Pennsylvania  
; COUNTRY: U.S.A.  
; ZIP: 19122

## COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb  
; COMPUTER: IBM PS/2  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: WordPerfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US92/05035  
; FILING DATE: 19920615  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/718,302  
; FILING DATE: June 18, 1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/869,911  
; FILING DATE: April 14, 1991  
; ATTORNEY/AGENT INFORMATION:

## NAME: Monaco, Daniel A.

; REGISTRATION NUMBER: 30,480  
; REFERENCE/DOCKET NUMBER: 6056-120 (CIP) 1

## TELECOMMUNICATION INFORMATION:

; TELEPHONE: (215) 568-8383  
; TELEFAX: (215) 568-5549  
; TELEX: None

## INFORMATION FOR SEQ ID NO: 11:

; SEQUENCE CHARACTERISTICS:  
; LENGTH: 22 Nucleotides  
; TYPE: NUCLEIC ACID  
; STRANDEDNESS: double stranded  
; TOPOLOGY: linear  
PCT-US92-05035-11

## Query Match

Best Local Similarity 100.0%; Pred. No. 0.082;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTACGGGAATGCTGTG 18  
DB 18 GGTACGGGAATGCTGTG 1

## RESULT 7

US-08-448-446B-1/c  
; Sequence 1, Application US/08448446B  
; Patent No. 6080851

## GENERAL INFORMATION:

; APPLICANT: Pachuk et al.  
; TITLE OF INVENTION: Compounds and Methods for the Treatment  
; TITLE OF INVENTION: of Leukemias  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Woodcock Washburn  
; ADDRESSEE: Kurtz Mackiewicz & No. 6080851ris  
; STREET: One Liberty Place - 46th Floor  
; CITY: Philadelphia  
; STATE: PA

;/ COUNTRY: USA  
;/ ZIP: 19103  
;/ COMPUTER READABLE FORM:  
;/ MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE  
;/ COMPUTER: IBM PS/2  
;/ OPERATING SYSTEM: PC-DOS  
;/ SOFTWARE: WORDPERFECT 5.1  
;/ CURRENT APPLICATION DATA:  
;/ APPLICATION NUMBER: US/08/448,446B  
;/ FILING DATE: July 10, 1995  
;/ CLASSIFICATION: 435  
;/ PRIOR APPLICATION DATA:  
;/ APPLICATION NUMBER: 07/989,852  
;/ FILING DATE: December 4, 1992  
;/ ATTORNEY/AGENT INFORMATION:  
;/ NAME: Doreen Yanko Trujillo  
;/ REGISTRATION NUMBER: 35,719  
;/ REFERENCE/DOCKET NUMBER: APOL-0020  
;/ TELECOMMUNICATION INFORMATION: C  
;/ TELEPHONE: (215) 568-3100  
;/ TELEFAX: (215) 568-3439  
;/ INFORMATION FOR SEQ ID NO: 1:  
;/ SEQUENCE CHARACTERISTICS:  
;/ LENGTH: 62  
;/ TYPE: Nucleic Acid  
;/ STRANDEDNESS: Single  
;/ TOPOLOGY: Linear  
;/ ANTI-SENSE: No  
;/ US-08-448-446B-1

Query Match 72.0%; Score 18; DB 3; Length 62;  
Best Local Similarity 100.0%; Pred. No. 0.082;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTCAGCGGAATGCTGTG 18  
||| ||||| ||||| |||||  
DB 18 GGTCAGCGGAATGCTGTG 1

RESULT 8  
US-08-448-446B-2  
; Sequence 2, Application US/08448446B  
; Patent No. 6080851  
; GENERAL INFORMATION:  
; APPLICANT: Pachuk et al.  
; TITLE OF INVENTION: Compounds and Methods for the Treatment  
; OF LEUKEMIA  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Woodcock Washburn  
; ADDRESSEE: Kurtz Mackiewicz & No. 6080851ris  
; STREET: One Liberty Place - 46th Floor  
; CITY: Philadelphia  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19103  
;/ COMPUTER READABLE FORM:  
;/ MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE  
;/ COMPUTER: IBM PS/2  
;/ OPERATING SYSTEM: PC-DOS  
;/ SOFTWARE: WORDPERFECT 5.1  
;/ CURRENT APPLICATION DATA:  
;/ APPLICATION NUMBER: US/08/448,446B  
;/ FILING DATE: July 10, 1995  
;/ CLASSIFICATION: 435  
;/ PRIOR APPLICATION DATA:  
;/ APPLICATION NUMBER: 07/989,852  
;/ FILING DATE: December 4, 1992  
;/ ATTORNEY/AGENT INFORMATION:  
;/ NAME: Doreen Yanko Trujillo  
;/ REGISTRATION NUMBER: 35,719  
;/ REFERENCE/DOCKET NUMBER: APOL-0020  
;/ TELECOMMUNICATION INFORMATION: C

;/ TELEPHONE: (215) 568-3100  
;/ TELEFAX: (215) 568-3439  
;/ INFORMATION FOR SEQ ID NO: 2:  
;/ SEQUENCE CHARACTERISTICS:  
;/ LENGTH: 81  
;/ TYPE: Nucleic Acid  
;/ STRANDEDNESS: Single  
;/ TOPOLOGY: Linear  
;/ ANTI-SENSE:  
;/ US-08-448-446B-2  
  
Query Match 72.0%; Score 18; DB 3; Length 81;  
Best Local Similarity 77.8%; Pred. No. 0.082;  
Matches 14; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTCAGCGGAATGCTGTG 18  
||| ||||| ||||| |||||  
DB 64 GGTCAGCGGAATGCTGTG 81

RESULT 9  
US-08-152-621-1/c  
; Sequence 1, Application US/08152621  
; Patent No. 5652222  
; GENERAL INFORMATION:  
; APPLICANT: Calabretta, Bruno  
; APPLICANT: Gewirtz, Alan M.  
; TITLE OF INVENTION: Selective Inhibition of  
; CELL GROWTH  
; TITLE OF INVENTION: Leukemic Cell Proliferation by bcr-abl  
; TITLE OF INVENTION: Antisense Oligonucleotides  
; NUMBER OF SEQUENCES: 34  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SEIDEL, GONDA, LAVORGNA  
; ADDRESSEE: & MONACO, P.C.  
; STREET: 1800 Two Penn Center  
; CITY: Philadelphia  
; STATE: Pennsylvania  
; COUNTRY: U.S.A.  
; ZIP: 19102

;/ COMPUTER READABLE FORM:  
;/ MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb  
;/ COMPUTER: IBM PS/2  
;/ OPERATING SYSTEM: MS-DOS  
;/ SOFTWARE: WordPerfect 5.1  
;/ CURRENT APPLICATION DATA:  
;/ APPLICATION NUMBER: US/08/152,621  
;/ FILING DATE: No. 5652222ember 15, 1993  
;/ CLASSIFICATION: 514  
;/ PRIOR APPLICATION DATA:  
;/ APPLICATION NUMBER: 07/718,302  
;/ FILING DATE: June 18, 1991  
;/ ATTORNEY/AGENT INFORMATION:  
;/ NAME: Monaco, Daniel A.  
;/ REGISTRATION NUMBER: 30,480  
;/ REFERENCE/DOCKET NUMBER: 6056-120 (CT.) 1  
;/ TELECOMMUNICATION INFORMATION:  
;/ TELEPHONE: (215) 568-8383  
;/ TELEFAX: (215) 568-5549  
;/ TELEX: No. 5652222e  
;/ INFORMATION FOR SEQ ID NO: 1:  
;/ SEQUENCE CHARACTERISTICS:  
;/ LENGTH: 257 Nucleotides  
;/ TYPE: nucleic acid  
;/ STRANDEDNESS: single stranded  
;/ TOPOLOGY: linear  
;/ US-08-152-621-1

Query Match 72.0%; Score 18; DB 1; Length 257;  
Best Local Similarity 100.0%; Pred. No. 0.082;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTCAGCGGAATGCTGTG 18  
||| ||||| ||||| |||||

Db 18 GGTACGCGGAATGCTGTG 1

## RESULT 10

US-08-306-691B-36/c  
; Sequence 36, Application US/08306691B  
; Patent No. 5734039

## GENERAL INFORMATION:

APPLICANT: Calabretta, Bruno

APPLICANT: Skorski, Tomasz

TITLE OF INVENTION: ANTISENSE

TITLE OF INVENTION: OLIGONUCLEOTIDES TARGETING COOPERATING ONCOGENES

NUMBER OF SEQUENCES: 55

## CORRESPONDENCE ADDRESS:

ADDRESSEE: Seidel, Gonda, Lavorigna & Monaco, P.C.

STREET: Two Penn Center, Suite 1800

CITY: Philadelphia

STATE: Pennsylvania

COUNTRY: U.S.A.

ZIP: 19102

## COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb

COMPUTER: IBM PS/2

OPERATING SYSTEM: MS-DOS

SOFTWARE: WordPerfect 5.1

## CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/306,691B

FILING DATE: September 15, 1994

CLASSIFICATION: 514

## PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Monaco, Daniel A.

REGISTRATION NUMBER: 30,480

REFERENCE/DOCKET NUMBER: 8321-8

## TELECOMMUNICATION INFORMATION:

TELEPHONE: (215) 568-8383

TELEFAX: (215) 568-5549

TELEX: No. 5734039e

INFORMATION FOR SEQ ID NO: 36:

## SEQUENCE CHARACTERISTICS:

LENGTH: 257 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-306-691B-36

Query Match 72.0%; Score 18; DB 1; Length 257;

Best Local Similarity 100.0%; Pred. No. 0.082;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTACGCGGAATGCTGTG 18

Db 18 GGTACGCGGAATGCTGTG 1

## RESULT 11

PCT-US92-05035-1/c

; Sequence 1, Application PC/TUS9205035

## GENERAL INFORMATION:

APPLICANT: Calabretta, Bruno

APPLICANT: Gewirtz, Alan M.

TITLE OF INVENTION: Selective Inhibition of

TITLE OF INVENTION: Leukemic Cell Proliferation by bcr-abl

TITLE OF INVENTION: Antisense Oligonucleotides

NUMBER OF SEQUENCES: 34

## CORRESPONDENCE ADDRESS:

ADDRESSEE: Temple University - Of The Common-

ADDRESSEE: wealth System of Higher Education

STREET: 406 University Services Building

CITY: Philadelphia

STATE: Pennsylvania

COUNTRY: U.S.A.  
ZIP: 19122

## COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb

COMPUTER: IBM PS/2

OPERATING SYSTEM: MS-DOS

SOFTWARE: WordPerfect 5.1

## CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US92/05035

FILING DATE: 19920615

CLASSIFICATION: 514

## PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/718,302

FILING DATE: June 18, 1991

## PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/869,911

FILING DATE: April 14, 1991

## ATTORNEY/AGENT INFORMATION:

NAME: Monaco, Daniel A.

REGISTRATION NUMBER: 30,480

REFERENCE/DOCKET NUMBER: 6056-120 (CIP) 1

## TELECOMMUNICATION INFORMATION:

TELEPHONE: (215) 568-8383

TELEFAX: (215) 568-5549

TELEX: None

INFORMATION FOR SEQ ID NO: 1:

## SEQUENCE CHARACTERISTICS:

LENGTH: 257 Nucleotides

TYPE: NUCLEIC ACID

STRANDEDNESS: single stranded

TOPOLOGY: linear

PCT-US92-05035-1

Query Match 72.0%; Score 18; DB 5; Length 257;

Best Local Similarity 100.0%; Pred. No. 0.082;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTACGCGGAATGCTGTG 18

Db 18 GGTACGCGGAATGCTGTG 1

## RESULT 12

US-09-341-955-2

; Sequence 2, Application US/09341955

; Patent No. 6251690

## GENERAL INFORMATION:

APPLICANT: Kulmala, Sakari

APPLICANT: Ala-Kleme, Timo

APPLICANT: Eskola, Jarkko

APPLICANT: Korpela, Timo

TITLE OF INVENTION: ELECTRICAL EXCITATION OF LABEL SUBSTANCES AT COATED

TITLE OF INVENTION: ELECTRODES

FILE REFERENCE: TUR-080

CURRENT APPLICATION NUMBER: US/09/341,955

CURRENT FILING DATE: 1999-07-21

EARLIER APPLICATION NUMBER: PCT/FI98/00114

EARLIER FILING DATE: 1999-02-10

NUMBER OF SEQ ID NOS: 2

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 2

LENGTH: 28

TYPE: DNA

ORGANISM: Artificial Sequence

## FEATURE:

OTHER INFORMATION: Description of Artificial Sequence:

OTHER INFORMATION: oligonucleotide containing an amino group

US-09-341-955-2

Query Match

Best Local Similarity 64.0%; Score 16; DB 3; Length 28;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTCAGCGGAATGCTG 16  
|||||  
Db 13 GGTCAGCGGAATGCTG 28

RESULT 13

US-09-779-881-2  
; Sequence 2, Application US/09779881  
; Patent No. 6645776  
; GENERAL INFORMATION:  
; APPLICANT: Kulmala, Sakari  
; APPLICANT: Ala-Kleme, Timo  
; APPLICANT: Eskola, Jarkko  
; APPLICANT: Korpela, Timo  
; TITLE OF INVENTION: ELECTRICAL EXCITATION OF LABEL SUBSTANCES AT COATED  
; TITLE OF INVENTION: ELECTRODES  
; FILE REFERENCE: TUR-080  
; CURRENT APPLICATION NUMBER: US/09/779,881  
; CURRENT FILING DATE: 2001-02-09  
; PRIOR APPLICATION NUMBER: 09/341,955  
; PRIOR FILING DATE: 1999-07-21  
; PRIOR APPLICATION NUMBER: PCT/FI98/00114  
; PRIOR FILING DATE: 1999-02-10  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 28  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:  
; OTHER INFORMATION: oligonucleotide containing an amino group

US-09-779-881-2  
Query Match 64.0%; Score 16; DB 4; Length 28;  
Best Local Similarity 100.0%; Pred. No. 1.2;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGTCAGCGGAATGCTG 16  
|||||  
Db 13 GGTCAGCGGAATGCTG 28

RESULT 14

US-09-489-039A-2414/C  
; Sequence 2414, Application US/09489039A  
; Patent No. 6610836  
; GENERAL INFORMATION:  
; APPLICANT: Gary Breton et. al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA  
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 2709.2004001  
; CURRENT APPLICATION NUMBER: US/09/489,039A  
; CURRENT FILING DATE: 2000-01-27  
; PRIOR APPLICATION NUMBER: US 60/117,747  
; PRIOR FILING DATE: 1999-01-29  
; NUMBER OF SEQ ID NOS: 14342  
; SEQ ID NO 2414  
; LENGTH: 864  
; TYPE: DNA  
; ORGANISM: Klebsiella pneumoniae  
US-09-489-039A-2414

Query Match 64.0%; Score 16; DB 4; Length 864;  
Best Local Similarity 100.0%; Pred. No. 1.2;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 3 TCAGCGGAATGCTGTG 18  
|||||  
Db 694 TCAGCGGAATGCTGTG 679

RESULT 15

US-08-448-446B-19  
; Sequence 19, Application US/08448446B  
; Patent No. 6080851  
; GENERAL INFORMATION:  
; APPLICANT: Pachuk et al.  
; TITLE OF INVENTION: Compounds and Methods for the Treatment  
; TITLE OF INVENTION: of Leukemias  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Woodcock Washburn  
; ADDRESSEE: Kurtz Mackiewicz & No. 6080851ris  
; STREET: One Liberty Place - 46th Floor  
; CITY: Philadelphia  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19103  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE  
; COMPUTER: IBM PS/2  
; OPERATING SYSTEM: PC-DOS  
; SOFTWARE: WORDPERFECT 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/448,446B  
; FILING DATE: July 10, 1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/989,852  
; FILING DATE: December 4, 1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Doreen Yanko Trujillo  
; REGISTRATION NUMBER: 35,719  
; REFERENCE/DOCKET NUMBER: APOL-0020  
; TELECOMMUNICATION INFORMATION: C  
; TELEPHONE: (215) 568-3100  
; TELEFAX: (215) 568-3439  
; INFORMATION FOR SEQ ID NO: 19:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 61  
; TYPE: Nucleic Acid  
; STRANDEDNESS: Single  
; TOPOLOGY: Linear  
; ANTI-SENSE:  
US-08-448-446B-19

Query Match 56.0%; Score 14; DB 3; Length 61;  
Best Local Similarity 100.0%; Pred. No. 18;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGTCAGCGGAATGC 14  
|||||  
Db 48 GGTCAGCGGAATGC 61

Search completed: May 27, 2004, 02:25:12  
Job time : 22.0702 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: May 27, 2004, 11:30:47 ; Search time 131.564 Seconds  
(without alignments)  
864.392 Million cell updates/sec

Title: US-09-121-239-11

Perfect score: 25  
Sequence: 1 GGTACCGGATGCTGTGCAGATC 25

Scoring table: OLIGO NUC  
Gapop 60.0 , Gapext 60.0

Searched: 2960401 seqs, 2274450654 residues

Word size : 0

Total number of hits satisfying chosen parameters: 5920802

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published Applications NA.\*

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- 3: /cgn2\_6/prodata/2/pubpna/US06\_NEW\_PUB.seq.\*
- 4: /cgn2\_6/prodata/2/pubpna/US06\_PUBCOMB.seq.\*
- 5: /cgn2\_6/prodata/2/pubpna/US07\_NEW\_PUB.seq.\*
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- 10: /cgn2\_6/prodata/2/pubpna/US09B\_PUBCOMB.seq.\*
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- 12: /cgn2\_6/prodata/2/pubpna/US09\_NEW\_PUB.seq.\*
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- 14: /cgn2\_6/prodata/2/pubpna/US10A\_PUBCOMB.seq.\*
- 15: /cgn2\_6/prodata/2/pubpna/US10B\_PUBCOMB.seq.\*
- 16: /cgn2\_6/prodata/2/pubpna/US10C\_PUBCOMB.seq.\*
- 17: /cgn2\_6/prodata/2/pubpna/US10\_NEW\_PUB.seq.\*
- 18: /cgn2\_6/prodata/2/pubpna/US60\_NEW\_PUB.seq.\*
- 19: /cgn2\_6/prodata/2/pubpna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	25	100.0	504	10	US-09-918-995-25454
C 2	25	100.0	542	9	US-09-796-692-8117
C 3	25	100.0	542	15	US-10-040-862-8117
C 4	25	100.0	542	16	US-10-057-475B-8117
C 5	25	100.0	542	16	US-10-154-884B-8117
C 6	25	100.0	596	9	US-09-796-692-8967
C 7	25	100.0	596	15	US-10-040-862-8967
C 8	25	100.0	596	16	US-10-057-475B-8967
C 9	25	100.0	596	16	US-10-154-884B-8967
C 10	25	100.0	1078	15	US-10-228-811-1
C 11	25	100.0	4739	9	US-09-954-531-586
C 12	25	100.0	4739	13	US-10-193-651-22
C 13	17	68.0	3664	15	US-10-128-714-206
C 14	17	68.0	3750	15	US-10-128-714-5206

Sequence 2, Appli	28	9	US-09-779-881-2
Sequence 4649, Ap	285	11	US-09-864-408A-4649
Sequence 9070, Ap	16	16	64.0
Sequence 8116, Ap	17	15	60.0
Sequence 8143, Ap	18	15	60.0
Sequence 39879, A	19	15	60.0
Sequence 39128, A	20	15	60.0
Sequence 39497, A	21	15	60.0
Sequence 133, Ap	22	15	60.0
Sequence 25393, A	23	15	60.0
Sequence 2109, Ap	24	15	60.0
Sequence 495, App	25	15	60.0
Sequence 5495, Ap	26	15	60.0
Sequence 988, App	27	15	60.0
Sequence 9, Appli	28	15	60.0
Sequence 1953, Ap	29	14	56.0
Sequence 1953, Ap	30	14	56.0
Sequence 1953, Ap	31	14	56.0
Sequence 1953, Ap	32	14	56.0
Sequence 7, Appli	33	14	56.0
Sequence 149, App	34	14	56.0
Sequence 156, App	35	14	56.0
Sequence 156, App	36	14	56.0
Sequence 156, App	37	14	56.0
Sequence 156, App	38	14	56.0
Sequence 2118, Ap	39	14	56.0
Sequence 68, Appli	40	14	56.0
Sequence 14682, A	41	14	56.0
Sequence 9876, Ap	42	14	56.0
Sequence 38733, A	43	14	56.0
Sequence 38, Appli	44	14	56.0
Sequence 3547, Ap	45	14	56.0

## ALIGNMENTS

### RESULT 1

US-09-918-995-25454/c  
; Sequence 25454, Application US/09918995  
; Publication No. US20030073623A1  
; GENERAL INFORMATION:  
; APPLICANT: Hyseq, Inc.  
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED  
; FILE REFERENCE: 20411-756  
; CURRENT APPLICATION NUMBER: US/09/918,995  
; CURRENT FILING DATE: 2001-07-30  
; PRIOR APPLICATION NUMBER: US/09/235,076  
; PRIOR FILING DATE: 1999-01-20  
; NUMBER OF SEQ ID NOS: 38054  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 25454  
; LENGTH: 504  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1)..(504)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-918-995-25454

Query Match 100.0%; Score 25; DB 10; Length 504;  
Best Local Similarity 100.0%; Pred. No. 2.6e-05;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTACCGGATGCTGTGCAGATC 25

Db 263 GGTACCGGATGCTGTGCAGATC 239

### RESULT 2

US-09-796-692-8117/c  
; Sequence 8117, Application US/09796692

```

; Publication No. US20020198362A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY
; TITLE OF INVENTION: HEMATOLOGICAL MALIGNANCIES
; FILE REFERENCE: 2077.001200
; CURRENT APPLICATION NUMBER: US/09/796,692
; CURRENT FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/222,903
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 60/223,416
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: 60/223,378
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: 60/222,903
; PRIOR FILING DATE: 2001-03-01
; NUMBER OF SEQ ID NOS: 9597
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8117
; LENGTH: 542
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-796-692-8117

Query Match 100.0%; Score 25; DB 9; Length 542;
Best Local Similarity 100.0%; Pred. No. 2.6e-05;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTCAGCGGAATGCTGTGGACAGTC 25
Db 457 GGTCAGCGGAATGCTGTGGACAGTC 433

RESULT 3
US-10-040-862-8117/c
; Sequence 8117, Application US/10040862
; Publication No. US20030078396A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; TITLE OF INVENTION: Hematological Malignancies
; FILE REFERENCE: 014058-01352005
; CURRENT APPLICATION NUMBER: US/10/040,862
; CURRENT FILING DATE: 2001-11-06
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303

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; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: US 60/223,416
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: US 60/223,378
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: US 09/796,692
; NUMBER OF SEQ ID NOS: 10467
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8117
; LENGTH: 542
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-040-862-8117

Query Match 100.0%; Score 25; DB 15; Length 542;
Best Local Similarity 100.0%; Pred. No. 2.6e-05;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTCAGCGGAATGCTGTGGACAGTC 25
Db 457 GGTCAGCGGAATGCTGTGGACAGTC 433

RESULT 4
US-10-057-475B-8117/c
; Sequence 8117, Application US/10057475B
; Publication No. US2004002068A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Clapper, Jonathan David
; APPLICANT: Wang, Aljun
; APPLICANT: Ordonez, Nadia
; APPLICANT: Carter, Lauren
; APPLICANT: McNeill, Patricia Dianne
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; TITLE OF INVENTION: Hematological Malignancies
; FILE REFERENCE: 014058-014402US
; CURRENT APPLICATION NUMBER: US/10/057,475B
; CURRENT FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14

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; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 10979
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8117
; LENGTH: 542
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-057-475B-8117

Query Match      100.0%; Score 25; DB 16; Length 542;
Best Local Similarity 100.0%; Pred. No. 2.6e-05;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGTGCGGGAATGCTGTGGACAGTC 25
Db      457 GGTGCGGGAATGCTGTGGACAGTC 433

RESULT 5
US-10-154-884B-8117/c
; Sequence 8117, Application US/10154884B
; Publication No. US20040005561A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc W.
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; TITLE OF INVENTION: Hematological Malignancies
; FILE REFERENCE: 014058-013521US
; CURRENT APPLICATION NUMBER: US/10/154,884B
; CURRENT FILING DATE: 2002-05-23
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: US 60/223,416
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: US 60/223,378
; PRIOR FILING DATE: 2000-08-07
; NUMBER OF SEQ ID NOS: 11290
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8117
; LENGTH: 542
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-154-884B-8117

Query Match      100.0%; Score 25; DB 16; Length 542;
Best Local Similarity 100.0%; Pred. No. 2.6e-05;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGTGCGGGAATGCTGTGGACAGTC 25
Db      457 GGTGCGGGAATGCTGTGGACAGTC 433

```

```

RESULT 6
US-09-796-692-8967/c
; Sequence 8967, Application US/09796692
; Publication No. US20020198362A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY
; TITLE OF INVENTION: HEMATOLOGICAL MALIGNANCIES
; FILE REFERENCE: 2077.001200
; CURRENT APPLICATION NUMBER: US/09/796,692
; CURRENT FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/222,903
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 60/223,416
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: 60/223,378
; PRIOR FILING DATE: 2000-08-07
; NUMBER OF SEQ ID NOS: 9597
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8967
; LENGTH: 596
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (13)
; OTHER INFORMATION: n=A,T,C or G
; NAME/KEY: unsure
; LOCATION: (47)
; OTHER INFORMATION: n=A,T,C or G
; NAME/KEY: unsure
; LOCATION: (49)
; OTHER INFORMATION: n=A,T,C or G
; NAME/KEY: unsure
; LOCATION: (58)
; OTHER INFORMATION: n=A,T,C or G
; NAME/KEY: unsure
; LOCATION: (63)
; OTHER INFORMATION: n=A,T,C or G
; NAME/KEY: unsure
; LOCATION: (81)
; OTHER INFORMATION: n=A,T,C or G
; NAME/KEY: unsure
; LOCATION: (155)
; OTHER INFORMATION: n=A,T,C or G
; NAME/KEY: unsure
; LOCATION: (196)
; OTHER INFORMATION: n=A,T,C or G
; NAME/KEY: unsure
; LOCATION: (211)
; OTHER INFORMATION: n=A,T,C or G
; NAME/KEY: unsure
; LOCATION: (267)

```

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; OTHER INFORMATION: n=A,T,C or G
; NAME/KEY: unsure
; LOCATION: (281)
; OTHER INFORMATION: n=A,T,C or G
; NAME/KEY: unsure
; LOCATION: (282)
; OTHER INFORMATION: n=A,T,C or G
; NAME/KEY: unsure
; LOCATION: (332)
; OTHER INFORMATION: n=A,T,C or G
; NAME/KEY: unsure
; LOCATION: (372)
; OTHER INFORMATION: n=A,T,C or G
; NAME/KEY: unsure
; LOCATION: (520)
; OTHER INFORMATION: n=A,T,C or G
; NAME/KEY: unsure
; LOCATION: (521)
; OTHER INFORMATION: n=A,T,C or G
; NAME/KEY: unsure
; LOCATION: (551)
; OTHER INFORMATION: n=A,T,C or G
; NAME/KEY: unsure
; LOCATION: (579)
; OTHER INFORMATION: n=A,T,C or G
; NAME/KEY: unsure
; LOCATION: (585)
; OTHER INFORMATION: n=A,T,C or G
; NAME/KEY: unsure
; LOCATION: (586)
; OTHER INFORMATION: n=A,T,C or G
; US-09-796-692-8967

Query Match 100.0%; Score 25; DB 9; Length 596;
Best Local Similarity 100.0%; Pred. No. 2.6e-05;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTGACGGGAATGCTGGGACAGTC 25
Db 457 GGTGACGGGAATGCTGGGACAGTC 433

RESULT 7
US-10-040-862-8967/c
; Sequence 8967, Application US/10040862
; Publication No. US20030078396A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; FILE REFERENCE: 014058-013520US
; CURRENT APPLICATION NUMBER: US/10/040,862
; CURRENT FILING DATE: 2001-11-06
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; OTHER APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; OTHER APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; OTHER APPLICATION NUMBER: US 60/223,416
; PRIOR FILING DATE: 2000-08-04
; OTHER APPLICATION NUMBER: US 60/223,378
; PRIOR FILING DATE: 2000-08-07
; OTHER APPLICATION NUMBER: US 09/796,692
; PRIOR FILING DATE: 2001-03-01
; NUMBER OF SEQ ID NOS: 10467
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8967
; LENGTH: 596
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (13)
; OTHER INFORMATION: n=A,T,C or G
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (47)
; OTHER INFORMATION: n=A,T,C or G
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (49)
; OTHER INFORMATION: n=A,T,C or G
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (58)
; OTHER INFORMATION: n=A,T,C or G
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (63)
; OTHER INFORMATION: n=A,T,C or G
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (81)
; OTHER INFORMATION: n=A,T,C or G
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (155)
; OTHER INFORMATION: n=A,T,C or G
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (196)
; OTHER INFORMATION: n=A,T,C or G
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (211)
; OTHER INFORMATION: n=A,T,C or G
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (267)
; OTHER INFORMATION: n=A,T,C or G
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (281)
; OTHER INFORMATION: n=A,T,C or G
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (282)
; OTHER INFORMATION: n=A,T,C or G
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (332)
; OTHER INFORMATION: n=A,T,C or G
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (372)
; OTHER INFORMATION: n=A,T,C or G
; FEATURE:
```

```
; NAME/KEY: unsure
; LOCATION: (520)
; OTHER INFORMATION: n=A,T,C or G
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (521)
; OTHER INFORMATION: n=A,T,C or G
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (551)
; OTHER INFORMATION: n=A,T,C or G
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (579)
; OTHER INFORMATION: n=A,T,C or G
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (585)
; OTHER INFORMATION: n=A,T,C or G
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (586)
; OTHER INFORMATION: n=A,T,C or G
US-10-040-862-8967
```

```
Query Match      100.0%; Score 25; DB 15; Length 596;
Best Local Similarity 100.0%; Pred. No. 2.6e-05;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1  GGTACGCGGAATGCTGTGGACAGTC 25
Db      457  GGTACGCGGAATGCTGTGGACAGTC 433
```

## RESULT 8

```
US-10-057-475B-8967/c
; Sequence 8967, Application US/10057475B
; Publication No. US20040002068A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Clappex, Jonathan David
; APPLICANT: Wang, Aijun
; APPLICANT: Ordonez, Nadia
; APPLICANT: Carter, Lauren
; APPLICANT: McNeill, Patricia Dianne
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; FILE REFERENCE: 014058-014402US
; CURRENT APPLICATION NUMBER: US/10/057,475B
; CURRENT FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 11290
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8967
; LENGTH: 596
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(596)
; OTHER INFORMATION: n = g, a, c or t
US-10-154-884B-8967
```

```
Query Match      100.0%; Score 25; DB 16; Length 596;
Best Local Similarity 100.0%; Pred. No. 2.6e-05;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 10979
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8967
; LENGTH: 596
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(596)
; OTHER INFORMATION: n = g, a, c or t
US-10-057-475B-8967
```

```
Query Match      100.0%; Score 25; DB 16; Length 596;
Best Local Similarity 100.0%; Pred. No. 2.6e-05;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1  GGTACGCGGAATGCTGTGGACAGTC 25
Db      457  GGTACGCGGAATGCTGTGGACAGTC 433
```

## RESULT 9

```
US-10-154-884B-8967/c
; Sequence 8967, Application US/10154884B
; Publication No. US20040005561A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc W.
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; FILE REFERENCE: 014058-013521US
; CURRENT APPLICATION NUMBER: US/10/154,884B
; CURRENT FILING DATE: 2002-05-23
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 11290
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8967
; LENGTH: 596
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(596)
; OTHER INFORMATION: n = g, a, c or t
US-10-154-884B-8967
```

```
Query Match      100.0%; Score 25; DB 16; Length 596;
Best Local Similarity 100.0%; Pred. No. 2.6e-05;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 GGTACGCGGAATGCTGTGGACAGTC 25  
 Db 457 GGTACGCGGAATGCTGTGGACAGTC 433

RESULT 10  
 US-10-228-811-1/c  
 ; Sequence 1, Application US/10228811  
 ; Publication No. US20030054392A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Wittig, Prof. Burghardt  
 ; APPLICANT: Jungmans, Claas  
 ; TITLE OF INVENTION: Design Principle for Constructing Expression Constructs for Gene  
 ; FILE REFERENCE: XI 597/99  
 ; CURRENT APPLICATION NUMBER: US/10/228,811  
 ; CURRENT FILING DATE: 2002-08-27  
 ; PRIOR APPLICATION NUMBER: DE 196 48 625.4  
 ; PRIOR FILING DATE: 1996-11-13  
 ; NUMBER OF SEQ ID NOS: 13  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 1  
 ; LENGTH: 1078  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; NAME/KEY: gene  
 ; LOCATION: (1)..(1078)  
 ; OTHER INFORMATION: bcr3=abl2; Oligo DNA Dumbbell  
 ; FEATURE:  
 ; NAME/KEY: misc.binding  
 ; LOCATION: (1)..(2)  
 ; OTHER INFORMATION: intramolecular binding site; the T-nucleotides at position 1 to  
 ; OTHER INFORMATION: 2 can be modified with amino or caroxy features  
 ; FEATURE:  
 ; NAME/KEY: misc.binding  
 ; LOCATION: (1077)..(1078)  
 ; OTHER INFORMATION: intramolecular binding site; the T-nucleotides at position 1077  
 ; OTHER INFORMATION: to 1078 can be modified with amino or caroxy features  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: Strandness: both; nucleic  
 ; OTHER INFORMATION: acid (linear), hypothetical: No. US20030054392A1 anti-sense: No  
 US-10-228-811-1

Query Match 100.0%; Score 25; DB 15; Length 1078;  
 Best Local Similarity 100.0%; Pred. No. 2.4e-05;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTACGCGGAATGCTGTGGACAGTC 25  
 Db 686 GGTACGCGGAATGCTGTGGACAGTC 662

RESULT 11  
 US-09-954-531-586/c  
 ; Sequence 586, Application US/09954531  
 ; Patent No. US20020165180A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Weaver, Zoe  
 ; TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Cand  
 ; FILE REFERENCE: 689290-77  
 ; CURRENT APPLICATION NUMBER: US/09/954,531  
 ; CURRENT FILING DATE: 2002-05-02  
 ; PRIOR APPLICATION NUMBER: US/60/233,133  
 ; PRIOR FILING DATE: 2000-09-18  
 ; PRIOR APPLICATION NUMBER: US/60/234,009  
 ; PRIOR FILING DATE: 2000-09-20  
 ; PRIOR APPLICATION NUMBER: US/60/234,034  
 ; PRIOR FILING DATE: 2000-09-20  
 ; PRIOR APPLICATION NUMBER: US/60/234,509  
 ; PRIOR FILING DATE: 2000-09-22

; PRIOR APPLICATION NUMBER: US/60/234,567  
 ; PRIOR FILING DATE: 2000-09-22  
 ; NUMBER OF SEQ ID NOS: 1392  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 586  
 ; LENGTH: 4739  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-09-954-531-586

Query Match 100.0%; Score 25; DB 9; Length 4739;  
 Best Local Similarity 100.0%; Pred. No. 2e-05;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTACGCGGAATGCTGTGGACAGTC 25  
 Db 3182 GGTACGCGGAATGCTGTGGACAGTC 3158

RESULT 12  
 US-10-193-651-22/c  
 ; Sequence 22, Application US/10193651  
 ; Publication No. US20030064061A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Zhao, Xun  
 ; APPLICANT: Ghaffari, Saghi  
 ; APPLICANT: Lodish, Harvey F.  
 ; APPLICANT: Malashkevich, Vladimir N.  
 ; APPLICANT: Kim, Peter S.  
 ; TITLE OF INVENTION: Bcr-Abl Oligomerization Domain  
 ; TITLE OF INVENTION: Polypeptides and Uses Therefor  
 ; FILE REFERENCE: 0399,2031-001  
 ; CURRENT APPLICATION NUMBER: US/10/193,651  
 ; CURRENT FILING DATE: 2002-11-19  
 ; PRIOR APPLICATION NUMBER: US 60/303,857  
 ; PRIOR FILING DATE: 2001-07-09  
 ; NUMBER OF SEQ ID NOS: 22  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 22  
 ; LENGTH: 4739  
 ; TYPE: DNA  
 ; ORGANISM: Homo Sapiens  
 ; FEATURE:  
 ; OTHER INFORMATION: Bcr nucleic acid  
 US-10-193-651-22

Query Match 100.0%; Score 25; DB 13; Length 4739;  
 Best Local Similarity 100.0%; Pred. No. 2e-05;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTACGCGGAATGCTGTGGACAGTC 25  
 Db 3182 GGTACGCGGAATGCTGTGGACAGTC 3158

RESULT 13  
 US-10-128-714-206/c  
 ; Sequence 206, Application US/10128714  
 ; Publication No. US20030119013A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Jiang, Bo  
 ; APPLICANT: Hu, Wengi  
 ; APPLICANT: Tishkoff, Daniel  
 ; APPLICANT: Zamudio, Carlos  
 ; APPLICANT: Eroshkin, Alexey M  
 ; APPLICANT: Lemieux, Sebastien M  
 ; TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and  
 ; TITLE OF INVENTION: Methods of Use  
 ; FILE REFERENCE: 10182-018-999  
 ; CURRENT APPLICATION NUMBER: US/10/128,714  
 ; CURRENT FILING DATE: 2002-04-23  
 ; PRIOR APPLICATION NUMBER: US 60/285,697  
 ; PRIOR FILING DATE: 2001-04-23

; PRIOR APPLICATION NUMBER: US 60/287,066  
 ; PRIOR FILING DATE: 2001-04-27  
 ; PRIOR APPLICATION NUMBER: US 60/295,890  
 ; PRIOR FILING DATE: 2001-06-05  
 ; PRIOR APPLICATION NUMBER: US 60/303,899  
 ; PRIOR FILING DATE: 2001-07-09  
 ; PRIOR APPLICATION NUMBER: US 60/316,362  
 ; PRIOR FILING DATE: 2001-08-31  
 ; NUMBER OF SEQ ID NOS: 8603  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 206  
 ; LENGTH: 3664  
 ; TYPE: DNA  
 ; ORGANISM: Aspergillus fumigatus  
 US-10-128-714-206

Query Match 68.0%; Score 17; DB 15; Length 3664;  
 Best Local Similarity 100.0%; Pred. No. 1.2; Indels 0; Gaps 0;  
 Matches 17; Conservative 0; Mismatches 0;

QY 5 AC CGGAATGCTGTGGAC 21  
 Db 3563 AC CGGAATGCTGTGGAC 3547

RESULT 14  
 US-10-128-714-5206/c  
 ; Sequence 5206, Application US/10128714  
 ; Publication No. US20030119013A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Jiang, Bo  
 ; APPLICANT: Hu, Weng  
 ; APPLICANT: Tishkoff, Daniel  
 ; APPLICANT: Zamudio, Carlos  
 ; APPLICANT: Broshkin, Alexey M  
 ; APPLICANT: Lemieux, Sebastien M  
 ; TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and  
 ; FILE OF INVENTION: Methods of Use  
 ; FILE REFERENCE: 10182-018-999  
 ; CURRENT APPLICATION NUMBER: US/10/128,714  
 ; PRIOR FILING DATE: 2002-04-23  
 ; PRIOR APPLICATION NUMBER: US 60/285,697  
 ; PRIOR FILING DATE: 2001-04-23  
 ; PRIOR APPLICATION NUMBER: US 60/287,066  
 ; PRIOR FILING DATE: 2001-04-27  
 ; PRIOR APPLICATION NUMBER: US 60/295,890  
 ; PRIOR FILING DATE: 2001-06-05  
 ; PRIOR APPLICATION NUMBER: US 60/303,899  
 ; PRIOR FILING DATE: 2001-07-09  
 ; PRIOR APPLICATION NUMBER: US 60/316,362  
 ; PRIOR FILING DATE: 2001-08-31  
 ; NUMBER OF SEQ ID NOS: 8603  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 5206  
 ; LENGTH: 3750  
 ; TYPE: DNA  
 ; ORGANISM: Aspergillus fumigatus  
 US-10-128-714-5206

Query Match 68.0%; Score 17; DB 15; Length 3750;  
 Best Local Similarity 100.0%; Pred. No. 1.2; Indels 0; Gaps 0;  
 Matches 17; Conservative 0; Mismatches 0;

QY 5 AC CGGAATGCTGTGGAC 21  
 Db 3652 AC CGGAATGCTGTGGAC 3636

RESULT 15  
 US-09-779-881-2  
 ; Sequence 2, Application US/09779881  
 ; Patent No. US20020081749A1  
 ; GENERAL INFORMATION:

; APPLICANT: Kulmala, Sakari  
 ; APPLICANT: Ala-Kleme, Timo  
 ; APPLICANT: Eskola, Jarkko  
 ; APPLICANT: Korpela, Timo  
 ; TITLE OF INVENTION: ELECTRICAL EXCITATION OF LABEL SUBSTANCES AT COATED  
 ; FILE OF INVENTION: ELECTRODES  
 ; FILE REFERENCE: TUR-080  
 ; CURRENT APPLICATION NUMBER: US/09/779,881  
 ; CURRENT FILING DATE: 2001-02-09  
 ; PRIOR APPLICATION NUMBER: 09/341,955  
 ; PRIOR FILING DATE: 1999-07-21  
 ; PRIOR APPLICATION NUMBER: PCT/FI98/00114  
 ; PRIOR FILING DATE: 1999-02-10  
 ; NUMBER OF SEQ ID NOS: 2  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 2  
 ; LENGTH: 28  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence:  
 ; OTHER INFORMATION: oligonucleotide containing an amino group  
 US-09-779-881-2

Query Match 64.0%; Score 16; DB 9; Length 28;  
 Best Local Similarity 100.0%; Pred. No. 8.6;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGT CAGCGGAATGCTG 16  
 Db 13 GGT CAGCGGAATGCTG 28

Search completed: May 27, 2004, 14:58:27  
 Job time : 131.564 secs

**THIS PAGE BLANK (USPTO)**

GenCore version 5.1.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 26, 2004, 15:22:41 ; Search time 882.692 Seconds  
(without alignments)  
845,770 Million cell updates/sec

Title: US-09-121-239-11

Perfect score: 25  
Sequence: 1 GGTACGGGAATGCTGTGGACAGTC 25

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 27513289 seqs, 14931090276 residues

Word size : 0

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

EST:\*

1: em\_estba:\*

2: em\_estba:\*

3: em\_estin:\*

4: em\_estmu:\*

5: em\_estov:\*

6: em\_estpl:\*

7: em\_estro:\*

8: em\_htc:\*

9: gb\_est1:\*

10: gb\_est2:\*

11: gb\_hic:\*

12: gb\_est3:\*

13: gb\_est4:\*

14: gb\_est5:\*

15: em\_estom:\*

16: em\_estom:\*

17: em\_gas\_hum:\*

18: em\_gas\_inv:\*

19: em\_gas\_pin:\*

20: em\_gas\_vrt:\*

21: em\_gas\_fun:\*

22: em\_gas\_nam:\*

23: em\_gas\_mus:\*

24: em\_gas\_pro:\*

25: em\_gas\_rod:\*

26: em\_gas\_phg:\*

27: em\_gas\_vrl:\*

28: gb\_gsl:\*

29: gb\_gsl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	25	100.0	181	14	H55545
C 2	25	100.0	314	14	D79153
C 3	25	100.0	360	10	BE168421
C 4	25	100.0	377	10	BF800308

C	5	25	100.0	401	14	R54267
C	6	25	100.0	437	10	BF873838
C	7	25	100.0	443	10	AW452440
C	8	25	100.0	531	12	BG927169
C	9	25	100.0	588	10	BF380221
C	10	25	100.0	588	10	BF094682
C	11	25	100.0	590	10	BF953848
C	12	25	100.0	597	10	BE396942
C	13	25	100.0	605	10	AW961897
C	14	25	100.0	621	10	BE267891
C	15	25	100.0	637	14	CB267185
C	16	25	100.0	653	12	BG829045
C	17	25	100.0	665	10	BE514596
C	18	25	100.0	684	10	BF530440
C	19	25	100.0	686	10	BE397010
C	20	25	100.0	712	10	BE397695
C	21	25	100.0	734	10	BE513555
C	22	25	100.0	741	10	BE265121
C	23	25	100.0	770	12	BE260004
C	24	25	100.0	777	13	B0597369
C	25	25	100.0	785	12	BG393462
C	26	25	100.0	797	12	BI225128
C	27	25	100.0	819	14	CF242964
C	28	25	100.0	844	14	CD652568
C	29	25	100.0	853	13	BQ227532
C	30	25	100.0	878	10	BF338795
C	31	25	100.0	880	13	BQ422888
C	32	25	100.0	880	13	B0539742
C	33	25	100.0	888	13	BU540933
C	34	25	100.0	895	13	EX368536
C	35	25	100.0	903	13	BQ441890
C	36	25	100.0	918	13	BQ212925
C	37	25	100.0	936	13	EX350695
C	38	25	100.0	955	13	BQ945725
C	39	25	100.0	975	12	BG392048
C	40	25	100.0	1021	13	BQ896733
C	41	24	96.0	104	10	AW998451
C	42	24	96.0	796	10	BE743192
C	43	24	96.0	813	12	BM050194
C	44	22	88.0	438	10	BE938059
C	45	20	80.0	750	10	BE513994

ALIGNMENTS

RESULT 1  
H55545/c  
LOCUS  
DEFINITION  
H55545  
VERSION  
H55545.1  
KEYWORDS  
EST.  
SOURCE  
Homo sapiens (human)  
ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE  
1 (bases 1 to 181)  
Trafletter, J.A., Long, K.R., Murrell, J.R., Stotler, C.J., Gusella, J.F. and Buckler, A.J.  
TITLE  
An expression-independent catalog of genes from human chromosome 22  
JOURNAL  
Genome Res. 5 (3), 214-224 (1995)  
MEDLINE  
96159527  
PubMed  
8593609  
COMMENT  
Contact: Buckler AJ  
Molecular Neurogenetics Unit  
Massachusetts General Hospital  
Building 149, 13th St., Charlestown MA 02129  
Tel: 6177249616  
Fax: 6177265736  
Email: buckler@helix.mgh.harvard.edu  
Seq primer: T3.

H55545  
CHR220484  
Chromosome 22  
exon Homo sapiens cDNA clone C22\_652 5',  
181 bp  
mRNA  
linear  
EST 07-DEC-1995  
mRNA sequence.

LOCUS



Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.

Shotgun sequencing of the human transcriptome with ORF expressed

sequence tags

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

20202663

10737800

#### COMMENT

Contact: Simpson A.J.G.

Laboratory of Cancer Genetics

Ludwig Institute for Cancer Research

Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,

Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome

Project. This entry can be seen in the following URL

(<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CM4&t2=CM4-CI0062-181000-370-b10&t3=2000-10-18&t4=1>)

Seq primer: puc 18 forward

High quality sequence start: 18

High quality sequence stop: 377.

#### FEATURES

source

1..377

Location/Qualifiers

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/dev\_stage="Adult"

/clone\_lib="CI0062"

/note="Organ: colon\_ins; Vector: puc18; Site 1: SmaI;

Site 2: SmaI; A mini-library was made by cloning products

derived from ORESSES PCR (U.S. Letters Patent application

No. 196,716 - Ludwig Institute for Cancer Research) of

profiles into the puc 18 vector. Reverse transcription of

tissue mRNA and cDNA amplification were performed under

low stringency conditions."

#### ORIGIN

Query Match 100.0%; Score 25; DB 10; Length 377;

Best Local Similarity 100.0%; Pred. No. 0.0035;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTACGCGGAATGCTGTGCAGATC 25

|||||

Db 274 GGTACGCGGAATGCTGTGCAGATC 250

#### RESULT 5

R54267/c

LOCUS

DEFINITION Y974h05.r1 Soares infant brain IN1B Homo sapiens cDNA clone

IMAGE:39270 5' similar to gb:U01147 BREAKPOINT CLUSTER REGION

PROTEIN (HUMAN) ; mRNA sequence.

R54267

ACCESSION R54267.1 GI:816169

VERSION

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 401)

AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,

Holman,M., Hultman,M., Kucaba,T., Le,M., Lemmon,G., Marra,M.,

Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,

Travaskis,E., Waterston,R., Williamson,A., Woldmann,P. and

Wilson.R.

The WashU-Merck EST Project

Unpublished (1995)

CONTACT: Wilson RK

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

Insert Size: 1872

High quality sequence stops: 342 Source: IMAGE Consortium, LLNL

This clone is available royalty-free through LLNL; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

Insert Length: 1872 Std Error: 0.00

Seq primer: M13RP1

High quality sequence stop: 342.

#### FEATURES

source

1..401

Location/Qualifiers

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="GDB:411811"

/db\_xref="taxon:9606"

/clone="IMAGE:39270"

/sex="female"

/dev\_stage="73 days post natal"

/lab\_host="DH10B (ampicillin resistant)"

/clone\_lib="Soares infant brain IN1B"

/note="Organ: whole brain; Vector: Lafmid BA; Site 1: Not

I; Site 2: Hind III; 1st strand cDNA was primed with a Not

I - oligo(GT) primer [5'

AACTGGAAGAATCGCCGCGAGAAATTTTTTTTTTTT 3'];

double-stranded cDNA was ligated to Hind III adaptors

(Pharmacia), digested with Not I and directionally cloned

into the Not I and Hind III sites of the Lafmid BA vector.

Library went through one round of normalization. Library

constructed by Bento Soares and M.Fatima Bonaldo."

#### ORIGIN

Query Match 100.0%; Score 25; DB 14; Length 401;

Best Local Similarity 100.0%; Pred. No. 0.0035;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTACGCGGAATGCTGTGCAGATC 25

|||||

Db 250 GGTACGCGGAATGCTGTGCAGATC 226

#### RESULT 6

BF873838

LOCUS

DEFINITION IL3-ET0114-071100-338-C02 ET0114 Homo sapiens cDNA, mRNA sequence.

ACCESSION BF873838

VERSION BF873838.1 GI:12264007

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 437)

AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,

Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,

Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,

Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,

O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and

Simpson,A.J.

Shotgun sequencing of the human transcriptome with ORF expressed

sequence tags

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

20202663

10737800

COMMENT

Contact: Simpson A.J.G.

Laboratory of Cancer Genetics

Ludwig Institute for Cancer Research

Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,

Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL  
 (http://www.ludwig.org.br/scripts/gethtml2.pl?tbl=IL3&t2=IL3-ET0114-071100-338-C02&t3=2000-11-07&t4=1)  
 Seq primer: puc 18 forward  
 High quality sequence stop: 390.

## FEATURES

## source

1. .437  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /dev\_stage="Adult"  
 /clone\_lib="ET0114"

/notes="Organ: lung tumor; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

## ORIGIN

Query Match 100.0%; Score 25; DB 10; Length 437;  
 Best Local Similarity 100.0%; Pred. No. 0.0036;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTACGCGGAATGCTGTGGACAGTC 25

Db 294 GGTACGCGGAATGCTGTGGACAGTC 318

## RESULT 7

## AW452440/C

LOCUS AW452440 443 bp mRNA linear EST 17-FEB-2000  
 DEFINITION UI-H-B13-als-c-04-0-UT.s1 NCI\_CGAP\_Sub5 Homo sapiens cDNA clone  
 IMAGE:3068526 3', mRNA sequence.

ACCESSION AW452440

VERSION AW452440.1 GI:6993216

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 443)

AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

TITLE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

JOURNAL National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

COMMENT Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgapsb@mail.nih.gov

is likely internal to the message. CDNA library Preparation: M.B. Soares Lab Clone distribution: NCI-CGAP clone distribution Information can be found through the I.M.A.G.E. Consortium/LINL at: www.bio.lnl.gov/bbrp/image/image.html The following repetitive elements were found in this cDNA sequence: 147-207, >HSR1RT

Seq primer: M13 Forward

POLYA-No.

## FEATURES

## source

1. .443  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:3068526"  
 /lab\_host="DHI0B (Life Technologies)"  
 /clone\_lib="NCI\_CGAP\_Sub5"

/notes="Vector: pT773D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; NCI CGAP Subs is a subtracted library derived from NCI CGAP Sub4. The NCI CGAP Sub5 library had 3 million recombinants. A single-stranded DNA preparation of NCI\_CGAP\_Sub4 was used as a tracer in a subtractive hybridization with a driver comprising: the IMAGE pool (NCI\_CGAP\_Kid3 pool 1 LLAM

3334-3337, 3682-3683, 3798-3803 (IMAGE CloneIDs 1322376-1323911, 1456008-1456775, 1500552-1502855);  
 NCI CGAP Kid5 pool 1 LLAM 3338-3342, 3722-3725, 3776-3778 (IMAGE CloneIDs 1323912-1325831, 1471368-1472903, 1492104-1493255); NCI\_CGAP\_Lu5 pool 1 LLAM 3575-3582, 3851-3854 (IMAGE CloneIDs 1414920-1417991, 1520904-1522439); NCI CGAP GC4 pool 1 LLAM 3164-3167, 3716-3720, 3733-3735 (IMAGE CloneIDs 1257096-1258631, 1469064-1470983, 1475592-1476743);  
 NCI CGAP Pr22 pool 1 LLAM 2457-2459, 2758-2759, 3062-3068 (IMAGE CloneIDs 985608-986759, 1101192-1101959, 1217928-1220615); NCI CGAP\_Co10 pool 1 LLAM 2644-2653, 2871-2872 (IMAGE CloneIDs 1057416-1061255, 1144584-1145351). (10% of the driver population), plus a pool of 3,840 arrayed clones from NCI CGAP Sub1 (IMAGE CloneIDs 2708616-2710535) and NCI\_CGAP\_Sub2 (IMAGE CloneIDs 2710536-2712455) (10% of the driver population), plus a pool of 11,136 clones from NCI CGAP Sub3 (IMAGE CloneIDs 2712456-2723591) (10% of the driver population), plus a pool of 5,472 clones from NCI CGAP Sub4 (IMAGE CloneIDs 2723592-2728969) (70% of the driver population). Subtraction was performed as previously described (Bonaldi, Lennon & Soares (1996): Normalization and Subtraction: Two Approaches To Facilitate Gene Discovery. Genome Research 6, 791-806.  
 TAG TISSUE=germ cell  
 TAG\_LIB=NCI\_CGAP\_GC4  
 TAG\_SEQ=AAATC"

## ORIGIN

Query Match 100.0%; Score 25; DB 10; Length 443;  
 Best Local Similarity 100.0%; Pred. No. 0.0036;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTACGCGGAATGCTGTGGACAGTC 25

Db 380 GGTACGCGGAATGCTGTGGACAGTC 356

## RESULT 8

## BG927169/c

## LOCUS

DEFINITION HNC18-1-D3.R.HC (Human Normal Cartilage) Homo sapiens cDNA, mRNA sequence.

ACCESSION BG927169

VERSION BG927169.1 GI:14321692

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 531)

AUTHORS Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Eukaryota; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Kumar, S., Connor, J.R., Dodds, R.A., Halsey, W., Van Horn, M., Mao, J.,

Sathe, G., Mui, P., Agarwal, P., Badger, A.M., Lee, J.C., Gowen, M. and

Lark, M.W.

Identification and initial characterization of 5000 expressed

sequenced tags (ESTs) each from adult human normal and

osteochondritic cartilage cDNA libraries

Osteoarthr. Cartil. 9 (7), 641-653 (2001)

JOURNAL MEDLINE

PUBMED 21482651

COMMENT Contact: Sanjay Kumar

UW2109

GlaxoSmithKline

709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA

Tel: 610-270-7245

Fax: 610-270-5598

Email: sanjay.kumar-1@gsk.com

Seq primer: T7

Location/Qualifiers

1. .531

/organism="Homo sapiens"

/mol\_type="mRNA"

Qy	1	GGTCAGCGGAATGCTGTGGACAGTC	25
Db	477	GGTCAGCGGAATGCTGTGGACAGTC	453
<p>RESULT 10</p> <p>BF094682/c</p> <p>LOCUS</p> <p>DEFINITION</p> <p>MR3-UT0050-130900-003-g03-UT0050</p> <p>ACCESSION</p> <p>BF094682</p> <p>VERSION</p> <p>BF094682.1</p> <p>KEYWORDS</p> <p>GI:10900392</p> <p>SOURCE</p> <p>Homo sapiens (human)</p> <p>ORGANISM</p> <p>Homo sapiens</p> <p>REFERENCE</p> <p>1 (bases 1 to 588)</p> <p>AUTHORS</p> <p>Dias Neto,E., Garcia Correa,R., Nagai,M.A., da Silva,W. Jr., Goldman,G.H., Carvalho,A.F., Martins Brunstein,A., deOliveira,P.S., O'Hare,M.J., Soares,F., Brentani Simpson,A.J.</p> <p>TITLE</p> <p>Shotgun sequencing of the human sequence tags</p> <p>JOURNAL</p> <p>Proc. Natl. Acad. Sci. U.S.A.</p> <p>MEDLINE</p> <p>20202663</p> <p>PUBMED</p> <p>10737800</p> <p>COMMENT</p> <p>Contact: Simpson A.J.G.</p> <p>Laboratory of Cancer Genetics</p> <p>Ludwig Institute for Cancer Research</p> <p>Rua Prof. Antonio Prudente 109, Brazil</p> <p>Tel: +55-11-2704922</p> <p>Fax: +55-11-2707001</p> <p>Email: asimpson@ludwig.org.br</p> <p>This sequence was derived from the Project. This entry can be seen (http://www.ludwig.org.br/scripts/900-003-g03&amp;t3=2000-09-13&amp;t4=1) Seq primer: puc 18 forward</p> <p>High quality sequence stop: 586</p> <p>FEATURES</p> <p>Location/Qualifiers</p> <p>1..588</p> <p>/organism="Homo sapiens"</p> <p>/mol_type="mRNA"</p> <p>/db_xref="taxon:9606"</p> <p>/dev_stage="Adult"</p> <p>/clone_lib="UT0050"</p> <p>/note="Organ: uterus"</p> <p>Site_2: SmaI; A mini-1 derived from ORESTES No. 196,716 - Ludwig profiles into the pUC tissue mRNA and cDNA at low stringency conditions</p>			
<p>ORIGIN</p> <p>Query Match 100.0%; Score 25</p> <p>Best Local Similarity 100.0%; Pred. No</p> <p>Matches 25; Conservative 0; Mismat</p>			
Qy	1	GGTCAGCGGAATGCTGTGGACAGTC	25
Db	477	GGTCAGCGGAATGCTGTGGACAGTC	453
<p>RESULT 11</p> <p>BF953848/c</p> <p>LOCUS</p> <p>DEFINITION</p> <p>MR0-NN1170-131100-302-f01-NN1170</p> <p>ACCESSION</p> <p>BF953848</p>			

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VERSION
KEYWORDS
SOURCE
ORGANISM
BF953848.1 GI:12371149
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 590)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W.Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
10737800
COMMENT
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?ti=MR0&t2=MR0-NN1170-
131100-302-f01&t3=2000-11-13&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 31
High quality sequence stop: 569.
FEATURES
source
1..590
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="NN1170"
/notes="Organ: nervous normal; Vector: puc18; Site 1: SmaI;
Site 2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
ORIGIN
Query Match 100.0%; Score 25; DB 10; Length 590;
Best Local Similarity 100.0%; Pred. No. 0.0037;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGTACGCGGAATGCTGTGGACAGTC 25
|||||
Db 212 GGTACGCGGAATGCTGTGGACAGTC 188
|||||

RESULT 12
BE396942/c
LOCUS
DEFINITION
601290652F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3621156.5',
mRNA sequence.
ACCESSION
BE396942
VERSION
BE396942.1 GI:9342307
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 597)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL
COMMENT
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA library Preparation: Ling Hong/Rubin Laboratory
cDNA library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCW294 row: 9 column: 13
High quality sequence stop: 597.
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/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 8"
/notes="Organ: lymph; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).".
ORIGIN
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Best Local Similarity 100.0%; Pred. No. 0.0037;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGTACGCGGAATGCTGTGGACAGTC 25
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Db 593 GGTACGCGGAATGCTGTGGACAGTC 569
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RESULT 13
AW961897/c
LOCUS
DEFINITION
EST373970 MAGE resequences, MAGG Homo sapiens cDNA, mRNA sequence.
ACCESSION
AW961897
VERSION
AW961897.1 GI:8151583
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 605)
Hegde,P., Qi,R., Abernathy,K., Dharap,S., Gaspard,R., Gay,C.,
Holt,J.E., Saeed,A.I., Shatov,V., Lee,N.H., Yeatman,T.J. and
Quackenbush,J.
Assessment of gene expression patterns in a model of colon tumor
metastasis using a 19,200 element cDNA microarray
Unpublished (2000)
Contact: John Quackenbush
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 3528
Fax: 301 838 0208
Email: johnq@tigr.org
Plate: 167
Seq primer: Reverse.
FEATURES
source
1..605
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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/notes="Vector: pBluescriptSm"
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QY 1 GGTACGCGGAATGCTGTGGACAGTC 25  
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 Db 437 GGTACGCGGAATGCTGTGGACAGTC 413

RESULT 14  
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 LOCUS  
 DEFINITION BE267891 621 bp mRNA linear EST 13-JUL-2000  
 mRNA sequence.

ACCESSION BE267891  
 VERSION BE267891.1 GI:9141488  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)

ORGANISM  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 621)  
 AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: [cgabbs@mail.nih.gov](mailto:cgabbs@mail.nih.gov)

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.  
 CDNA Library Preparation: Ling Hong/Rubin Laboratory  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at: [image.llnl.gov](http://image.llnl.gov)  
 Plate: LLCW132 row: h column: 13  
 High quality sequence stop: 619.

## FEATURES

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 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
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 /note="Organ: lymph; Vector: pOTB7; Site 1: XhoI; Site 2:  
 EcoRI; cDNA made by oligo-dT priming. Directionally  
 cloned into EcoRI/XhoI sites using the following 5'  
 adaptor: GGACGAG(G). Size-selected >500bp for average  
 insert size 1.8kb. Library constructed by Ling Hong in  
 the laboratory of Gerald M. Rubin (University of  
 California, Berkeley) using ZAP-cDNA synthesis kit  
 (Stratagene) and Superscript II RT (Life Technologies)."

## ORIGIN

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 Db 208 GGTACGCGGAATGCTGTGGACAGTC 184

RESULT 15  
 CB267185/c  
 LOCUS  
 DEFINITION CB267185 637 bp mRNA linear EST 20-FEB-2003  
 1006091 Human Fat Cell 5'-Stretch Plus cDNA Library Homo sapiens  
 cDNA 5', mRNA sequence.  
 ACCESSION CB267185  
 VERSION CB267185.1 GI:28441771  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)

## ORGANISM

Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 637)  
 AUTHORS Yang, R.-Z., Shuldiner, A. and Gong, D.-W.  
 TITLE EST analysis of human adipose gene expression  
 JOURNAL Unpublished (2002)  
 COMMENT Contact: Gong Da-Wei  
 Division of Endocrinology, Diabetes and Nutrition  
 University of Maryland  
 660 Redwood St, HH497, Baltimore, MD 21201, USA

Tel: 410 706 1672  
 Fax: 410 706 1622  
 Email: [dgong@medicine.umaryland.edu](mailto:dgong@medicine.umaryland.edu)  
 PCR Primers  
 FORWARD: AATACGACTCACTATAGGGAATTGG  
 BACKWARD: CTCGGGAAGCGCCATTGTGTGTGGT

Seq primer: GTTGTACCGGAATTC.

## FEATURES

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 Db 428 GGTACGCGGAATGCTGTGGACAGTC 404

Search completed: May 26, 2004, 22:44:24  
 Job time : 882.692 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 26, 2004, 16:00:31 ; Search time 532.065 Seconds  
(without alignments)  
2036.547 Million cell updates/sec

Title: US-09-121-239-12

Perfect score: 25

Sequence: 1 GGUCAGCCGAUUGUGUGACAGUC 25

Scoring table: OLIGO NUC

Gapop 60.0 , Gapext 60.0

Searched: 3470272 seqs, 21671516995 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

GenEmbl.\*

1: gb\_ba.\*

2: gb\_hgt.\*

3: gb\_in.\*

4: gb\_om.\*

5: gb\_ov.\*

6: gb\_pat.\*

7: gb\_ph.\*

8: gb\_pl.\*

9: gb\_pr.\*

10: gb\_ro.\*

11: gb\_sts.\*

12: gb\_sy.\*

13: gb\_un.\*

14: gb\_vt.\*

15: em\_ba.\*

16: em\_fun.\*

17: em\_hum.\*

18: em\_in.\*

19: em\_mu.\*

20: em\_om.\*

21: em\_or.\*

22: em\_ov.\*

23: em\_pat.\*

24: em\_ph.\*

25: em\_pl.\*

26: em\_ro.\*

27: em\_sts.\*

28: em\_un.\*

29: em\_vt.\*

30: em\_hgt\_hum.\*

31: em\_hgt\_inv.\*

32: em\_hgt\_other.\*

33: em\_hgt\_mus.\*

34: em\_hgt\_pln.\*

35: em\_hgt\_rtd.\*

36: em\_hgt\_mam.\*

37: em\_hgt\_vrt.\*

38: em\_sy.\*

39: em\_hgt\_hum.\*

40: em\_hgt\_mus.\*

41: em\_hgt\_other.\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
C 1	25	100.0	25	6	BD222531	BD222531 Methods f
C 2	25	100.0	25	6	BD222532	BD222532 Methods f
C 3	25	100.0	25	6	BD222533	BD222533 Methods f
C 4	25	100.0	25	6	BD222534	BD222534 Methods f
C 5	25	100.0	56	6	I12447	I12447 Sequence 17
C 6	25	100.0	56	6	I14509	I14509 Sequence 17
C 7	25	100.0	210	9	AY043457	AY043457 Homo sapi
C 8	25	100.0	250	9	AF321981	AF321981 Homo sapi
C 9	25	100.0	305	9	AF192533	AF192533 Homo sapi
C 10	25	100.0	350	6	BD222546	BD222546 Methods f
C 11	25	100.0	561	9	HUMMK562B	M19695 Human myelo
C 12	25	100.0	679	9	HUMABLB	M30832 Human bcr/a
C 13	25	100.0	854	9	HUMABLD	M30829 Human bcr/a
C 14	25	100.0	922	9	HSAL131467	AJ131467 Homo sapi
C 15	25	100.0	997	9	HSAL131466	AJ131466 Homo sapi
C 16	25	100.0	1078	6	A92081	A92081 Sequence 5
C 17	25	100.0	1078	6	AR230688	AR230688 Sequence
C 18	25	100.0	1157	6	BD177069	BD177069 Standard
C 19	25	100.0	2255	6	E00984	E00984 Probe detec
C 20	25	100.0	2255	6	I04527	I04527 Sequence 1
C 21	25	100.0	2541	9	HUMBCRX	M55395 Human break
C 22	25	100.0	2811	6	AX780333	AX780333 Sequence
C 23	25	100.0	3481	9	AK128501	AK128501 Homo sapi
C 24	25	100.0	4714	9	HSBCR	Y0661 Human bcr m
C 25	25	100.0	4739	6	AX331144	AX331144 Sequence
C 26	25	100.0	4739	9	HSBCRR	X02596 Human mRNA
C 27	25	100.0	5000	9	HUMBCRE	L02935 Human major
C 28	25	100.0	111249	9	AP000343	AP000343 Homo sapi
C 29	25	100.0	152141	9	HSU07000	U07000 Human break
C 30	24	96.0	26	6	I83632	I83632 Sequence 6
C 31	24	96.0	40	6	E16986	E16986 Sense prime
C 32	21	84.0	468	9	HUMKMLCABL	M25946 Human chro
C 33	21	84.0	468	9	HUMKMLCABL	M13096 Human chine
C 34	21	84.0	219210	2	AC145066	AC145066 Pan trogl
C 35	21	84.0	240115	2	AC138021	AC138021 Pan trogl
C 36	18	72.0	22	6	I58643	I58643 Sequence 11
C 37	18	72.0	62	6	AR100681	AR100681 Sequence
C 38	18	72.0	81	6	AR100682	AR100682 Sequence
C 39	18	72.0	205	6	I02402	I02402 Sequence 1
C 40	18	72.0	257	6	I58633	I58633 Sequence 1
C 41	18	72.0	257	6	I58633	I58633 Sequence 1
C 42	17	68.0	60	6	A50293	A50293 Sequence 13
C 43	17	68.0	13980	1	AE001036	AE001036 Archaeogl
C 44	17	68.0	80526	2	AC145976	AC145976 Gallus ga
C 45	17	68.0	110000	2	AC107201_3	Continuation (4 of

ALIGNMENTS

RESULT 1  
BD222531/c  
LOCUS BD222531  
DEFINITION Methods for detecting and measuring spliced nucleic acids.  
ACCESSION BD222531  
VERSION BD222531.1 GI:33032301  
KEYWORDS JP 2002521037-A/9.  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1 (bases 1 to 25)  
AUTHORS Harvey, R.C. and Eastman, P.S.  
TITLE Methods for detecting and measuring spliced nucleic acids  
JOURNAL Patent: JP 2002521037-A 9 16-JUL-2002;  
GEN PROBE INC

```

COMMENT      OS      Artificial Sequence
              PN      JP 2002521037-A/9
              PD      16-JUL-2002
              PP      23-JUL-1999 JP 2000561364
              PR      23-JUL-1998 US 09/121239
              PT      RICHARD C HARVEY, PAUL S EASTMAN
              PC      C12Q1/68, C12N15/09, C12N15/00
              CC      Description of Artificial Sequence: Probe for bcr b2 sequence
              PH      Key Location/Qualifiers
              FT      source 1..25
                   /organism='Artificial Sequence'.
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source       Location/Qualifiers
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              /db_xref="taxon:32630"
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Query Match      100.0%; Score 25; DB 6; Length 25;
Best Local Similarity 80.0%; Pred. No. 3.9e-05;
Matches 20; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGUCAGCGGAUGCUGGACAGUC 25
        ||:|||||:|:|:|:|:|:|
        25 GGTACGCGGAATGCTGTGGACAGTC 1

RESULT 2
BD222532/c
LOCUS      BD222532      25 bp      RNA      linear      PAT 17-JUL-2003
DEFINITION Methods for detecting and measuring spliced nucleic acids.
ACCESSION  BD222532
VERSION     BD222532.1 GI:33032302
KEYWORDS    JP 2002521037-A/10.
SOURCE      synthetic construct
ORGANISM    artificial sequences.
REFERENCE   1 (bases 1 to 25)
AUTHORS     Harvey, R.C. and Eastman, P.S.
TITLES      Methods for detecting and measuring spliced nucleic acids
JOURNALS    Patent: JP 2002521037-A 10 16-JUL-2002;
            GEN PROBE INC
COMMENT      OS      Artificial Sequence
              PN      JP 2002521037-A/10
              PD      16-JUL-2002
              PP      23-JUL-1999 JP 2000561364
              PR      23-JUL-1998 US 09/121239
              PT      RICHARD C HARVEY, PAUL S EASTMAN
              PC      C12Q1/68, C12N15/09, C12N15/00
              CC      Description of Artificial Sequence: RNA version of SEQ ID NO:9
              PH      Key Location/Qualifiers
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Query Match      100.0%; Score 25; DB 6; Length 25;
Best Local Similarity 80.0%; Pred. No. 3.9e-05;
Matches 20; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

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        25 GGTACGCGGAATGCTGTGGACAGTC 1

RESULT 3
BD222533
LOCUS      BD222533      25 bp      DNA      linear      PAT 17-JUL-2003
DEFINITION Methods for detecting and measuring spliced nucleic acids.

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ACCESSION  BD222533
VERSION     BD222533.1 GI:33032303
KEYWORDS    JP 2002521037-A/11.
SOURCE      synthetic construct
ORGANISM    artificial sequences.
REFERENCE   1 (bases 1 to 25)
AUTHORS     Harvey, R.C. and Eastman, P.S.
TITLES      Methods for detecting and measuring spliced nucleic acids
JOURNALS    Patent: JP 2002521037-A 11 16-JUL-2002;
            GEN PROBE INC
COMMENT      OS      Artificial Sequence
              PN      JP 2002521037-A/11
              PD      16-JUL-2002
              PP      23-JUL-1999 JP 2000561364
              PR      23-JUL-1998 US 09/121239
              PT      RICHARD C HARVEY, PAUL S EASTMAN
              PC      C12Q1/68, C12N15/09, C12N15/00
              CC      Description of Artificial Sequence: Reverse complement of SEQ
                   ID NO:9
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              /mol_type="genomic DNA"
              /db_xref="taxon:32630"
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Query Match      100.0%; Score 25; DB 6; Length 25;
Best Local Similarity 80.0%; Pred. No. 3.9e-05;
Matches 20; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGUCAGCGGAUGCUGGACAGUC 25
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        1 GGTACGCGGAATGCTGTGGACAGTC 25

RESULT 4
BD222534
LOCUS      BD222534      25 bp      RNA      linear      PAT 17-JUL-2003
DEFINITION Methods for detecting and measuring spliced nucleic acids.
ACCESSION  BD222534
VERSION     BD222534.1 GI:33032304
KEYWORDS    JP 2002521037-A/12.
SOURCE      synthetic construct
ORGANISM    artificial sequences.
REFERENCE   1 (bases 1 to 25)
AUTHORS     Harvey, R.C. and Eastman, P.S.
TITLES      Methods for detecting and measuring spliced nucleic acids
JOURNALS    Patent: JP 2002521037-A 12 16-JUL-2002;
            GEN PROBE INC
COMMENT      OS      Artificial Sequence
              PN      JP 2002521037-A/12
              PD      16-JUL-2002
              PP      23-JUL-1999 JP 2000561364
              PR      23-JUL-1998 US 09/121239
              PT      RICHARD C HARVEY, PAUL S EASTMAN
              PC      C12Q1/68, C12N15/09, C12N15/00
              CC      Description of Artificial Sequence: RNA version of SEQ ID NO:
                   9
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ORIGIN

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[illegible]

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Query Match      100.0%; Score 25; DB 9; Length 305;
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Matches 20; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY      1  GGUCAGCGGAAGUCUGGACAGUC  25
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Db      112  GGTGACGGGAATGCTGTGACAGTC  88

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RESULT 10	BD222546	350 bp	DNA	linear	PAT 17-JUL-2003
LOCUS	BD222546/c				
DEFINITION	Methods for detecting and measuring spliced nucleic acids.				
ACCESSION	BD222546				
VERSION	BD222546.1	GI:33032316			
KEYWORDS	JP 2002521037-A/24.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				

REFERENCE	1 (bases 1 to 350)
AUTHORS	Harvey, K.C. and Eastman, P.S.
TITLE	Methods for detecting and measuring spliced nucleic acids
JOURNAL	Patent: JP 2002521037-A 24 16-JUL-2002;
COMMENT	GEN PROBE INC OS Homo sapiens (human) PN JP 2002521037-A/24

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D 18-JUL-2002 JP 2000561364
PF 23-JUL-1999 JP 2000561364
PR 23-JUL-1998 US 09/121239
PI RICHARD C HARVEY, PAUL S EASTMAN
PC C12Q1/68, C12N15/09, C12N15/00
CC Methods for detecting and measuring spliced nucleic acids FH
Key Location/Qualifiers
FT source 1..350
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ORIGIN

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Query Match      100.0%; Score 25; DB 6; Length 350;
Best Local Similarity 80.0%; Pred.NO. 4.1e-05;
Matches 20; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGUCAGCGGAAGUCUGUGACAGUC 25
    ||:|||||:|:|:|:|:|:|
Db 113 GGTACGCGGAATCTGTGGACATC 89

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RESULT 11
HUMMS62B/c
LOCUS
HUMMS62B
561 bp
mRNA
linear
PRI 27-APR-1993
DEFINITION
Human myelocytic chimeric bcr and chromosome 9 fusion gene, exons

ACCESSION	M19695	
VERSION	M19695.1	GI:188567
KEYWORDS	.	
SOURCE	Homo sapiens (human)	
ORGANISM	Homo sapiens	

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 561)  
**REFERENCE**  
**AUTHORS**  
 Grosveld, G., Verwoerd, T., van Aegthoven, T., de Klein, A., Ramachandran, K. L., Heisterkamp, N., Stam, K. and Groffen, J.  
**TITLE**  
 The chronic myelocytic cell line K562 contains a breakpoint in bcr and produces a chimeric bcr/c-abl transcript  
**JOURNAL**  
 Mol. Cell. Biol. 6 (2), 607-616 (1986)  
**MEDLINE**  
 87064346

**MEDLINE** 87064348  
**PUBMED** 3023859

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line, cDNA to mRNA, clone 8E.
The bcr region of the fusion protein is located on chromosome
22q11; the abl region was translocated from chromosome 9q34.
Location/Qualifiers
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            /mol_type="mRNA"
            /db_xref="taxon:9606"
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            /note="cDNA 8E 3' end (AA at 1)"
ORIGIN
Chromosome 22q11.

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Best Local Similarity 80.0%; Pred. No. 4.1e-05;
Matches 20; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy      1  GGUCAGCGGAUUGCUGUGGACAGUC 25
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Db      108  GGTGACGGGAATGCTGTGGCAGTC 84

RESULT 12
HUMABL/c
LOCUS
DEFINITION Human bcr/abl fusion protein, partial cds, clone E3.
ACCESSION M30832
VERSION M30832.1 GI:177944
KEYWORDS Philadelphia chromosome; abl proto-oncogene; translocation.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 679)
AUTHORS Shtivelman,E., Lifshitz,B., Gale,R.P. and Canaani,E.
TITLE Fused transcript of abl and bcr genes in chronic myelogenous
        leukaemia
JOURNAL Nature 315 (6020), 550-554 (1985)
MEDLINE 85240529
PUBMED 2389692
COMMENT Original source text: Homo sapiens (clone: E3.) cDNA to mRNA.
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            /cell_line="chronic myelogenous leukemia cell line EM2"
            <1..>679
            /note="putative"
            /codon_start=3
            /product="bcr/abl fusion protein"
            /protein_id="AAA87612.1"
            /db_xref="GI:1185071"
            /translation="ISOIKSDIQREKRVKSGKATERLKKKLSQESLLLLMSPSWAF
            VHSRPTNGKDESYFLIISDYAEARVREINREQKCFKFSLSASVELQMLTNSCVKIQLOT
            RVSLPTINKEDDESPLYGLVFNIVHSATGFKQSKLQRPVASFDPQGLSEARWNIS
            KENLLAAPSENDPNLFVALYDFVAGSDNTLSITKGEKRLVLYGNHNCEWCEATKTIQ
            GWVPSNY"
CDS
            <1..>561
            /note="chronic myelogenous leukemia cell line EM2"

ORIGIN
Chromosome 22q11.

Query Match      100.0%; Score 25; DB 9; Length 679;
Best Local Similarity 80.0%; Pred. No. 4.2e-05;
Matches 20; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy      1  GGUCAGCGGAUUGCUGUGGACAGUC 25
        ||:|||||:|:|:|:|:|:|:|:|
Db      326  GGTGACGGGAATGCTGTGGCAGTC 302

RESULT 13
HUMABL/c
LOCUS
DEFINITION Human bcr/abl fusion protein mRNA, partial cds, clone K28.

```



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/gene="abl"
/number=3
844. .997
/gene="abl"
844. .>997
/gene="abl"
/number=4
```

gene  
exon

ORIGIN

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Query Match      100.0%; Score 25; DB 9; Length 997;
Best Local Similarity 80.0%; Pred. No. 4.2e-05;
Matches 20; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GGUCAGCGGAUUGCUGGACAGUC 25
        ||:|||||:|:|:|:|:|:|:|
Db      285 GGTGAGCGGAATGCTGTGGACATC 261
```

Search completed: May 27, 2004, 02:16:39  
Job time : 532.065 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 26, 2004, 14:55:11 ; Search time 111.497 Seconds  
(without alignments)  
952.539 Million cell updates/sec

Title: US-09-121-239-12

Perfect score: 25

Sequence: 1 GGUCAGCGAUGCUGGACAGUC 25

Scoring table: OLIGO NUC

Gapop 60.0 , Gapext 60.0

Searched: 3373863 seqs, 2124099041 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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- 2: geneseqn1990s:\*
- 3: geneseqn2000s:\*
- 4: geneseqn2001as:\*
- 5: geneseqn2001bs:\*
- 6: geneseqn2002s:\*
- 7: geneseqn2003as:\*
- 8: geneseqn2003bs:\*
- 9: geneseqn2003cs:\*
- 10: geneseqn2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	25	100.0	25	3	Aaz60850 Oligonucleotide
2	25	100.0	25	3	Aaz60849 Oligonucleotide
3	25	100.0	25	3	Aaz60851 Oligonucleotide
4	25	100.0	25	3	Aaz60848 Oligonucleotide
5	25	100.0	45	9	ADC38532 Template
6	25	100.0	56	2	Aaq46951 Branched
7	25	100.0	200	2	Aat88785 Leukaemic
8	25	100.0	250	6	Abs73175 Human tra
9	25	100.0	305	6	Abs73174 DNA encod
10	25	100.0	350	3	Aaz60863 Region su
11	25	100.0	504	5	Aas85023 DNA encod
12	25	100.0	504	8	Ach38242 Human end
13	25	100.0	561	8	Abs73169 Human tra
14	25	100.0	679	6	Abs73172 DNA encod
15	25	100.0	766	5	Abv29306 Human pro
16	25	100.0	766	5	Abv23449 Human pro
17	25	100.0	854	6	Abs73170 DNA encod
18	25	100.0	921	5	Aas85025 DNA encod
19	25	100.0	922	6	Abs73180 DNA encod
20	25	100.0	997	6	Abs73173 DNA encod
21	25	100.0	1097	2	Aat91764 Chimeric
22	25	100.0	1157	9	Adc64640 Hepatitis
23	25	100.0	1212	5	Aas85028 DNA encod

# ALIGNMENTS

## RESULT 1

AAZ60850	AAZ60850 standard; DNA; 25 BP.				
XX	AAZ60850;				
XX	16-MAY-2000 (first entry)				
XX	Oligonucleotide used to detect bcr b3-abl fusion transcripts.				
DE	Fusion transcript; translocation; bcr b3 region; abl gene;				
KW	amplification assay; detection assay; medical diagnosis;				
KW	clinical monitoring; chimeric RNA; fusion RNA; condition marker;				
KW	disease marker; cancer; leukemia; ss.				
XX	Synthetic.				
OS	WO200005418-A1.				
PN	03-FEB-2000.				
PD	23-JUL-1999; 99WO-US016832.				
XX	23-JUL-1998; 98US-00121239.				
XX	(GENP-) GEN-PROBE INC.				
PA	Harvey RC, Eastman PS;				
PI	WPI; 2000-182730/16.				
XX	Novel methods for preparing RNA from biological samples, used for the				
DR	detection and measurement of nucleic acids and fusion nucleic acids.				
PT	Claim 19; Page 41; 49pp; English.				
XX	Oligonucleotides AAZ60840-62 and AAZ60865-66 are used in the method of				
PS	the invention to detect fusion transcripts produced from a translocation				
CC	between the bcr b3 region and the abl gene. The specification describes a				
CC	method for detecting a fusion nucleic acid (particularly chimeric mRNA				
CC	species), in a biological sample. The method comprises contacting a				
CC	sample of fusion nucleic acid with primers, amplifying the hybridized				
CC	fusion nucleic acid, and detecting the target hybrid. The method is used				
CC	for the sample and rapid preparation of RNA from a biological sample,				
CC	particularly from the cytoplasm of eukaryotic cells, which is suitable				
CC	for use in an amplification and detection assay. The methods are used for				

AA60228	Sequence
Aas76375	DNA encod
Ab163316	Breast ca
Acc00031	Human Bcr
Aas85030	DNA encod
Aas76377	DNA encod
Aas85031	DNA encod
ACa64961	Human BCR
Aas1830	bcr mRNA
Aav58775	Forward p
Abs73171	Human tra
Aat91761	Primer DE
Aas91782	Primer BB
Aaq4635	Human bcr
Aaq66774	L6(1)31 r
Aan91666	Bcr-abl f
Aan91666	Bcr-abl f
Aaq34625	Human bcr
Aav20458	Human bcr
Aaz91685	PCR prime
Adb68429	PCR prime
Add06158	Bcr-abl f

c 24	25	100.0	2255	1	AA60228
c 25	25	100.0	4725	5	AAS76375
c 26	25	100.0	4739	6	ABL63316
c 27	25	100.0	4739	7	ACC00031
c 28	25	100.0	4756	5	AAS85030
c 29	25	100.0	4775	5	AAS76377
c 30	25	100.0	5795	5	AAS85031
c 31	25	100.0	152141	7	ACA64961
c 32	24	96.0	26	2	AAV51830
c 33	24	96.0	40	2	AAV58775
c 34	21	84.0	468	6	ABS73171
c 35	20	80.0	20	2	AAT91761
c 36	19	76.0	45	2	AAT91782
c 37	18	72.0	22	2	AAQ34635
c 38	18	72.0	62	2	AAQ66774
c 39	18	72.0	81	2	AAQ66775
c 40	18	72.0	205	1	AAQ91666
c 41	18	72.0	257	2	AAQ34625
c 42	18	72.0	257	2	AAV20458
c 43	17	68.0	20	3	AAZ91685
c 44	17	68.0	20	8	ADB68429
c 45	17	68.0	20	9	ADD06158

CC the analysis and detection of nucleic acids in biological samples. The  
 CC methods are useful in the human medical and veterinary fields, for  
 CC medical diagnoses and clinical monitoring of a patient's response to  
 CC therapy where a disease or medical condition is associated with a  
 CC particular type and/or level of mRNA present in the sample. The methods  
 CC are also useful for detecting or quantifying fusion or chimeric RNA  
 CC species, and for detecting a translocation as a marker for a given  
 CC condition or disease, e.g. translocations associate with cancers,  
 CC particularly forms of leukemia  
 XX  
 SQ Sequence 25 BP; 5 A; 5 C; 10 G; 5 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 25; DB 3; Length 25;  
 Best Local Similarity 80.0%; Pred. No. 0.00021;  
 Matches 20; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGUCAGCGGAUUCUGGACAGUC 25  
 ||:|||||:|:|:|:|:|:|:  
 Db 1 GGTACGCGGAATGCTGTGGACAGTC 25

RESULT 2  
 AAZ60849/c  
 ID AAZ60849 standard; RNA; 25 BP.  
 XX  
 AC AAZ60849;  
 XX  
 DT 16-MAY-2000 (first entry)  
 XX  
 DE Oligonucleotide used to detect bcr b3-abl fusion transcripts.  
 KW Fusion transcript; translocation; bcr b3 region; abl gene;  
 KW amplification assay; detection assay; medical diagnosis;  
 KW clinical monitoring; chimeric RNA; fusion RNA; condition marker;  
 KW disease marker; cancer; leukemia; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200005418-A1.  
 XX  
 PD 03-FEB-2000.  
 XX  
 PF 23-JUL-1999; 99WO-US016832.  
 XX  
 PR 23-JUL-1998; 98US-00121239.  
 XX  
 PA (GENP-) GEN-PROBE INC.  
 XX  
 PI Harvey RC, Eastman PS;  
 XX  
 DR WPI; 2000-182730/16.  
 XX  
 PT Novel methods for preparing RNA from biological samples, used for the  
 PT detection and measurement of nucleic acids and fusion nucleic acids.  
 XX  
 PS Claim 19; Page 41; 49pp; English.  
 XX  
 CC Oligonucleotides AAZ60840-62 and AAZ60865-66 are used in the method of  
 CC the invention to detect fusion transcripts produced from a translocation  
 CC between the bcr b3 region and the abl gene. The specification describes a  
 CC method for detecting a fusion nucleic acid (particularly chimeric mRNA  
 CC species), in a biological sample. The method comprises contacting a  
 CC sample of fusion nucleic acid with primers, amplifying the hybridized  
 CC fusion nucleic acid, and detecting the target hybrid. The method is used  
 CC for the simple and rapid preparation of RNA from a biological sample,  
 CC particularly from the cytoplasm of eukaryotic cells, which is suitable  
 CC for use in an amplification and detection assay. The methods are used for  
 CC the analysis and detection of nucleic acids in biological samples. The  
 CC methods are useful in the human medical and veterinary fields, for  
 CC medical diagnoses and clinical monitoring of a patient's response to  
 CC therapy where a disease or medical condition is associated with a  
 CC particular type and/or level of mRNA present in the sample. The methods  
 CC are also useful for detecting or quantifying fusion or chimeric RNA  
 CC species, and for detecting a translocation as a marker for a given  
 CC condition or disease, e.g. translocations associate with cancers,  
 CC particularly forms of leukemia  
 XX  
 SQ Sequence 25 BP; 5 A; 5 C; 10 G; 5 T; 0 U; 0 Other;

CC species, and for detecting a translocation as a marker for a given  
 CC condition or disease, e.g. translocations associate with cancers,  
 CC particularly forms of leukemia  
 XX  
 SQ Sequence 25 BP; 5 A; 10 C; 5 G; 0 T; 5 U; 0 Other;  
 Query Match 100.0%; Score 25; DB 3; Length 25;  
 Best Local Similarity 80.0%; Pred. No. 0.00021;  
 Matches 20; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGUCAGCGGAUUCUGGACAGUC 25  
 ||:|||||:|:|:|:|:|:|:  
 Db 25 GGTACGCGGAATGCTGTGGACAGTC 1

RESULT 3  
 AAZ60851  
 ID AAZ60851 standard; RNA; 25 BP.  
 XX  
 AC AAZ60851;  
 XX  
 DT 16-MAY-2000 (first entry)  
 XX  
 DE Oligonucleotide used to detect bcr b3-abl fusion transcripts.  
 KW Fusion transcript; translocation; bcr b3 region; abl gene;  
 KW amplification assay; detection assay; medical diagnosis;  
 KW clinical monitoring; chimeric RNA; fusion RNA; condition marker;  
 KW disease marker; cancer; leukemia; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200005418-A1.  
 XX  
 PD 03-FEB-2000.  
 XX  
 PF 23-JUL-1999; 99WO-US016832.  
 XX  
 PR 23-JUL-1998; 98US-00121239.  
 XX  
 PA (GENP-) GEN-PROBE INC.  
 XX  
 PI Harvey RC, Eastman PS;  
 XX  
 DR WPI; 2000-182730/16.  
 XX  
 PT Novel methods for preparing RNA from biological samples, used for the  
 PT detection and measurement of nucleic acids and fusion nucleic acids.  
 XX  
 PS Claim 19; Page 41; 49pp; English.  
 XX  
 CC Oligonucleotides AAZ60840-62 and AAZ60865-66 are used in the method of  
 CC the invention to detect fusion transcripts produced from a translocation  
 CC between the bcr b3 region and the abl gene. The specification describes a  
 CC method for detecting a fusion nucleic acid (particularly chimeric mRNA  
 CC species), in a biological sample. The method comprises contacting a  
 CC sample of fusion nucleic acid with primers, amplifying the hybridized  
 CC fusion nucleic acid, and detecting the target hybrid. The method is used  
 CC for the simple and rapid preparation of RNA from a biological sample,  
 CC particularly from the cytoplasm of eukaryotic cells, which is suitable  
 CC for use in an amplification and detection assay. The methods are used for  
 CC the analysis and detection of nucleic acids in biological samples. The  
 CC methods are useful in the human medical and veterinary fields, for  
 CC medical diagnoses and clinical monitoring of a patient's response to  
 CC therapy where a disease or medical condition is associated with a  
 CC particular type and/or level of mRNA present in the sample. The methods  
 CC are also useful for detecting or quantifying fusion or chimeric RNA  
 CC species, and for detecting a translocation as a marker for a given  
 CC condition or disease, e.g. translocations associate with cancers,  
 CC particularly forms of leukemia  
 XX  
 SQ Sequence 25 BP; 5 A; 5 C; 10 G; 0 T; 5 U; 0 Other;



```

Db      . 25 GGTGACGGGAATGCTGTGGACAGTC 1

RESULT 5
ADC38532/c
ID  ADC38532 standard; DNA; 45 BP.
XX
XX  AC  ADC38532;
XX
XX  18-DEC-2003 (first entry)
XX
XX  Template translocation oligonucleotide SEQ ID 9.
XX
XX  Chromosome translocation; cancer; leukaemia; lymphoma; ss.
XX
XX  Synthetic.
XX
XX  WO2003044486-A2.
XX
XX  30-MAY-2003.
XX
XX  20-NOV-2002; 2002WO-US037507.
XX
XX  20-NOV-2001; 2001US-0335716P.
XX
XX  (REGC ) UNIV CALIFORNIA.
XX
XX  Nolan JP, Zhou F;
XX
XX  WPI; 2003-468806/44.
XX
XX  Detecting chromosome translocations in a target nucleic acid sequence for
XX  diagnosing cancers associated with chromosome translocations, by using
XX  microsphere arrays.
XX
XX  Claim 52; Fig 7; 57pp; English.
XX
XX  The present invention relates to a method (M) for detecting chromosome
XX  translocation. The method comprises amplifying a target nucleic acid
XX  sequence from a sample, hybridizing oligonucleotides (ONTs) specific for
XX  regions of the translocation to the amplified target, where the ONTs
XX  comprise capture tags, extending the ONTs to produce labelled extended
XX  ONTs, hybridizing the ONTs to address tags on solid support and detecting
XX  the presence of labelled extended ONTs on the solid support. (M) is
XX  useful for detecting a chromosomal translocation in a target nucleic acid
XX  sequence, preferably a cdna from a biological sample from a human. The
XX  chromosome translocation is associated with cancer (e.g. leukaemia) and
XX  this method is especially useful for diagnosing cancer, especially
XX  leukaemia, and also lymphoma. The present sequence is a template
XX  translocation oligonucleotide used to illustrate the invention.
XX
XX  Sequence 45 BP; 15 A; 14 C; 8 G; 8 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 9; Length 45;
Best Local Similarity 80.0%; Pred. No. 0.00021;
Matches 20; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GGUCAGCGGAUUCGUGGACAGUC 25
         ||:|||||:|:|:|:|:|:|
Db      31 GGTGACGGGAATGCTGTGGACAGTC 7

RESULT 6
AAQ46951/c
ID  AAQ46951 standard; DNA; 56 BP.
XX
XX  AC  AAQ46951;
XX
XX  25-MAR-2003 (revised)
XX
XX  21-JAN-1994 (first entry)
XX
XX  Branched probe to CMLb translocation region of chromosome 22.
XX

```

KW Chronic myelogenous leukaemia; CMLb; abl region;  
 KW acute lymphocytic leukaemia; ALL; genetic translocation; chromosome 22;  
 KW target sequence; universal detection oligomer; branched probe;  
 KW chemiluminescent acridinium ester; ss.  
 XX  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT misc\_feature 1..40  
 FT /tag= a  
 FT /note= "complementary to region of chromosome 22  
 FT associated with CMLb translocation"  
 FT 41..56  
 FT /tag= b  
 FT /note= "complementary to nucleotides 16-1 of universal  
 FT detection probe AAQ46949"  
 FT  
 XX EP552931-A1.  
 XX  
 XX  
 PD 28-JUL-1993.  
 XX  
 XX  
 PF 20-JAN-1993; 93EP-00300377.  
 XX  
 XX 22-JAN-1992; 92US-00827021.  
 XX (GENP-) GEN PROBE INC.  
 XX  
 XX Hogan JJ, Arnold LJ, Nelson NC, Bezverkov R;  
 XX WPI; 1993-236606/30.  
 XX  
 XX Nucleic acid molecules which hybridise in presence of target nucleic acid  
 PT - are used as probes in hybridisation assays or as therapeutic agents for  
 PT diseases.  
 XX  
 PS Example 6; Fig 12B; 58pp; English.  
 XX  
 CC Chimeric targets were synthesised homologous to 3 different genetic  
 CC translocations between a constant abl region of chromosome 9 and various  
 CC regions of chromosome 22; two are the most common translocations  
 CC associated with chronic myelogenous leukaemia (CMLa and CMLb) and the  
 CC other is associated with acute lymphocytic leukaemia (ALL). An AB-  
 CC labelled universal detection oligomer (AAQ46949) specific for the abl  
 CC region was synthesised. Three different strands were designed to contain  
 CC a probe region specific for one of the translocated chromosome 22 regions  
 CC as well as an arm region complementary to part of the universal probe  
 CC (AAQ46950-2). The probe mixes were found to detect only the correct  
 CC chimeric targets and did not cross-react significantly with the other  
 CC targets. (Updated on 25-MAR-2003 to correct PN field.) (Updated on 25-MAR  
 CC -2003 to correct PA field.)  
 XX  
 SQ Sequence 56 BP; 18 A; 18 C; 9 G; 11 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 25; DB 2; Length 56;  
 Best Local Similarity 80.0%; Pred. No. 0.00021;  
 Matches 20; Conservative 5; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GGUCAGCGGAUUCUGUGGACAGUC 25  
 ||:|||||:|:|:|:|:|:|  
 DB 27 GGTACGCGGAATGCTGTGGACAGTC 3  
 RESULT 7  
 AAT88785/C  
 ID AAT88785 standard; DNA; 200 BP.  
 XX  
 XX AAT88785;  
 XX  
 XX  
 DT 23-MAR-1998 (first entry)  
 XX  
 DE Leukaemic cell BCR-ABL mRNA PCR product target sequence.  
 XX  
 KW Leukaemia; BCR-ABL; cell line K562; target; immunoassay; probe;

KW hybridisation; diagnostic; luciferase; genetic disease; ss.  
 XX Unidentified.  
 XX  
 PN CA2186998-A.  
 XX  
 PD 31-MAY-1997.  
 XX  
 XX 02-OCT-1996; 96CA-02186998.  
 XX  
 PR 30-NOV-1995; 95US-00565055.  
 XX (UYWI-) UNIV WINDSOR.  
 XX  
 XX Christopoulos TK;  
 XX WPI; 1997-415964/39.  
 XX  
 XX Immunoassays and nucleic acid hybridisation assays - using protein-  
 PT encoding nucleic acid fragments as labels.  
 XX  
 PS Disclosure; Page 26; 39pp; English.  
 XX  
 CC A novel assay has been developed for determining an analyte. The assay  
 CC comprises labelling the analyte with a nucleic acid fragment that encodes  
 CC a protein, expressing the nucleic acid, and detecting the protein. The  
 CC present sequence represents a target sequence from a leukaemic cell (cell  
 CC line K562), used in an example of the present assay. The assay is used  
 CC for the determination of antigens or nucleic acids for diagnostic or  
 CC research purposes, e.g. detecting low levels of tumour markers, analysing  
 CC nucleic acid mutations associated with genetic diseases, diagnosing and  
 CC monitoring pathogen infections, or searching for new disease markers. The  
 CC immunoassay when using a luciferase for detection is more sensitive than  
 CC an enzyme-amplified, time-resolved fluorometric immunoassay and does not  
 CC require preparation of a luciferase-antibody conjugate  
 XX  
 SQ Sequence 200 BP; 49 A; 52 C; 51 G; 48 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 25; DB 2; Length 200;  
 Best Local Similarity 80.0%; Pred. No. 0.0002; Indels 0; Gaps 0;  
 Matches 20; Conservative 5; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GGUCAGCGGAUUCUGUGGACAGUC 25  
 ||:|||||:|:|:|:|:|:|  
 DB 64 GGTACGCGGAATGCTGTGGACAGTC 40  
 RESULT 8  
 ABS73175/C  
 ID ABS73175 standard; DNA; 250 BP.  
 XX  
 XX ABS73175;  
 XX  
 DT 04-DEC-2002 (first entry)  
 XX  
 DE Human translocation (9: 22)(q34: q11) #3.  
 XX  
 KW Chromosome aberration; oncogenic fusion protein; cancer;  
 KW proliferative disease; cellular protein isoform; heat shock protein 90;  
 KW HSP-90; rheumatoid arthritis; cancer; haematopoietic disorder;  
 KW T cell lymphoma; B cell lymphoma; chronic myeloid leukaemia; CML;  
 KW acute myeloid leukaemia; AML; chronic myelomonocytic leukaemia; CMML;  
 KW acute lymphoblastic leukaemia; ALL; APL; solid tumour;  
 KW papillary thyroid carcinoma; Ewing's sarcoma; melanoma; liposarcoma;  
 KW rhabdomyosarcoma; synovial sarcoma; viral infection; gene; ds.  
 XX  
 XX Homo sapiens.  
 XX  
 XX WO200269900-A2.  
 PN  
 XX  
 XX 12-SEP-2002.  
 PD  
 XX  
 XX 01-MAR-2002; 2002WO-US006518.

```

XX 01-MAR-2001; 2001US-0272751P.
XX (CONF-) CONFORMA THERAPEUTICS CORP.
XX Fritz LC, Burrows FJ;
XX WPI; 2002-698710/75.
XX P-PSDB; ABG95013.
XX Treating genetically-defined disease associated with chromosomal
XX aberrations yielding oncogenic fusion proteins, e.g. cell proliferative
XX diseases, involves administering an inhibitor of heat shock protein 90.
XX Disclosure; Page 97; 389pp; English.
XX The invention describes a method of treating genetically-defined disease
XX associated with chromosomal aberrations yielding oncogenic fusion
XX proteins (I), treating cancerous cells containing (I) in a heterogeneous
XX cell population, treating proliferative diseases associated with mutant
XX protein or cellular protein isoforms (II) dependent on heat shock protein
XX (HSP)-90, or selectively treating cells expressing (II) involving
XX administering HSP90-inhibitor. The method is useful for treating
XX genetically-defined disease with chromosomal aberration yielding
XX oncogenic fusion protein, treating cancerous cells containing fusion
XX protein in heterogeneous cell population, treating proliferative disease
XX (e.g. rheumatoid arthritis or cancer) associated with mutant protein or
XX cellular protein isoform dependent on heat shock protein (HSP)-90 (e.g.
XX p53), or selectively treating cells expressing mutant protein or cellular
XX protein isoform in a patient heterozygous for (II). The method is useful
XX for treating a disease e.g. haematopoietic disorder such as T or B cell
XX lymphoma, chronic myeloid leukaemia (CML), ALL, AML, NHL and CMMU,
XX or a disease characterised by a solid tumour such as papillary thyroid
XX carcinoma, Ewing's sarcoma, melanoma, liposarcoma, rhabdomyosarcoma and
XX synovial sarcoma. The method is also useful for treating viral
XX infections. This represents the DNA sequence of a chromosome aberration
XX Sequence 250 BP; 65 A; 62 C; 63 G; 60 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 25; DB 6; Length 250;
XX Best Local Similarity 80.0%; Pred. No. 0.0002;
XX Matches 20; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 GGUCAGCGGAUUGCUGGACAGUC 25
DB 65 GGTACGCGGAATGCTGTGCACGTC 41
XX
RESULT 9
ABS73174/c
ID ABS73174 standard; DNA; 305 BP.
XX
XX AC ABS73174;
XX
XX DT 04-DEC-2002 (first entry)
XX
XX DE DNA encoding human translocation (9: 22) (q34: q11) protein #5.
XX
XX KW Chromosome aberration; oncogenic fusion protein; cancer;
XX proliferative disease; cellular protein isoform; heat shock protein 90;
XX HSP-90; rheumatoid arthritis; cancer; haematopoietic disorder;
XX T cell lymphoma; B cell lymphoma; chronic myeloid leukaemia; CML;
XX acute myeloid leukaemia; ALL; chronic myelomonocytic leukaemia; CMMU;
XX acute lymphoblastic leukaemia; ALL; NHL; solid tumour;
XX papillary thyroid carcinoma; Ewing's sarcoma; melanoma; liposarcoma;
XX rhabdomyosarcoma; synovial sarcoma; viral infection; gene; ds.
XX
XX OS Homo sapiens.
XX
XX PN WO200269900-A2.
XX
XX PD 12-SEP-2002.
XX
XX PF 01-MAR-2002; 2002WO-US006518.
XX
XX
XX 01-MAR-2001; 2001US-0272751P.
XX (CONF-) CONFORMA THERAPEUTICS CORP.
XX Fritz LC, Burrows FJ;
XX WPI; 2002-698710/75.
XX P-PSDB; ABG95013.
XX Treating genetically-defined disease associated with chromosomal
XX aberrations yielding oncogenic fusion proteins, e.g. cell proliferative
XX diseases, involves administering an inhibitor of heat shock protein 90.
XX Disclosure; Page 97; 389pp; English.
XX The invention describes a method of treating genetically-defined disease
XX associated with chromosomal aberrations yielding oncogenic fusion
XX proteins (I), treating cancerous cells containing (I) in a heterogeneous
XX cell population, treating proliferative diseases associated with mutant
XX protein or cellular protein isoforms (II) dependent on heat shock protein
XX (HSP)-90, or selectively treating cells expressing (II) involving
XX administering HSP90-inhibitor. The method is useful for treating
XX genetically-defined disease with chromosomal aberration yielding
XX oncogenic fusion protein, treating cancerous cells containing fusion
XX protein in heterogeneous cell population, treating proliferative disease
XX (e.g. rheumatoid arthritis or cancer) associated with mutant protein or
XX cellular protein isoform dependent on heat shock protein (HSP)-90 (e.g.
XX p53), or selectively treating cells expressing mutant protein or cellular
XX protein isoform in a patient heterozygous for (II). The method is useful
XX for treating a disease e.g. haematopoietic disorder such as T or B cell
XX lymphoma, chronic myeloid leukaemia (CML), ALL, AML, NHL and CMMU,
XX or a disease characterised by a solid tumour such as papillary thyroid
XX carcinoma, Ewing's sarcoma, melanoma, liposarcoma, rhabdomyosarcoma and
XX synovial sarcoma. The method is also useful for treating viral
XX infections. This represents the DNA sequence of a chromosome aberration
XX Sequence 305 BP; 77 A; 79 C; 77 G; 72 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 25; DB 6; Length 305;
XX Best Local Similarity 80.0%; Pred. No. 0.0002;
XX Matches 20; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 GGUCAGCGGAUUGCUGGACAGUC 25
DB 112 GGTACGCGGAATGCTGTGCACGTC 88
XX
RESULT 10
AAZ60863/c
ID AAZ60863 standard; DNA; 350 BP.
XX
XX AC AAZ60863;
XX
XX DT 16-MAY-2000 (first entry)
XX
XX DE Region surrounding a bcr-able splice junction.
XX
XX KW Fusion transcript; translocation; bcr b3 region; abl gene;
XX amplification assay; detection assay; medical diagnosis;
XX clinical monitoring; chimeric RNA; fusion RNA; condition marker;
XX disease marker; cancer; leukemia; ss.
XX
XX OS Unidentified.
XX
XX PN WO200005418-A1.
XX
XX PD 03-FEB-2000.
XX
XX PF 23-JUL-1999; 99WO-US016832.
XX
XX PR 23-JUL-1998; 98US-00121239.
XX
XX

```

PA (GENP-) GEN-PROBE INC.  
 XX Harvey RC, Eastman PS;  
 XX WPI; 2000-182730/16.  
 XX  
 PT Novel methods for preparing RNA from biological samples, used for the  
 PT detection and measurement of nucleic acids and fusion nucleic acids.  
 XX  
 PS Disclosure; Fig 2; 49pp; English.  
 XX  
 CC The present sequence represents a region surrounding a bcr-able splice  
 CC junction. The specification describes oligonucleotides which are used to  
 CC detect fusion transcripts produced from a translocation between the bcr  
 CC b3 region and the abl gene. The specification also describes a method for  
 CC detecting a fusion nucleic acid (particularly chimeric mRNA species), in  
 CC a biological sample. The method comprises contacting a sample of fusion  
 CC nucleic acid with primer, amplifying the hybridized fusion nucleic acid,  
 CC and detecting the target hybrid. The method is used for the simple and  
 CC rapid preparation of RNA from a biological sample, particularly from the  
 CC cytoplasm of eukaryotic cells, which is suitable for use in an  
 CC amplification and detection assay. The methods are used for the analysis  
 CC and detection of nucleic acids in biological samples. The methods are  
 CC useful in the human medical and veterinary fields, for medical diagnoses  
 CC and clinical monitoring of a patient's response to therapy where a disease  
 CC or medical condition is associated with a particular type and/or level of  
 CC mRNA present in the sample. The methods are also useful for detecting or  
 CC quantifying fusion or chimeric RNA species, and for detecting a  
 CC translocation as a marker for a given condition or disease, e.g.  
 CC translocations associate with cancers, particularly forms of leukemia  
 XX  
 SQ Sequence 350 BP; 85 A; 92 C; 89 G; 84 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 3; Length 350;  
 Best Local Similarity 80.0%; Pred. No. 0.0002;  
 Matches 20; Conservative 5; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GGUCAGCGGAAGUCUGGACAGUC 25  
 ||:|||||:|||||:|||||:  
 Db 113 GGTACGCGGAATGCTGTGCACATC 89

RESULT 11  
 AAS85023/c  
 ID AAS85023 standard; cDNA; 504 BP.  
 AC AAS85023;  
 XX  
 DT 13-FEB-2002 (first entry)  
 DE  
 DE DNA encoding novel human diagnostic protein #20827.  
 XX  
 KW Human; chromosome mapping; gene mapping; gene therapy; forensic;  
 KW food supplement; medical imaging; diagnostic; genetic disorder; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200175067-A2.  
 XX  
 PD 11-OCT-2001.  
 XX  
 PF 30-MAR-2001; 2001WO-US008631.  
 XX  
 PR 31-MAR-2000; 2000US-00540217.  
 PR 23-AUG-2000; 2000US-00649167.  
 XX  
 PA (HYSE-) HYSEQ INC.  
 XX  
 PI Drmanac RT, Liu C, Tang YT;  
 XX  
 DR WPI; 2001-639362/73.  
 DR P-PSDB; ABG20836.  
 XX  
 XX

PT New isolated polynucleotide and encoded polypeptides, useful in  
 PT diagnostics, forensics, gene mapping, identification of mutations  
 PT responsible for genetic disorders or other traits and to assess  
 PT biodiversity.  
 XX  
 PS Claim 1; SEQ ID NO 20827; 103pp; English.  
 XX  
 CC The invention relates to isolated polynucleotide (I) and polypeptide (II)  
 CC sequences. (I) is useful as hybridisation probes, polymerase chain  
 CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,  
 CC and in recombinant production of (II). The polynucleotides are also used  
 CC in diagnostics as expressed sequence tags for identifying expressed  
 CC genes. (I) is useful in gene therapy techniques to restore normal  
 CC activity of (II) or to treat disease states involving (II). (II) is  
 CC useful for generating antibodies against it, detecting or quantitating a  
 CC polypeptide in tissue, as molecular weight markers and as a food  
 CC supplement. (II) and its binding partners are useful in medical imaging  
 CC of sites expressing (II). (I) and (II) are useful for treating disorders  
 CC involving aberrant protein expression or biological activity. The  
 CC polypeptide and polynucleotide sequences have applications in  
 CC diagnostics, forensics, gene mapping, identification of mutations  
 CC responsible for genetic disorders or other traits to assess biodiversity  
 CC and to produce other types of data and products dependent on DNA and  
 CC amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic  
 CC coding sequences of the invention. Note: The sequence data for this  
 CC patent did not appear in the printed specification, but was obtained in  
 CC electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 504 BP; 119 A; 122 C; 144 G; 117 T; 0 U; 2 Other;

Query Match 100.0%; Score 25; DB 5; Length 504;  
 Best Local Similarity 80.0%; Pred. No. 0.0002;  
 Matches 20; Conservative 5; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GGUCAGCGGAAGUCUGGACAGUC 25  
 ||:|||||:|||||:|||||:  
 Db 263 GGTACGCGGAATGCTGTGCACATC 239

RESULT 12  
 ACH38242/c  
 ID ACH38242 standard; cDNA; 504 BP.  
 XX  
 AC ACH38242;  
 XX  
 DT 13-OCT-2003 (first entry)  
 DE  
 DE Human endothelial cell cDNA #6375.  
 XX  
 KW Human; ss; sequencing by hybridisation; SBH; expressed sequence tag; EST;  
 KW genome mapping; biodiversity; genetic disorder.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US2003073623-A1.  
 XX  
 PD 17-APR-2003.  
 XX  
 PF 30-JUL-2001; 2001US-00918995.  
 XX  
 PR 30-JUL-2001; 2001US-00918995.  
 XX  
 PA (DRMA/) DRMANAC R T.  
 PA (LABA/) LABAT I.  
 PA (STAC/) STACHE-CRAIN B.  
 PA (DICK/) DICKSON M C.  
 PA (JONE/) JONES L W.  
 XX  
 PI Drmanac RT, Labat I, Stache-Crain B, Dickson MC, Jones LW;  
 XX  
 DR WPI; 2003-615964/58.  
 XX  
 XX

PT aberrations yielding oncogenic fusion proteins, e.g. cell proliferative

**Treating genetically-defined disease associated with chromosomal**

PT aberrations yielding oncogenic fusion proteins, e.g. cell proliferative  
 PT diseases, involves administering an inhibitor of heat shock protein 90.  
 XX  
 PS Disclosure; Page 94-95; 389pp; English.  
 XX  
 CC The invention describes a method of treating genetically-defined disease  
 CC associated with chromosomal aberrations yielding oncogenic fusion  
 CC proteins (I), treating cancerous cells containing (I) in a heterogeneous  
 CC cell population, treating proliferative diseases associated with mutant  
 CC protein or cellular protein isoforms (II) dependent on heat shock protein  
 CC (HSP)-90, or selectively treating cells expressing (II) involving  
 CC administering HSP90-inhibitor. The method is useful for treating  
 CC genetically-defined disease with chromosomal aberration yielding  
 CC oncogenic fusion protein, treating cancerous cells containing fusion  
 CC protein in heterogeneous cell population, treating proliferative disease  
 CC (e.g. rheumatoid arthritis or cancer) associated with mutant protein or  
 CC cellular protein isoform dependent on heat shock protein (HSP)-90 (e.g.  
 CC p53), or selectively treating cells expressing mutant protein or cellular  
 CC protein isoform in a patient heterozygous for (II). The method is useful  
 CC for treating a disease e.g. haematopoietic disorder such as T or B cell  
 CC lymphoma, chronic myeloid leukaemia (CML), APL, ALL, NHL and CML,  
 CC or a disease characterised by a solid tumour such as papillary thyroid  
 CC carcinoma, Ewing's sarcoma, melanoma, liposarcoma, rhabdomyosarcoma and  
 CC synovial sarcoma. The method is also useful for treating viral  
 CC infections. This represents the DNA sequence of a chromosome aberration  
 XX  
 SQ Sequence 679 BP; 186 A; 165 C; 184 G; 144 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 6; Length 679;  
 Best Local Similarity 80.0%; Pred. No. 0.0002;  
 Matches 20; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGUCAGCGGAUUCUGUGACAGUC 25  
 DB 326 GGTACGCGGAATGCTGTGGACAGTC 302

RESULT 15  
 ABV29306  
 ID ABV29306 standard; cDNA; 766 BP.  
 AC ABV29306;  
 XX  
 DT 16-SEP-2002 (first entry)  
 XX  
 DE Human prostate expression marker cDNA 29297.  
 XX  
 KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;  
 KW pharmacogenomic marker; gene; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200160860-A2.  
 XX  
 PD 23-AUG-2001.  
 XX  
 XX 20-FEB-2001; 2001WO-US005171.  
 XX  
 PR 17-FEB-2000; 2000US-0183319P.  
 PR 16-MAR-2000; 2000US-0189862P.  
 PR 25-MAY-2000; 2000US-0207454P.  
 PR 09-JUN-2000; 2000US-0211314P.  
 PR 18-JUL-2000; 2000US-0219007P.  
 PR 13-DEC-2000; 2000US-0255281P.  
 XX  
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
 XX  
 PI Schlegel R, Endege WO, Monahan JE;  
 XX  
 DR WPI; 2001-662795/76.  
 XX  
 PT Novel isolated nucleic acid molecule associated with cancerous state of  
 PT prostate cells and correlating with presence of prostate cancer, useful

PT for detecting presence of prostate cancer, stage of prostate cancer.  
 XX  
 PS Claim 1; Page 6267; 11750pp; English.  
 XX  
 CC The invention relates to an isolated nucleic acid molecule (I) comprising  
 CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the  
 CC specification or its complement. (I) is useful for: (a) assessing whether  
 CC a patient is afflicted with prostate cancer; (b) monitoring the  
 CC progression of prostate cancer in a patient; (c) assessing the efficacy  
 CC of a test compound to inhibit prostate cancer in a patient; (d) assessing  
 CC the efficacy of a therapy for inhibiting prostate cancer in a patient;  
 CC (e) selecting a composition for inhibiting prostate cancer in a patient;  
 CC (f) assessing the prostate cell carcinogenic potential of a compound; (g)  
 CC determining whether prostate cancer has metastasized in a patient; (h)  
 CC assessing the aggressiveness or indolence of prostate cancer in a patient  
 CC ; (I) is also useful as a pharmacodynamic or pharmacogenomic marker  
 XX  
 SQ Sequence 766 BP; 166 A; 237 C; 193 G; 170 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 25; DB 5; Length 766;  
 Best Local Similarity 80.0%; Pred. No. 0.0002;  
 Matches 20; Conservative 5; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 GGUCAGCGGAUUCUGUGACAGUC 25  
 DB 529 GGTACGCGGAATGCTGTGGACAGTC 553

Search completed: May 26, 2004, 16:52:17  
 Job time : 111.497 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: May 26, 2004, 16:02:51 ; Search time 21.0702 Seconds  
(without alignments)  
658.454 Million cell updates/sec

Title: US-09-121-239-12

Perfect score: 25  
Sequence: 1 GGUCAGCGGAUGCUGGACAGUC 25

Scoring table: OLIGO NUC  
Gapop 60.0 , Gapext 60.0

Searched: 682709 seqs, 277475446 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents NA.\*  
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2: /cgn2\_6/prodata/2/ina/5B\_COMB.seq.\*  
3: /cgn2\_6/prodata/2/ina/6A\_COMB.seq.\*  
4: /cgn2\_6/prodata/2/ina/6B\_COMB.seq.\*  
5: /cgn2\_6/prodata/2/ina/PCTUS\_COMB.seq.\*  
6: /cgn2\_6/prodata/2/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	25	100.0	56	1	US-07-940-652-17
C 2	25	100.0	56	1	US-08-255-553-17
C 3	25	100.0	1078	4	US-09-310-842-1
C 4	24	96.0	26	1	US-08-363-233B-6
C 5	18	72.0	22	1	US-08-152-621-11
C 6	18	72.0	22	5	PCT-US92-05035-11
C 7	18	72.0	62	3	US-08-448-446B-1
C 8	18	72.0	81	3	US-08-448-446B-2
C 9	18	72.0	257	1	US-08-152-621-1
C 10	18	72.0	257	1	US-08-306-691B-36
C 11	18	72.0	257	5	PCT-US92-05035-1
C 12	16	64.0	28	3	US-09-341-955-2
C 13	16	64.0	28	4	US-09-779-881-2
C 14	16	64.0	864	4	US-09-489-039A-2414
C 15	14	56.0	61	3	US-08-448-446B-19
C 16	14	56.0	363	3	US-08-905-223-206
C 17	14	56.0	500	4	US-09-621-976-9874
C 18	14	56.0	930	4	US-09-252-991A-11373
C 19	14	56.0	981	4	US-09-252-991A-11296
C 20	14	56.0	1094	4	US-09-280-116-243
C 21	14	56.0	1197	4	US-09-252-991A-6737
C 22	14	56.0	1269	4	US-09-149-476-143
C 23	14	56.0	1272	4	US-09-252-991A-6952
C 24	14	56.0	1361	4	US-09-280-116-197
C 25	14	56.0	1427	4	US-09-907-794A-152
C 26	14	56.0	1427	4	US-09-905-125A-152
C 27	14	56.0	1427	4	US-09-902-775A-152

28	14	56.0	1620	1	US-07-616-022C-9	Sequence 9, Appli
29	14	56.0	1869	4	US-09-406-045-2	Sequence 2, Appli
C 30	14	56.0	2346	4	US-09-252-991A-6782	Sequence 6782, Ap
31	14	56.0	3041	4	US-09-339-159B-31	Sequence 31, Appl
32	14	56.0	36519	3	US-08-923-137-2	Sequence 2, Appli
C 33	14	56.0	786431	4	US-09-751-389-3	Sequence 3, Appli
34	13	52.0	277	4	US-09-313-294A-1791	Sequence 1791, Ap
35	13	52.0	288	4	US-09-134-000C-2182	Sequence 2182, Ap
C 36	13	52.0	396	4	US-09-621-976-16576	Sequence 16576, A
C 37	13	52.0	403	4	US-09-621-976-16577	Sequence 16577, A
C 38	13	52.0	437	4	US-09-221-017B-243	Sequence 243, App
39	13	52.0	444	4	US-09-252-991A-6828	Sequence 6828, Ap
C 40	13	52.0	458	4	US-09-621-976-16578	Sequence 16578, A
41	13	52.0	477	4	US-09-489-039A-1314	Sequence 1314, Ap
42	13	52.0	489	4	US-09-252-991A-12619	Sequence 12619, A
C 43	13	52.0	504	3	US-09-328-111-120	Sequence 120, App
C 44	13	52.0	792	4	US-09-489-039A-1358	Sequence 1358, Ap
45	13	52.0	857	4	US-09-660-176-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1  
US-07-940-652-17/c  
; Sequence 17, Application US/07940652  
; Patent No. 5424413  
; GENERAL INFORMATION:  
; APPLICANT: James J. Hogan et al.  
; TITLE OF INVENTION: BRANCHED NUCLEIC ACID PROBES  
; NUMBER OF SEQUENCES: 31  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; CITY: 611 West Sixth Street  
; STATE: California  
; COUNTRY: USA  
; ZIP: 90017  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: IBM P.C. DOS Version 3.30  
; SOFTWARE: WordPerfect (Version 5.1)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/940,652  
; FILING DATE: 19920904  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/07/827,021  
; FILING DATE: 22-JAN-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Warburg, Richard J.  
; REGISTRATION NUMBER: 32,327  
; REFERENCE/DOCKET NUMBER: 199/201  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (213) 489-1600  
; TELEFAX: (213) 955-0440  
; TELEX: 67-3510  
; INFORMATION FOR SEQ ID NO: 17:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 56  
; TYPE: NUCLEIC ACID  
; STRANDEDNESS: single  
; TOPOLOGY: linear

US-07-940-652-17  
Query Match 100.0%; Score 25; DB 1; Length 56;  
Best Local Similarity 80.0%; Pred. No. 6.5e-06;  
Matches 20; Conservative 5; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGUCAGCGGAUGCUGGACAGUC 25  
DB 27 GGTCAGCGGAATGCTGTGACAGTC 3

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RESULT 2
US-08-255-553-17/c
; Sequence 17, Application US/08255553
; Patent No. 5451503
; GENERAL INFORMATION:
; APPLICANT: James J. Hogan et al.
; TITLE OF INVENTION: BRANCHED NUCLEIC ACID PROBES
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 611 West Sixth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90017
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS Version 3.30
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/255,553
; FILING DATE: 07-JUN-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/940,652
; FILING DATE: 04-SEP-1992
; APPLICATION NUMBER: US/07/827,021
; FILING DATE: 22-JAN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 199/201
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 56
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-255-553-17
Query Match 100.0%; Score 25; DB 1; Length 56;
Best Local Similarity 80.0%; Pred. No. 6.5e-06;
Matches 20; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGUCACGGGAUUCUGGACAGUC 25
DB 27 GGTACGCGGAATGCTGTGGACGTC 3

RESULT 3
US-09-310-842-1/c
; Sequence 1, Application US/09310842A
; Patent No. 6451593
; GENERAL INFORMATION:
; APPLICANT: Wittig, Prof. Burghardt
; APPLICANT: Jungmans, Claas
; TITLE OF INVENTION: Design Principle for Constructing Expression Constructs for Gene
; TITLE OF INVENTION: Therapy
; FILE REFERENCE: XI 597/99
; CURRENT APPLICATION NUMBER: US/09/310,842A
; CURRENT FILING DATE: 1999-05-12
; EARLIER APPLICATION NUMBER: DE 196 48 625.4
; EARLIER FILING DATE: 1996-11-13
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1

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; LENGTH: 1078
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: gene
; LOCATION: (1)..(1078)
; OTHER INFORMATION: bcr3=abl2; Oligo DNA Dumbbell
; FEATURE:
; NAME/KEY: misc_binding
; LOCATION: (1)..(2)
; OTHER INFORMATION: intramolecular binding site; the T-nucleotides at position 1 to
; OTHER INFORMATION: 2 can be modified with amino or caroxy features
; FEATURE:
; NAME/KEY: misc_binding
; LOCATION: (1077)..(1078)
; OTHER INFORMATION: intramolecular binding site; the T-nucleotides at position 1077
; OTHER INFORMATION: to 1078 can be modified with amino or caroxy features
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Strandness: both; nucleic
; OTHER INFORMATION: acid (linear), hypothetical: No. 6451593 anti-sense: No
US-09-310-842-1
Query Match 100.0%; Score 25; DB 4; Length 1078;
Best Local Similarity 80.0%; Pred. No. 6.5e-06;
Matches 20; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGUCACGGGAUUCUGGACAGUC 25
DB 686 GGTACGCGGAATGCTGTGGACGTC 662

RESULT 4
US-08-363-233B-6/c
; Sequence 6, Application US/08363233B
; Patent No. 5714383
; GENERAL INFORMATION:
; APPLICANT: Thompson, James D.
; TITLE OF INVENTION: METHOD AND REAGENT FOR TREATING CHRONIC
; TITLE OF INVENTION: MYELOGENOUS LEUKEMIA
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/363,233B
; FILING DATE: December 23, 1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION DATA: including application
; PRIOR APPLICATION DATA: described below: 2
; APPLICATION NUMBER: 07/882,822
; FILING DATE: May 14, 1992
; APPLICATION NUMBER: 08/193,922
; FILING DATE: February 7, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 209/165
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510

```



```

; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-363-233B-6

Query Match          96.0%; Score 24; DB 1; Length 26;
Best Local Similarity 79.2%; Pred. No. 2.5e-05;
Matches 19; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 2 GUCACGGGAUUCUGGACAGUC 25
Db 26 GTCACGGGAATGCTGTGGACATC 3

RESULT 5
US-08-152-621-11/c
; Sequence 11, Application US/08152621
; Patent No. 5652222
; GENERAL INFORMATION:
; APPLICANT: Calabretta, Bruno
; APPLICANT: Gewirtz, Alan M.
; TITLE OF INVENTION: Selective Inhibition of
; TITLE OF INVENTION: Leukemic Cell Proliferation by bcr-abl
; TITLE OF INVENTION: Antisense Oligonucleotides
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEIDEL, GONDA, LAVORGNA
; ADDRESSEE: & MONACO, P.C.
; STREET: 1800 Two Penn Center
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: U.S.A.
; ZIP: 19102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/152,621
; FILING DATE: No. 5652222ember 15, 1993
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/718,302
; FILING DATE: June 18, 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Monaco, Daniel A.
; REGISTRATION NUMBER: 30,480
; REFERENCE/DOCKET NUMBER: 6056-120 (CT.) 1
; TELEPHONE: (215) 568-8383
; TELEFAX: (215) 568-5549
; TELEX: None
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 Nucleotides
; TYPE: NUCLEIC ACID
; STRANDEDNESS: double stranded
; TOPOLOGY: linear
PCT-US92-05035-11

Query Match          72.0%; Score 18; DB 1; Length 22;
Best Local Similarity 77.8%; Pred. No. 0.082;
Matches 14; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGUCACGGGAUUCUGUG 18
Db 18 GGTACGGGAATGCTGTG 1

RESULT 7
US-08-448-446B-1/c
; Sequence 1, Application US/08448446B
; Patent No. 6080851
; GENERAL INFORMATION:
; APPLICANT: Pachuk et al.
; TITLE OF INVENTION: Compounds and Methods for the Treatment
; TITLE OF INVENTION: of Leukemias
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn
; ADDRESSEE: Kurtz Mackiewicz & No. 6080851iris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA

```

; COUNTRY: USA  
; ZIP: 19103  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE  
; COMPUTER: IBM PS/2  
; OPERATING SYSTEM: PC-DOS  
; SOFTWARE: WORDPERFECT 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/448,446B  
; FILING DATE: July 10, 1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/989,852  
; FILING DATE: December 4, 1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Doreen Yanko Trujillo  
; REGISTRATION NUMBER: 35,719  
; REFERENCE/DOCKET NUMBER: APOL-0020  
; TELECOMMUNICATION INFORMATION: C  
; TELEPHONE: (215) 568-3100  
; TELEFAX: (215) 568-3439  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 62  
; TYPE: Nucleic Acid  
; STRANDEDNESS: Single  
; TOPOLOGY: Linear  
; ANTI-SENSE: No  
; US-08-448-446B-1

Query Match 72.0%; Score 18; DB 3; Length 62;  
Best Local Similarity 77.8%; Pred. No. 0.082;  
Matches 14; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGUCAGCGGAUGCUG 18  
Db 18 GGTACGCGGAATGCTGTG 1

RESULT 8  
US-08-448-446B-2  
; Sequence 2, Application US/08448446B  
; Patent No. 6080851  
; GENERAL INFORMATION:  
; APPLICANT: Pachuk et al.  
; TITLE OF INVENTION: Compounds and Methods for the Treatment  
; OF LEUKEMIA  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Woodcock Washburn  
; ADDRESSEE: Kurtz Mackiewicz & No. 6080851ris  
; STREET: One Liberty Place - 46th Floor  
; CITY: Philadelphia  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19103  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE  
; COMPUTER: IBM PS/2  
; OPERATING SYSTEM: PC-DOS  
; SOFTWARE: WORDPERFECT 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/448,446B  
; FILING DATE: July 10, 1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/989,852  
; FILING DATE: December 4, 1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Doreen Yanko Trujillo  
; REGISTRATION NUMBER: 35,719  
; REFERENCE/DOCKET NUMBER: APOL-0020  
; TELECOMMUNICATION INFORMATION: C

; TELEPHONE: (215) 568-3100  
; TELEFAX: (215) 568-3439  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 81  
; TYPE: Nucleic Acid  
; STRANDEDNESS: Single  
; TOPOLOGY: Linear  
; ANTI-SENSE:  
; US-08-448-446B-2

Query Match 72.0%; Score 18; DB 3; Length 81;  
Best Local Similarity 100.0%; Pred. No. 0.082;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGUCAGCGGAUGCUG 18  
Db 64 GGUCAGCGGAUGCUG 81

RESULT 9  
US-08-152-621-1/c  
; Sequence 1, Application US/08152621  
; Patent No. 5652222  
; GENERAL INFORMATION:  
; APPLICANT: Calabretta, Bruno  
; APPLICANT: Gewirtz, Alan M.  
; TITLE OF INVENTION: Selective Inhibition of  
; CELL PROLIFERATION  
; TITLE OF INVENTION: Leukemic Cell Proliferation by bcr-abl  
; TITLE OF INVENTION: Antisense Oligonucleotides  
; NUMBER OF SEQUENCES: 34  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SEIDEL, GONDA, LAVORGNA  
; ADDRESSEE: & MONACO, P.C.  
; STREET: 1800 Two Penn Center  
; CITY: Philadelphia  
; STATE: Pennsylvania  
; COUNTRY: U.S.A.  
; ZIP: 19102  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb  
; COMPUTER: IBM PS/2  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: WordPerfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/152,621  
; FILING DATE: No. 5652222ember 15, 1993  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/718,302  
; FILING DATE: June 18, 1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Monaco, Daniel A.  
; REGISTRATION NUMBER: 30,480  
; REFERENCE/DOCKET NUMBER: 6056-120 (CT.) 1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (215) 568-8383  
; TELEFAX: (215) 568-5549  
; TELEX: No. 5652222e  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 257 Nucleotides  
; TYPE: nucleic acid  
; STRANDEDNESS: single stranded  
; TOPOLOGY: linear  
; US-08-152-621-1

Query Match 72.0%; Score 18; DB 1; Length 257;  
Best Local Similarity 77.8%; Pred. No. 0.082;  
Matches 14; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGUCAGCGGAUGCUG 18  
Db 18 GGTACGCGGAATGCTGTG 1

Db 18 GGTACGCGGAATGCTGTG 1

RESULT 10

US-08-306-691B-36/c  
Sequence 36, Application US/08306691B  
Patent No. 5734039

GENERAL INFORMATION:

APPLICANT: Calabretta, Bruno

APPLICANT: Skorski, Tomasz

TITLE OF INVENTION: ANTISENSE

TITLE OF INVENTION: OLIGONUCLEOTIDES TARGETING COOPERATING ONCOGENES

NUMBER OF SEQUENCES: 55

CORRESPONDENCE ADDRESS:

ADDRESSEE: Seidel, Gonda, Lavorgna & Monaco, P.C.

STREET: Two Penn Center, Suite 1800

CITY: Philadelphia

STATE: Pennsylvania

COUNTRY: U.S.A.

ZIP: 19102

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb

COMPUTER: IBM PS/2

OPERATING SYSTEM: MS-DOS

SOFTWARE: WordPerfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/306,691B

FILING DATE: September 15, 1994

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Monaco, Daniel A.

REGISTRATION NUMBER: 30,480

REFERENCE/DOCKET NUMBER: 8321-8

TELECOMMUNICATION INFORMATION:

TELEPHONE: (215) 568-8383

TELEFAX: (215) 568-5549

INFORMATION FOR SEQ ID NO: 36:

SEQUENCE CHARACTERISTICS:

LENGTH: 257 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-306-691B-36

Query Match 72.0%; Score 18; DB 1; Length 257;

Best Local Similarity 77.8%; Pred. No. 0.082;

Matches 14; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGUCAGCGGAUUGCUG 18

Db 18 GGTACGCGGAATGCTGTG 1

RESULT 11

PCT-US92-05035-1/c

Sequence 1, Application PC/TUS9205035

GENERAL INFORMATION:

APPLICANT: Calabretta, Bruno

APPLICANT: Gewirtz, Alan M.

TITLE OF INVENTION: Selective Inhibition of

TITLE OF INVENTION: Leukemic Cell Proliferation by bcr-abl

TITLE OF INVENTION: Antisense Oligonucleotides

NUMBER OF SEQUENCES: 34

CORRESPONDENCE ADDRESS:

ADDRESSEE: Temple University - Of The Common-

ADDRESSEE: wealth System of Higher Education

STREET: 406 University Services Building

CITY: Philadelphia

STATE: Pennsylvania

COUNTRY: U.S.A.

ZIP: 19102

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb

COMPUTER: IBM PS/2

OPERATING SYSTEM: MS-DOS

SOFTWARE: WordPerfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US92/05035

FILING DATE: 19920615

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Monaco, Daniel A.

REGISTRATION NUMBER: 30,480

REFERENCE/DOCKET NUMBER: 6056-120 (CIP) 1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (215) 568-8383

TELEFAX: (215) 568-5549

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 257 Nucleotides

TYPE: NUCLEIC ACID

STRANDEDNESS: single stranded

TOPOLOGY: linear

PCT-US92-05035-1

Query Match 72.0%; Score 18; DB 5; Length 257;

Best Local Similarity 77.8%; Pred. No. 0.082;

Matches 14; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGUCAGCGGAUUGCUG 18

Db 18 GGTACGCGGAATGCTGTG 1

RESULT 12

US-09-341-955-2

Sequence 2, Application US/09341955

Patent No. 6251690

GENERAL INFORMATION:

APPLICANT: Kulmala, Sakari

APPLICANT: Ala-Kleme, Timo

APPLICANT: Eskola, Jarkko

APPLICANT: Korpela, Timo

TITLE OF INVENTION: ELECTRICAL EXCITATION OF LABEL SUBSTANCES AT COATED

TITLE OF INVENTION: ELECTRODES

FILE REFERENCE: TUR-080

CURRENT APPLICATION NUMBER: US/09/341,955

CURRENT FILING DATE: 1999-07-21

EARLIER APPLICATION NUMBER: PCT/FI98/00114

EARLIER FILING DATE: 1999-02-10

NUMBER OF SEQ ID NOS: 2

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 2

LENGTH: 28

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence:

OTHER INFORMATION: oligonucleotide containing an amino group

US-09-341-955-2

Query Match 64.0%; Score 16; DB 3; Length 28;

Best Local Similarity 81.2%; Pred. No. 1.2;

Matches 13; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGUCAGCGGAAGCUG 16  
||:|||||:|:|  
Db 13 GGTCAGCGGAATGCTG 28

## RESULT 13

US-09-779-881-2  
; Sequence 2, Application US/09779881  
; Patent No. 6645776  
; GENERAL INFORMATION:  
; APPLICANT: Kulmala, Sakari  
; APPLICANT: Ala-Kleme, Timo  
; APPLICANT: Eskola, Jarkko  
; APPLICANT: Korpela, Timo  
; TITLE OF INVENTION: ELECTRICAL EXCITATION OF LABEL SUBSTANCES AT COATED  
; TITLE OF INVENTION: ELECTRODES  
; FILE REFERENCE: TUR-080  
; CURRENT APPLICATION NUMBER: US/09779,881  
; CURRENT FILING DATE: 2001-02-09  
; PRIOR APPLICATION NUMBER: 09/341,955  
; PRIOR FILING DATE: 1999-07-21  
; PRIOR APPLICATION NUMBER: PCT/FI98/00114  
; PRIOR FILING DATE: 1999-02-10  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: Patent In Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 28  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:  
; OTHER INFORMATION: oligonucleotide containing an amino group  
US-09-779-881-2

Query Match 64.0%; Score 16; DB 4; Length 28;  
Best Local Similarity 81.2%; Pred. No. 1.2;  
Matches 13; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGUCAGCGGAAGCUG 16  
||:|||||:|:|  
Db 13 GGTCAGCGGAATGCTG 28

## RESULT 14

US-09-489-039A-2414/c  
; Sequence 2414, Application US/09489039A  
; Patent No. 6610836  
; GENERAL INFORMATION:  
; APPLICANT: Gary Breton et. al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA  
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 2709.2004001  
; CURRENT APPLICATION NUMBER: US/09/489,039A  
; CURRENT FILING DATE: 2000-01-27  
; PRIOR APPLICATION NUMBER: US 60/117,747  
; PRIOR FILING DATE: 1999-01-29  
; NUMBER OF SEQ ID NOS: 14342  
; SEQ ID NO 2414  
; LENGTH: 864  
; TYPE: DNA  
; ORGANISM: Klebsiella pneumoniae  
US-09-489-039A-2414

Query Match 64.0%; Score 16; DB 4; Length 864;  
Best Local Similarity 75.0%; Pred. No. 1.2;  
Matches 12; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 3 UCAGCGGAAGCUG 18  
:|||||:|:|  
Db 694 TCAGCGGAATGCTGTG 679

## RESULT 15

US-08-448-446B-19  
; Sequence 19, Application US/08448446B  
; Patent No. 6080851  
; GENERAL INFORMATION:  
; APPLICANT: Pachuk et al.  
; TITLE OF INVENTION: Compounds and Methods for the Treatment  
; TITLE OF INVENTION: of Leukemias  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Woodcock Washburn  
; ADDRESSEE: Kurtz Mackiewicz & No. 6080851ris  
; STREET: One Liberty Place - 46th Floor  
; CITY: Philadelphia  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19103  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE  
; COMPUTER: IBM PS/2  
; OPERATING SYSTEM: PC-DOS  
; SOFTWARE: WORDPERFECT 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/448,446B  
; FILING DATE: July 10, 1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/989,852  
; FILING DATE: December 4, 1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Doreen Yanko Trujillo  
; REGISTRATION NUMBER: 35,719  
; REFERENCE/DOCKET NUMBER: APOL-0020  
; TELECOMMUNICATION INFORMATION: C  
; TELEPHONE: (215) 568-3100  
; TELEFAX: (215) 568-3439  
; INFORMATION FOR SEQ ID NO: 19:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 61  
; TYPE: Nucleic Acid  
; STRANDEDNESS: Single  
; TOPOLOGY: Linear  
; ANTI-SENSE:  
US-08-448-446B-19

Query Match 56.0%; Score 14; DB 3; Length 61;  
Best Local Similarity 85.7%; Pred. No. 18;  
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGUCAGCGGAATGC 14  
||:|||||:|:|  
Db 48 GGTCAGCGGAATGC 61

Search completed: May 27, 2004, 02:25:12  
Job time : 21.0702 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: May 27, 2004, 11:30:47 ; Search time 131.564 Seconds  
(without alignments)  
864.392 Million cell updates/sec

Title: US-09-121-239-12

Perfect score: 25  
Sequence: 1 GGUCAGCGGAUGCUGGACAGUC 25

Scoring table: OLIGO\_NUC  
Gapop\_60.0 , Gapext 60.0

Searched: 2960401 seqs, 2274450654 residues

Word size : 0  
Total number of hits satisfying chosen parameters: 5920802

Minimum DB seq length: 0  
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Post-processing: Listing first 45 summaries

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2: /cgn2\_6/ptodata/2/pubpna/PT\_NEW\_PUB.seq.\*  
3: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq.\*  
4: /cgn2\_6/ptodata/2/pubpna/US06\_PUBCOMB.seq.\*  
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19: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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C 2	25	100.0	542	9	US-09-796-692-8117
C 3	25	100.0	542	15	US-10-040-862-8117
C 4	25	100.0	542	16	US-10-057-475B-8117
C 5	25	100.0	542	16	US-10-154-884B-8117
C 6	25	100.0	596	9	US-09-796-692-8967
C 7	25	100.0	596	15	US-10-040-862-8967
C 8	25	100.0	596	16	US-10-057-475B-8967
C 9	25	100.0	596	16	US-10-154-884B-8967
C 10	25	100.0	1078	15	US-10-228-811-1
C 11	25	100.0	4739	9	US-09-954-531-586
C 12	25	100.0	4739	13	US-10-193-651-22
C 13	17	68.0	3664	15	US-10-128-714-206
C 14	17	68.0	3750	15	US-10-128-714-5206

15	16	64.0	28	9	US-09-779-881-2	Sequence 2, Appli
16	16	64.0	285	11	US-09-864-408A-4649	Sequence 4649, Ap
c 17	15	60.0	383	9	US-09-960-352-9070	Sequence 9070, Ap
18	15	60.0	483	9	US-09-974-300-8116	Sequence 8116, Ap
19	15	60.0	501	9	US-09-974-300-8143	Sequence 8143, Ap
c 20	15	60.0	765	16	US-10-369-433-39879	Sequence 39879, A
c 21	15	60.0	804	16	US-10-369-433-39128	Sequence 39128, A
c 22	15	60.0	804	16	US-10-369-493-39497	Sequence 39497, A
c 23	15	60.0	828	16	US-10-388-934-133	Sequence 133, App
c 24	15	60.0	837	13	US-10-282-122A-25393	Sequence 25393, A
c 25	15	60.0	933	9	US-09-974-300-2109	Sequence 2109, Ap
c 26	15	60.0	3076	15	US-10-128-714-495	Sequence 495, App
c 27	15	60.0	3076	15	US-10-128-714-5495	Sequence 5495, Ap
c 28	15	60.0	203264	13	US-10-087-192-988	Sequence 988, App
c 29	14	56.0	16	9	US-09-068-817-9	Sequence 9, Appli
c 30	14	56.0	21	10	US-09-864-436A-1953	Sequence 1953, Ap
c 31	14	56.0	21	11	US-09-864-456A-1953	Sequence 1953, Ap
c 32	14	56.0	21	15	US-10-084-839-1953	Sequence 1953, Ap
c 33	14	56.0	28	9	US-09-747-165-7	Sequence 7, Appli
c 34	14	56.0	80	12	US-10-384-245-179	Sequence 179, App
c 35	14	56.0	134	15	US-10-029-386-26303	Sequence 26303, A
c 36	14	56.0	268	13	US-10-052-283-149	Sequence 149, App
c 37	14	56.0	335	9	US-09-815-343-156	Sequence 156, App
c 38	14	56.0	335	13	US-10-097-105-156	Sequence 156, App
c 39	14	56.0	430	10	US-09-918-995-2118	Sequence 2118, Ap
c 40	14	56.0	460	9	US-09-969-347-68	Sequence 68, Appl
c 41	14	56.0	461	10	US-09-918-995-14682	Sequence 14682, A
c 42	14	56.0	462	10	US-09-918-995-9876	Sequence 9876, Ap
c 43	14	56.0	474	16	US-10-369-433-38733	Sequence 38733, A
c 44	14	56.0	493	13	US-10-052-283-38	Sequence 38, Appl
c 45	14	56.0	501	15	US-10-060-036-3547	Sequence 3547, Ap

ALIGNMENTS

RESULT 1  
US-09-918-995-25454/c  
; Sequence 25454, Application US/09918995  
; Publication No. US20030073623A1  
; GENERAL INFORMATION:  
; APPLICANT: Hyseq, Inc.  
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED  
; FILE REFERENCE: 20411-756  
; CURRENT APPLICATION NUMBER: US/09/918,995  
; CURRENT FILING DATE: 2001-07-30  
; PRIOR APPLICATION NUMBER: US/09/235,076  
; PRIOR FILING DATE: 1999-01-20  
; NUMBER OF SEQ ID NOS: 38054  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 25454  
; LENGTH: 504  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1)..(504)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-918-995-25454

Query Match 100.0%; Score 25; DB 10; Length 504;  
Best Local Similarity 80.0%; Pred. No. 2.6e-05;  
Matches 20; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGUCAGCGGAUGCUGGACAGUC 25  
||:|||||||:|||||||:  
Db 263 GGTCAGCGGAATGCTGTGCAGATC 239

RESULT 2  
US-09-796-692-8117/c  
; Sequence 8117, Application US/09796692

```

; Publication No. US20020198362A1
;
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
;
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY
; OF HEMATOLOGICAL MALIGNANCIES
;
; FILE REFERENCE: 2077.001200
;
; CURRENT APPLICATION NUMBER: US/09/796,692
;
; CURRENT FILING DATE: 2001-03-01
;
; PRIOR APPLICATION NUMBER: 60/186,126
;
; PRIOR FILING DATE: 2000-03-01
;
; PRIOR APPLICATION NUMBER: 60/190,479
;
; PRIOR FILING DATE: 2000-03-17
;
; PRIOR APPLICATION NUMBER: 60/200,545
;
; PRIOR FILING DATE: 2000-04-27
;
; PRIOR APPLICATION NUMBER: 60/200,303
;
; PRIOR FILING DATE: 2000-04-28
;
; PRIOR APPLICATION NUMBER: 60/200,779
;
; PRIOR FILING DATE: 2000-04-28
;
; PRIOR APPLICATION NUMBER: 60/200,999
;
; PRIOR FILING DATE: 2000-05-01
;
; PRIOR APPLICATION NUMBER: 60/202,084
;
; PRIOR FILING DATE: 2000-05-04
;
; PRIOR APPLICATION NUMBER: 60/206,201
;
; PRIOR FILING DATE: 2000-05-22
;
; PRIOR APPLICATION NUMBER: 60/218,950
;
; PRIOR FILING DATE: 2000-07-14
;
; PRIOR APPLICATION NUMBER: 60/222,903
;
; PRIOR FILING DATE: 2000-08-03
;
; PRIOR APPLICATION NUMBER: 60/223,416
;
; PRIOR FILING DATE: 2000-08-04
;
; PRIOR APPLICATION NUMBER: 60/223,378
;
; PRIOR FILING DATE: 2000-08-07
;
; NUMBER OF SEQ ID NOS: 9597
;
; SOFTWARE: FastSeq for Windows Version 3.0
;
; SEQ ID NO 8117
;
; LENGTH: 542
;
; TYPE: DNA
;
; ORGANISM: Homo sapiens
;
US-09-796-692-8117

Query Match 100.0%; Score 25; DB 9; Length 542;
Best Local Similarity 80.0%; Pred. No. 2.6e-05;
Matches 20; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGUCAGCGGAUUGCUGUGGACAGUC 25
Db 457 GGTGACGGGAATGCTGTGGACAGTC 433
||:|||||||:|||||:|
|:|||||||:|||||:|

RESULT 3
US-10-040-862-8117/c
; Sequence 8117, Application US/10040862
; Publication No. US20030078396A1
;
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc
; APPLICANT: Corixa Corporation
;
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; OF HEMATOLOGICAL MALIGNANCIES
;
; FILE REFERENCE: 014058-013520US
;
; CURRENT APPLICATION NUMBER: US/10/040,862
;
; CURRENT FILING DATE: 2001-11-06
;
; PRIOR APPLICATION NUMBER: US 60/186,126
;
; PRIOR FILING DATE: 2000-03-01
;
; PRIOR APPLICATION NUMBER: US 60/190,479
;
; PRIOR FILING DATE: 2000-03-17
;
; PRIOR APPLICATION NUMBER: US 60/200,545
;
; PRIOR FILING DATE: 2000-04-27
;
; PRIOR APPLICATION NUMBER: US 60/200,303

```

;; PRIOR APPLICATION NUMBER: US 60/222,903  
;; PRIOR FILING DATE: 2000-08-03  
;; Remaining Prior Application data removed - See File Wrapper or PALM.  
;; NUMBER OF SEQ ID NOS: 10979  
;; SOFTWARE: FastSeq for Windows Version 3.0  
;; SEQ ID NO 8117  
;; LENGTH: 542  
;; TYPE: DNA  
;; ORGANISM: Homo sapiens  
US-10-057-475B-8117

Query Match 100.0%; Score 25; DB 16; Length 542;  
Best Local Similarity 80.0%; Pred. No. 2.6e-05;  
Matches 20; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGUCAGCGGAUUGCUGGACAGUC 25  
||:|||||:|||||:|||||:|||||:  
Db 457 GGTACGGGAATGCTGTGCACATC 433

RESULT 5

US-10-154-884B-8117/c  
;; Sequence 8117, Application US/10154884B  
;; Publication No. US200400055611  
;; GENERAL INFORMATION:  
;; APPLICANT: Gaiger, Alexander  
;; APPLICANT: Algate, Paul A.  
;; APPLICANT: Mannion, Jane  
;; APPLICANT: Retter, Marc W.  
;; APPLICANT: Corixa Corporation  
;; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy  
;; FILE REFERENCE: 014058-013521US  
;; CURRENT APPLICATION NUMBER: US/10/154,884B  
;; CURRENT FILING DATE: 2002-05-23  
;; PRIOR APPLICATION NUMBER: US 60/186,126  
;; PRIOR FILING DATE: 2000-03-01  
;; PRIOR APPLICATION NUMBER: US 60/190,479  
;; PRIOR FILING DATE: 2000-03-17  
;; PRIOR APPLICATION NUMBER: US 60/200,545  
;; PRIOR FILING DATE: 2000-04-27  
;; PRIOR APPLICATION NUMBER: US 60/200,303  
;; PRIOR FILING DATE: 2000-04-28  
;; PRIOR APPLICATION NUMBER: US 60/200,779  
;; PRIOR FILING DATE: 2000-04-28  
;; PRIOR APPLICATION NUMBER: US 60/200,999  
;; PRIOR FILING DATE: 2000-05-01  
;; PRIOR APPLICATION NUMBER: US 60/202,084  
;; PRIOR FILING DATE: 2000-05-04  
;; PRIOR APPLICATION NUMBER: US 60/206,201  
;; PRIOR FILING DATE: 2000-05-01  
;; PRIOR APPLICATION NUMBER: US 60/218,950  
;; PRIOR FILING DATE: 2000-07-14  
;; PRIOR APPLICATION NUMBER: US 60/222,903  
;; PRIOR FILING DATE: 2000-08-03  
;; PRIOR APPLICATION NUMBER: 60/223,416  
;; PRIOR FILING DATE: 2000-08-04  
;; PRIOR APPLICATION NUMBER: 60/223,378  
;; PRIOR FILING DATE: 2000-08-07  
;; NUMBER OF SEQ ID NOS: 11290  
;; SOFTWARE: FastSeq for Windows Version 3.0  
;; SEQ ID NO 8117  
;; LENGTH: 542  
;; TYPE: DNA  
;; ORGANISM: Homo sapiens  
US-10-154-884B-8117

Query Match 100.0%; Score 25; DB 16; Length 542;  
Best Local Similarity 80.0%; Pred. No. 2.6e-05;  
Matches 20; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGUCAGCGGAUUGCUGGACAGUC 25  
||:|||||:|||||:|||||:|||||:  
Db 457 GGTACGGGAATGCTGTGCACATC 433

RESULT 6

US-09-796-692-8967/c  
;; Sequence 8967, Application US/09796692  
;; Publication No. US20020198362A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Gaiger, Alexander  
;; APPLICANT: Algate, Paul A.  
;; APPLICANT: Mannion, Jane  
;; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY  
;; FILE REFERENCE: 2077.001200  
;; CURRENT APPLICATION NUMBER: US/09/796,692  
;; CURRENT FILING DATE: 2001-03-01  
;; PRIOR APPLICATION NUMBER: 60/186,126  
;; PRIOR FILING DATE: 2000-03-01  
;; PRIOR APPLICATION NUMBER: 60/190,479  
;; PRIOR FILING DATE: 2000-03-17  
;; PRIOR APPLICATION NUMBER: 60/200,545  
;; PRIOR FILING DATE: 2000-04-27  
;; PRIOR APPLICATION NUMBER: 60/200,303  
;; PRIOR FILING DATE: 2000-04-28  
;; PRIOR APPLICATION NUMBER: 60/200,779  
;; PRIOR FILING DATE: 2000-04-28  
;; PRIOR APPLICATION NUMBER: 60/200,999  
;; PRIOR FILING DATE: 2000-05-01  
;; PRIOR APPLICATION NUMBER: 60/202,084  
;; PRIOR FILING DATE: 2000-05-04  
;; PRIOR APPLICATION NUMBER: 60/206,201  
;; PRIOR FILING DATE: 2000-05-22  
;; PRIOR APPLICATION NUMBER: 60/218,950  
;; PRIOR FILING DATE: 2000-07-14  
;; PRIOR APPLICATION NUMBER: 60/222,903  
;; PRIOR FILING DATE: 2000-08-03  
;; PRIOR APPLICATION NUMBER: 60/223,416  
;; PRIOR FILING DATE: 2000-08-04  
;; PRIOR APPLICATION NUMBER: 60/223,378  
;; PRIOR FILING DATE: 2000-08-07  
;; NUMBER OF SEQ ID NOS: 9597  
;; SOFTWARE: FastSeq for Windows Version 3.0  
;; SEQ ID NO 8967  
;; LENGTH: 596  
;; TYPE: DNA  
;; ORGANISM: Homo sapiens  
;; FEATURE:  
;; NAME/KEY: unsure  
;; LOCATION: (13)  
;; OTHER INFORMATION: n=A, T, C or G  
;; NAME/KEY: unsure  
;; LOCATION: (47)  
;; OTHER INFORMATION: n=A, T, C or G  
;; NAME/KEY: unsure  
;; LOCATION: (49)  
;; OTHER INFORMATION: n=A, T, C or G  
;; NAME/KEY: unsure  
;; LOCATION: (58)  
;; OTHER INFORMATION: n=A, T, C or G  
;; NAME/KEY: unsure  
;; LOCATION: (63)  
;; OTHER INFORMATION: n=A, T, C or G  
;; NAME/KEY: unsure  
;; LOCATION: (81)  
;; OTHER INFORMATION: n=A, T, C or G  
;; NAME/KEY: unsure  
;; LOCATION: (155)  
;; OTHER INFORMATION: n=A, T, C or G  
;; NAME/KEY: unsure  
;; LOCATION: (196)  
;; OTHER INFORMATION: n=A, T, C or G  
;; NAME/KEY: unsure  
;; LOCATION: (211)  
;; OTHER INFORMATION: n=A, T, C or G  
;; NAME/KEY: unsure  
;; LOCATION: (267)

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; OTHER INFORMATION: n=A,T,C or G
; NAME/KEY: unsure
; LOCATION: (281)
; OTHER INFORMATION: n=A,T,C or G
; NAME/KEY: unsure
; LOCATION: (282)
; OTHER INFORMATION: n=A,T,C or G
; NAME/KEY: unsure
; LOCATION: (332)
; OTHER INFORMATION: n=A,T,C or G
; NAME/KEY: unsure
; LOCATION: (372)
; OTHER INFORMATION: n=A,T,C or G
; NAME/KEY: unsure
; LOCATION: (520)
; OTHER INFORMATION: n=A,T,C or G
; NAME/KEY: unsure
; LOCATION: (521)
; OTHER INFORMATION: n=A,T,C or G
; NAME/KEY: unsure
; LOCATION: (551)
; OTHER INFORMATION: n=A,T,C or G
; NAME/KEY: unsure
; LOCATION: (579)
; OTHER INFORMATION: n=A,T,C or G
; NAME/KEY: unsure
; LOCATION: (585)
; OTHER INFORMATION: n=A,T,C or G
; NAME/KEY: unsure
; LOCATION: (586)
; OTHER INFORMATION: n=A,T,C or G
; OTHER INFORMATION: n=A,T,C or G
US-09-796-692-8967

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Query Match 100.0%; Score 25; DB 9; Length 596;  
 Best Local Similarity 80.0%; Pred. NO. 2.6e-05;  
 Matches 20; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

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QY 1 GGTCAGCGGAAGUCUGGACAGUC 25
Db 457 GGTCAGCGGAATGCTGTGACAGTC 433

```

```

RESULT 7
US-10-040-862-8967/c
; Sequence 8967, Application US/10040862
; Publication No. US20030078396A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; FILE OF INVENTION: Hematological Malignancies
; FILE REFERENCE: 014058-013520US
; CURRENT APPLICATION NUMBER: US/10/040,862
; CURRENT FILING DATE: 2001-11-06
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22

```

```

; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: US 60/223,416
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: US 60/223,378
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: US 09/796,692
; PRIOR FILING DATE: 2001-03-01
; NUMBER OF SEQ ID NOS: 10467
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8967
; LENGTH: 596
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (13)
; OTHER INFORMATION: n=A,T,C or G
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (47)
; OTHER INFORMATION: n=A,T,C or G
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (49)
; OTHER INFORMATION: n=A,T,C or G
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (58)
; OTHER INFORMATION: n=A,T,C or G
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (63)
; OTHER INFORMATION: n=A,T,C or G
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (81)
; OTHER INFORMATION: n=A,T,C or G
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (155)
; OTHER INFORMATION: n=A,T,C or G
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (196)
; OTHER INFORMATION: n=A,T,C or G
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (211)
; OTHER INFORMATION: n=A,T,C or G
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (267)
; OTHER INFORMATION: n=A,T,C or G
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (281)
; OTHER INFORMATION: n=A,T,C or G
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (282)
; OTHER INFORMATION: n=A,T,C or G
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (332)
; OTHER INFORMATION: n=A,T,C or G
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (372)
; OTHER INFORMATION: n=A,T,C or G
; FEATURE:

```



```

; NAME/KEY: unsure
; LOCATION: (520)
; OTHER INFORMATION: n=A,T,C or G
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (521)
; OTHER INFORMATION: n=A,T,C or G
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (551)
; OTHER INFORMATION: n=A,T,C or G
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (579)
; OTHER INFORMATION: n=A,T,C or G
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (585)
; OTHER INFORMATION: n=A,T,C or G
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (586)
; OTHER INFORMATION: n=A,T,C or G
US-10-040-862-8967

```

```

Query Match      100.0%; Score 25; DB 15; Length 596;
Best Local Similarity 80.0%; Pred. No. 2.6e-05;
Matches 20; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 GGUCAGCGGAUGCUGGACAGUC 25
DB 457 GGTGACGGAATGCTGTGGACATC 433

```

# RESULT 8

```

US-10-057-475B-8967/c
; Sequence 8967, Application US/10057475B
; Publication No. US20040002068A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Mannion, Jane
; APPLICANT: Clapper, Jonathan David
; APPLICANT: Wang, Aijun
; APPLICANT: Carder, Lauren
; APPLICANT: Ordonez, Nadia
; APPLICANT: McNeill, Patricia Dianne
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; FILE REFERENCE: 014058-014402US
; CURRENT APPLICATION NUMBER: US/10/057,475B
; CURRENT FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 11290
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8967
; LENGTH: 596
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(596)
; OTHER INFORMATION: n = g, a, c or t
US-10-040-862-8967

```

```

Query Match      100.0%; Score 25; DB 15; Length 596;
Best Local Similarity 80.0%; Pred. No. 2.6e-05;
Matches 20; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

```

```

; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 10979
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8967
; LENGTH: 596
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(596)
; OTHER INFORMATION: n = g, a, c or t
US-10-057-475B-8967

```

```

Query Match      100.0%; Score 25; DB 16; Length 596;
Best Local Similarity 80.0%; Pred. No. 2.6e-05;
Matches 20; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 GGUCAGCGGAUGCUGGACAGUC 25
DB 457 GGTGACGGAATGCTGTGGACATC 433

```

# RESULT 9

```

US-10-154-884B-8967/c
; Sequence 8967, Application US/10154884B
; Publication No. US2004000561A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc W.
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; FILE REFERENCE: 014058-013521US
; CURRENT APPLICATION NUMBER: US/10/154,884B
; CURRENT FILING DATE: 2002-05-23
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 11290
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8967
; LENGTH: 596
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(596)
; OTHER INFORMATION: n = g, a, c or t
US-10-154-884B-8967

```

```

Query Match      100.0%; Score 25; DB 16; Length 596;
Best Local Similarity 80.0%; Pred. No. 2.6e-05;
Matches 20; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1  GGUCAGCGGAUUGCUGUGGACAGUC 25
Db      457  GGTACGCGGAATGCTGTGGACAGTC 433
          |||:|||||:|:|:|||||:|
          |||:|||||:|:|:|||||:|

RESULT 10
US-10-228-811-1/c
; Sequence 1, Application US/10228811
; Publication No. US20030054392A1
; GENERAL INFORMATION:
; APPLICANT: Wittig, Prof. Burghardt
; APPLICANT: Junghans, Claas
; TITLE OF INVENTION: Design Principle for Constructing Expression Constructs for Gene
; TITLE OF INVENTION: Therapy
; FILE REFERENCE: XI 597/99
; CURRENT APPLICATION NUMBER: US/10/228,811
; CURRENT FILING DATE: 2002-08-27
; PRIOR APPLICATION NUMBER: DE 196 48 625.4
; PRIOR FILING DATE: 1996-11-13
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1078
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: gene
; LOCATION: (1)..(1078)
; OTHER INFORMATION: bcr3=abl2; Oligo DNA Dumbbell
; FEATURE:
; NAME/KEY: misc binding
; LOCATION: (1)..(2)
; OTHER INFORMATION: intramolecular binding site; the T-nucleotides at position 1 to
; OTHER INFORMATION: 2 can be modified with amino or caroxy features
; FEATURE:
; NAME/KEY: misc binding
; LOCATION: (1077)..(1078)
; OTHER INFORMATION: intramolecular binding site; the T-nucleotides at position 1077
; OTHER INFORMATION: to 1078 can be modified with amino or caroxy features
; OTHER INFORMATION: Description of Artificial Sequence: Strandness: both; nucleic
; OTHER INFORMATION: acid (linear), hypothetical: No. US20030054392A1 anti-sense: No.
US-10-228-811-1

Query Match      100.0%; Score 25; DB 15; Length 1078;
Best Local Similarity 80.0%; Pred. No. 2.4e-05;
Matches 20; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY      1  GGUCAGCGGAUUGCUGUGGACAGUC 25
Db      686  GGTACGCGGAATGCTGTGGACAGTC 662
          |||:|||||:|:|:|||||:|
          |||:|||||:|:|:|||||:|

RESULT 11
US-09-954-531-586/c
; Sequence 586, Application US/09954531
; Patent No. US20020165180A1
; GENERAL INFORMATION:
; APPLICANT: Weaver, Zoe
; TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Can
; TITLE OF INVENTION: Gene Sets
; FILE REFERENCE: 689290-77
; CURRENT APPLICATION NUMBER: US/09/954,531
; CURRENT FILING DATE: 2002-05-02
; PRIOR APPLICATION NUMBER: US/60/233,133
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US/60/234,009
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: US/60/234,034
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: US/60/234,509
; PRIOR FILING DATE: 2000-09-22

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RESULT 15  
US-09-779-881-2  
; Sequence 2, Application US/09779881  
; Patent No. US20020081749A1  
; GENERAL INFORMATION:

Search completed: May 27, 2004, 14:58:27  
Job time : 131.564 secs

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GenCore version 5.1.1.6  
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OM nucleic - nucleic search, using sw model

Run on: May 26, 2004, 15:22:41 ; Search time 882.692 Seconds  
(without alignments)  
845.770 Million cell updates/sec

Title: US-09-121-239-12

Perfect score: 25

Sequence: 1 GGUCAGCGAUGCUGGACAGUC 25

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 27513289 seqs, 14931090276 residues

Word size : 0

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

EST:

1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estin:\*  
4: em\_estmu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_htc:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_hcc:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_estom:\*  
17: em\_gss\_hum:\*  
18: em\_gss\_inv:\*  
19: em\_gss\_pin:\*  
20: em\_gss\_vrt:\*  
21: em\_gss\_fun:\*  
22: em\_gss\_nam:\*  
23: em\_gss\_mus:\*  
24: em\_gss\_pro:\*  
25: em\_gss\_rtd:\*  
26: em\_gss\_phg:\*  
27: em\_gss\_vrl:\*  
28: gb\_gsl1:\*  
29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	25	100.0	181	14	H55545 CHR220484 C
C 2	25	100.0	314	14	D79153 HUM532H11B
C 3	25	100.0	360	10	BE168421 QV3-HT051
C 4	25	100.0	377	10	BF800308 CM4-CI006

C	5	25	100.0	401	14	R54267
C	7	25	100.0	437	10	BF873838
C	8	25	100.0	443	10	AW452440
C	9	25	100.0	531	12	BG927169
C	10	25	100.0	588	10	BF380221
C	11	25	100.0	588	10	BF094682
C	12	25	100.0	590	10	BF953848
C	13	25	100.0	605	10	BE396942
C	14	25	100.0	621	10	AW961897
C	15	25	100.0	637	14	CB267185
C	16	25	100.0	653	12	BG829045
C	17	25	100.0	665	10	BE514596
C	18	25	100.0	684	10	BF530440
C	19	25	100.0	686	10	BE397010
C	20	25	100.0	712	10	BE397695
C	21	25	100.0	734	10	BE513555
C	22	25	100.0	741	10	BE265121
C	23	25	100.0	770	12	BE26004
C	24	25	100.0	777	13	B0597369
C	25	25	100.0	785	12	BG393462
C	26	25	100.0	797	12	BI225128
C	27	25	100.0	819	14	CF242964
C	28	25	100.0	844	14	CD652568
C	29	25	100.0	853	13	BQ227532
C	30	25	100.0	878	10	BF338795
C	31	25	100.0	880	13	BQ422888
C	32	25	100.0	880	13	B0539742
C	33	25	100.0	888	13	B0540933
C	34	25	100.0	895	13	BX368536
C	35	25	100.0	903	13	BQ441890
C	36	25	100.0	918	13	BQ212925
C	37	25	100.0	936	13	BX350695
C	38	25	100.0	955	13	BQ945725
C	39	25	100.0	975	12	BG392048
C	40	25	100.0	1021	13	BQ896733
C	41	24	96.0	104	10	AW998451
C	42	24	96.0	796	10	BE743192
C	43	24	96.0	813	12	BM050194
C	44	22	88.0	438	10	BE938059
C	45	20	80.0	750	10	BE513994

#### ALIGNMENTS

RESULT 1  
H55545/c  
LOCUS  
DEFINITION  
H55545  
VERSION  
H55545.1  
KEYWORDS  
EST.  
SOURCE  
Homo sapiens (human)  
ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE  
1 (bases 1 to 181)  
Trafatter,J.A., Long,K.R., Murrell,J.R., Stotler,C.J., Gusella,J.F. and Buckler,A.J.  
AUTHORS  
An expression-independent catalog of genes from human chromosome 22  
JOURNAL  
Genome Res. 5 (3), 214-224 (1995)  
MEDLINE  
96159527  
PUBMED  
8593609  
COMMENT  
Contact: Buckler AJ  
Molecular Neurogenetics Unit  
Massachusetts General Hospital  
Building 149, 13th St., Charlestown MA 02129  
Tel: 6177249616  
Fax: 6177265736  
Email: buckler@helix.mgh.harvard.edu  
Seq primer: T3.

H55545  
CHR220484  
Chromosome 22  
exon Homo sapiens  
cDNA clone C22\_652 5',  
181 bp  
mRNA  
linear  
EST 07-DEC-1995  
mRNA sequence.

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FEATURES
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      /organism="Homo sapiens"
      /mol_type="mRNA"
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      /clone="C22_652"
      /lab_host="E. coli DH5a"
      /clone_lib="Chromosome 22 exon"
      /notes="Vector: pBluescriptIIKS+; Site 1: Sal I; Site 2:
      Bam HI (destroyed); Exons were isolated from human
      chromosome 22 specific cosmids using a modification of
      the method of exon amplification (Proc. Natl. Acad. Sci.
      USA 88:4005-4009, 1991). Amplified exons were digested
      with Sal I and Bgl II and subsequently cloned into
      pBluescriptIIKS+ at the Sal I and Bam HI sites."

ORIGIN
Query Match      100.0%; Score 25; DB 14; Length 181;
Best Local Similarity 80.0%; Pred. No. 0.0033;
Matches 20; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGUCAGCGGAUCCUGGACAGUC 25
    ||:|||||:||||:||||:|
Db 168 GGTACGCGGAATGCTGTGGACAGTC 144

RESULT 2
D79153/c
LOCUS
DEFINITION
  HUM532H11B Human placenta polyA+ (TFujiwara) Homo sapiens cDNA
  clone GEN-532H11 5', mRNA sequence.
ACCESSION
  D79153
VERSION
  D79153.1 GI:1181026
KEYWORDS
  EST.
SOURCE
  Homo sapiens (human)
  ORGANISM
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  REFERENCE
    1 (bases 1 to 314)
    Fujiwara, T., Hirano, H., Katagiri, T., Kawai, A., Kuga, Y., Nagata, M.,
    Okuno, S., Ozaki, K., Shimizu, F., Shimada, Y., Shinomiya, H.,
    Takaichi, A., Takeda, S., Watanabe, T., Takahashi, E., Hirai, Y.,
    Maeiawa, H., Shin, S. and Nakamura, Y.
    Fujiwara et al. (1995)
    TITLE
      Unpublished (1995)
    JOURNAL
      Contact: Tsutomu Fujiwara
    COMMENT
      Otsuka GEN Research Institute
      Otsuka Pharmaceutical Co., Ltd
      463-10 Kagasuno Kawauchi-cho, Tokushima, Tokushima, 771-01 Japan
      Tel: 0886-65-2888
      Fax: 0886-37-1035.

FEATURES
source
  Location/Qualifiers
    1..314
      /organism="Homo sapiens"
      /mol_type="mRNA"
      /db_xref="taxon:9606"
      /clone="GEN-532H11"
      /tissue_type="placenta"
      /clone_lib="Human placenta polyA+ (TFujiwara)"

ORIGIN
Query Match      100.0%; Score 25; DB 14; Length 314;
Best Local Similarity 80.0%; Pred. No. 0.0035;
Matches 20; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGUCAGCGGAUCCUGGACAGUC 25
    ||:|||||:||||:||||:|
Db 77 GGTACGCGGAATGCTGTGGACAGTC 53

RESULT 3
BE168421
LOCUS
DEFINITION
  QV3-HT0513-060400-148-b11 HT0513 Homo sapiens cDNA, mRNA sequence.
  BE168421.1 GI:8631051
  EST.
  SOURCE
    Homo sapiens (human)
    ORGANISM
      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
      REFERENCE
        1 (bases 1 to 360)
        Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
        Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
        Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,
        Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V.,
        O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
        Simpson, A.J.
        Shotgun sequencing of the human transcriptome with ORF expressed
        sequence tags
        Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
        MEDLINE
          20202663
        PUBMED
          10737800
        COMMENT
          Contact: Simpson A.J.G.
          Laboratory of Cancer Genetics
          Ludwig Institute for Cancer Research
          Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
          Brazil
          Tel: +55-11-2704922
          Fax: +55-11-2707001
          Email: asimpson@ludwig.org.br
          This sequence was derived from the FAPESP/LICR Human Cancer Genome
          Project. This entry can be seen in the following URL
          (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=&t2=QV3-HT0513-060
          400-148-b11&t3=2000-04-06&t4=1)
          Seq primer: puc 18 forward
          High quality sequence start: 31
          High quality sequence stop: 359.

FEATURES
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      /mol_type="mRNA"
      /db_xref="taxon:9606"
      /dev_stage="Adult"
      /clone_lib="HT0513"
      /note="Organ: head neck; Vector: puc18; Site 1: SmaI;
      Site 2: SmaI; A mini-library was made by cloning products
      derived from ORESTES PCR (U.S. Letters Patent application
      No. 196,716 - Ludwig Institute for Cancer Research)
      profiles into the pUC 18 vector. Reverse transcription of
      tissue mRNA and cDNA amplification were performed under
      low stringency conditions."

ORIGIN
Query Match      100.0%; Score 25; DB 10; Length 360;
Best Local Similarity 80.0%; Pred. No. 0.0035;
Matches 20; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGUCAGCGGAUCCUGGACAGUC 25
    ||:|||||:||||:||||:|
Db 304 GGTACGCGGAATGCTGTGGACAGTC 328

RESULT 4
BF800308/c
LOCUS
DEFINITION
  CM4-CI0062-181000-370-b10 CI0062 Homo sapiens cDNA, mRNA sequence.
  BF800308
  EST.
  SOURCE
    Homo sapiens (human)
    ORGANISM
      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
      REFERENCE
        1 (bases 1 to 377)
        Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,

```

Washington University School of Medicine

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL  
 (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=IL3&t2=IL3-ET0114-071100-338-C02&t3=2000-11-07&t4=1)  
 Seq primer: puc 18 forward  
 High quality sequence stop: 390.

## FEATURES

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 /dev\_stage="Adult"  
 /clone\_lib="ET0114"

/notes="Organ: lung tumor; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

## ORIGIN

Query Match 100.0%; Score 25; DB 10; Length 437;

Best Local Similarity 80.0%; Pred. No. 0.0036;  
 Matches 20; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGUCAGCGGAUUGCUGGACAGUC 25

Db 294 GGTACGCGGAATGCTGTGGACAGTC 318

## RESULT 7

AW452440/C

LOCUS AW452440 443 bp mRNA linear EST 17-FEB-2000  
 DEFINITION UI-H-B13-als-c-04-0-UI.sl NCI\_CGAP\_Sub5 Homo sapiens cDNA clone  
 IMAGE:3068526 3', mRNA sequence.

ACCESSION AW452440

VERSION AW452440.1 GI:6993216

KEYWORDS EST.

SOURCE Homo sapiens (human)

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 443)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Oligo-dT track not found. Not 1 site shown in beginning of sequence  
 is likely internal to the message. cDNA library Preparation: M.B.

Scorates Lab Clone distribution: NCI-CGAP clone distribution  
 Information can be found through the I.M.A.G.E. Consortium/LLNL at:

www.bio.llnl.gov/bbrp/image/image.html The following repetitive

elements were found in this cDNA sequence: 147-207, >HSR1T

Seq primer: M13 Forward

POLYA-No. Location/Qualifiers

## FEATURES

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1. .443  
 Location/Qualifiers  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:3068526"  
 /lab\_host="DH10B (Life Technologies)"  
 /clone\_lib="NCI\_CGAP\_Sub5"

/notes="Vector: pT773D-Pac (Pharmacia) with a modified  
 polylinker; Site 1: Not I; Site 2: Eco RI; NCI CGAP Sub5  
 is a subtracted library derived from NCI CGAP Sub4. The  
 NCI CGAP Sub5 library had 3 million recombinants. A  
 single-stranded DNA preparation of NCI\_CGAP\_Sub4 was used  
 as a tracer in a subtractive hybridization with a driver  
 comprising: the IMAGE pool (NCI\_CGAP\_Kid3 pool 1 LLAM

3334-3337, 3682-3683, 3798-3803 (IMAGE CloneIDs  
 1322376-1323911, 1456008-1456775, 1500852-1502855);  
 NCI\_CGAP\_Kid5 pool 1 LLAM 3338-3342, 3722-3725, 3776-3778  
 (IMAGE CloneIDs 1323912-1325831, 1471368-1472903,  
 1492104-1493255); NCI\_CGAP\_Lus pool 1 LLAM 3575-3582,  
 3851-3854 (IMAGE CloneIDs  
 1414920-1417991, 1520904-1522439); NCI\_CGAP\_GC4 pool 1 LLAM  
 3164-3167, 3716-3720, 3733-3735 (IMAGE CloneIDs  
 1257096-1258631, 1469064-1470983, 1475592-1476743);  
 NCI\_CGAP\_Pr22 pool 1 LLAM 2457-2459, 2758-2759, 3062-3068  
 (IMAGE CloneIDs 985608-986759, 1101192-1101959,  
 1217928-1220615); NCI\_CGAP\_Co10 pool 1 LLAM 2644-2653,  
 2871-2872 (IMAGE CloneIDs  
 1057416-1061255, 1144584-1145351). (10% of the driver  
 population), plus a pool of 3,840 arrayed clones from  
 NCI\_CGAP\_Sub1 (IMAGE CloneIDs 2708616-2710535) and  
 NCI\_CGAP\_Sub2 (IMAGE CloneIDs 2710536-2712455) (10% of  
 the driver population), plus a pool of 11,136 clones from  
 NCI\_CGAP\_Sub3 (IMAGE CloneIDs 2712456-2723591) (10% of the  
 driver population), plus a pool of 5,472 clones from  
 NCI\_CGAP\_Sub4 (IMAGE CloneIDs 2723592-2728969) (70% of the  
 driver population). Subtraction was performed as  
 previously described [Bonaldi, Lennon & Soares (1996):  
 Normalization and Subtraction: Two Approaches To  
 Facilitate Gene Discovery. Genome Research 6, 791-806.  
 TAG\_TISSUE=germ cell  
 TAG\_LIB=NCI\_CGAP\_GC4  
 TAG\_SEQ=AAATC"

## ORIGIN

Query Match 100.0%; Score 25; DB 10; Length 443;

Best Local Similarity 80.0%; Pred. No. 0.0036;  
 Matches 20; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGUCAGCGGAUUGCUGGACAGUC 25

Db 380 GGTACGCGGAATGCTGTGGACAGTC 356

## RESULT 8

BG927169/c

LOCUS

DEFINITION HNC18-1-D3.R HNC (Human Normal Cartilage) Homo sapiens cDNA, mRNA  
 sequence.

ACCESSION BG927169

VERSION BG927169.1 GI:14321692

KEYWORDS EST.

SOURCE Homo sapiens (human)

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 531)

Kumar, S., Connor, J.R., Dodds, R.A., Halsey, W., Van Horn, M., Mao, J.,  
 Sathe, G., Mui, P., Agarwal, P., Badger, A.M., Lee, J.C., Gowen, M. and  
 Lark, M.W.

Identification and initial characterization of 5000 expressed

sequenced tags (ESTs) each from adult human normal and

osteoarthritic cartilage cDNA libraries

Osteoarthr. Cartil. 9 (7), 641-653 (2001)

JOURNAL MEDLINE

PUBMED 21482651

COMMENT

Contact: Sanjay Kumar

UW2109

GlaxoSmithKline

709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA

Tel: 610-270-7245

Fax: 610-270-5598

Email: sanjay.kumar-1@gsk.com

Seq primer: T7

Location/Qualifiers

source

1. .531

/organism="Homo sapiens"

/mol\_type="mRNA"



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/db_xref="taxon:9606"
/tissue_type="cartilage"
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/clone_lib="HNC (Human Normal Cartilage)"
/note="Vector: pSPORT I; Site_1: SalI; Site_2: NotI; Directional"

ORIGIN
Query Match      100.0%; Score 25; DB 12; Length 531;
Best Local Similarity 80.0%; Pred. No. 0.0036;
Matches 20; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGUCAGCGGAAGUCUGGACAGUC 25
Db 463 GGTACGCGGAATGCTGTGGACAGTC 439

RESULT 9
BF380221/c
LOCUS
DEFINITION MR3-UT0050-250900-003-g03 UT0050 Homo sapiens cDNA, mRNA sequence.
ACCESSION BF380221
VERSION BF380221.1 GI:11369346
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 588)
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
PUBMED 10737800
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=MR3&t2=MR3-UT0050-250900-003-g03&t3=2000-09-25&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 586.
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/clone_lib="UT0050"
/note="Organ: uterus tumor; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

FEATURES
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/dev_stage="Adult"
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ORIGIN
Query Match      100.0%; Score 25; DB 10; Length 588;
Best Local Similarity 80.0%; Pred. No. 0.0037;
Matches 20; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGUCAGCGGAAGUCUGGACAGUC 25
Db 477 GGTACGCGGAATGCTGTGGACAGTC 453

RESULT 11
BF953848/c
LOCUS
DEFINITION MR0-NN1170-131100-302-f01 NN1170 Homo sapiens cDNA, mRNA sequence.
ACCESSION BF953848

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```

QY 1 GGUCAGCGGAAGUCUGGACAGUC 25
Db 477 GGTACGCGGAATGCTGTGGACAGTC 453

RESULT 10
BF094682/c
LOCUS
DEFINITION MR3-UT0050-130900-003-g03 UT0050 Homo sapiens cDNA, mRNA sequence.
ACCESSION BF094682
VERSION BF094682.1 GI:10900392
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 588)
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
PUBMED 10737800
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=MR3&t2=MR3-UT0050-130900-003-g03&t3=2000-09-13&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 586.
location/Qualifiers
1..588
/organism="Homo sapiens"
/mol_type="mRNA"
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/dev_stage="Adult"
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/note="Organ: uterus tumor; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

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QY 1 GGUCAGCGGAAGUCUGGACAGUC 25
Db 477 GGTACGCGGAATGCTGTGGACAGTC 453

RESULT 11
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LOCUS
DEFINITION MR0-NN1170-131100-302-f01 NN1170 Homo sapiens cDNA, mRNA sequence.
ACCESSION BF953848

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source
1. .bz1
/organism="Homo sapiens"
/mol type="mRNA"

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 26, 2004, 16:00:31 ; Search time 425.652 Seconds  
(without alignments)  
2036.547 Million cell updates/sec

Title: US-09-121-239-13

Perfect score: 20  
Sequence: 1 CAAAGGAGCAGGGAAGG 20

Scoring table: OLIGO\_NUC  
Gapop\_60.0 , Gapext 60.0

Searched: 3470272 seqs, 21671516995 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

GenEmbl.\*

1: gb\_ba.\*

2: gb\_hgt.\*

3: gb\_in.\*

4: gb\_om.\*

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7: gb\_ph.\*

8: gb\_pl.\*

9: gb\_pr.\*

10: gb\_ro.\*

11: gb\_sts.\*

12: gb\_sy.\*

13: gb\_un.\*

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26: em\_ro.\*

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29: em\_vi.\*

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33: em\_hgt\_mus.\*

34: em\_hgt\_pin.\*

35: em\_hgt\_rod.\*

36: em\_hgt\_mam.\*

37: em\_hgt\_vrt.\*

38: em\_sy.\*

39: em\_hgt\_hum.\*

40: em\_hgt\_mus.\*

41: em\_hgt\_other.\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

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C 4	20	100.0	299	6	BD222547	BD222547 Methods f
C 5	20	100.0	532	9	HUMABEBA	M14753 Human abl m
C 6	20	100.0	1346	10	BC005711	BC005711 Mus muscu
C 7	20	100.0	2795	9	HUMABL1B	M17310 Human c-abl
C 8	20	100.0	35737	10	AL732315	AL732315 Mouse DNA
C 9	20	100.0	35962	6	AX598662	AX598662 Sequence
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C 13	20	100.0	173463	9	AL359092	AL359092 Human DNA
C 14	20	100.0	235338	2	AL357893	AL357893 Homo sapi
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C 16	19	95.0	171026	9	AL590416	AL590416 Human DNA
C 17	19	95.0	184509	2	AC113237	AC113237 Canis fam
C 18	18	90.0	396	6	AX337450	AX337450 Sequence
C 19	18	90.0	543	11	G28197	G28197 human STS S
C 20	18	90.0	1345	6	AX380370	AX380370 Sequence
C 21	18	90.0	1726	6	AX832877	AX832877 Sequence
C 22	18	90.0	1726	9	AK094084	AK094084 Homo sapi
C 23	18	90.0	1835	9	BC004172	BC004172 Homo sapi
C 24	18	90.0	1835	9	BC019324	BC019324 Homo sapi
C 25	18	90.0	1869	6	AR339213	AR339213 Sequence
C 26	18	90.0	3868	9	AL627389	AL627389 Human DNA
C 27	18	90.0	3994	10	AL714015	AL714015 Mouse DNA
C 28	18	90.0	87430	9	AL139400	AL139400 Human DNA
C 29	18	90.0	142422	9	AC113935	AC113935 Homo sapi
C 30	18	90.0	158911	2	AC113803	AC113803 Rattus no
C 31	18	90.0	161692	2	AL138797	AL138797 Homo sapi
C 32	18	90.0	172613	9	AC093433	AC093433 Homo sapi
C 33	18	90.0	173995	2	AC073027	AC073027 Homo sapi
C 34	18	90.0	184660	2	AC123734	AC123734 Mus muscu
C 35	18	90.0	189149	2	AC046171	AC046171 Homo sapi
C 36	18	90.0	189616	2	AC128538	AC128538 Rattus no
C 37	18	90.0	203295	10	AL663049	AL663049 Mouse DNA
C 38	18	90.0	203812	2	AC026874	AC026874 Homo sapi
C 39	18	90.0	204746	9	AC055866	AC055866 Homo sapi
C 40	18	90.0	209083	10	AC113999	AC113999 Mus muscu
C 41	18	90.0	217415	2	AC123346	AC123346 Rattus no
C 42	18	90.0	218127	2	AC132713	AC132713 Rattus no
C 43	18	90.0	218800	2	AC094410	AC094410 Rattus no
C 44	18	90.0	237998	2	BX544886	BX544886 Mus muscu
C 45	18	90.0	238075	2	AC127907	AC127907 Rattus no

ALIGNMENTS

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LOCUS Methods for detecting and measuring spliced nucleic acids.  
DEFINITION BD222535  
ACCESSION BD222535  
VERSION BD222535.1 GI:33032305  
KEYWORDS JP 2002521037-A/13.  
SOURCE synthetic construct  
ORGANISM artificial sequences.  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Harvey R.C. and Eastman, P.S.  
TITLE Methods for detecting and measuring spliced nucleic acids  
JOURNAL Patent: JP 2002521037-A 13 16-JUL-2002;  
GEN PROBE INC

```

COMMENT      OS      Artificial Sequence
PN      JP 2002521037-A/13
PD      16-JUL-2002
PF      23-JUL-1999 JP 2000561364
PR      23-JUL-1998 US 09/121239
PI      RICHARD C HARVEY, PAUL S EASTMAN
PC      C12Q1/68, C12N15/09, C12N15/00
CC      Description of Artificial Sequence: Primer sequence for abl-1
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Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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LOCUS
DEFINITION      Methods for detecting and measuring spliced nucleic acids.
ACCESSION      BD222536
VERSION      BD222536.1 GI:33032306
KEYWORDS      JP 2002521037-A/14.
SOURCE      synthetic construct
ORGANISM      artificial sequences.
REFERENCE      1 (bases 1 to 20)
AUTHORS      Harvey, R.C. and Eastman, P.S.
TITLE      Methods for detecting and measuring spliced nucleic acids
JOURNAL      Patent: JP 2002521037-A 14 16-JUL-2002;
COMMENT      OS      Artificial Sequence
PN      JP 2002521037-A/14
PD      16-JUL-2002
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PR      23-JUL-1998 US 09/121239
PI      RICHARD C HARVEY, PAUL S EASTMAN
PC      C12Q1/68, C12N15/09, C12N15/00
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QY      1 CAAAGGAGCAGGGAAGG 20
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Db
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LOCUS
DEFINITION      Methods for detecting and measuring spliced nucleic acids.
ACCESSION      BD222537
VERSION      BD222537.1 GI:33032307
KEYWORDS      JP 2002521037-A/15.
SOURCE      synthetic construct
ORGANISM      artificial sequences.
REFERENCE      1 (bases 1 to 20)
AUTHORS      Harvey, R.C. and Eastman, P.S.
TITLE      Methods for detecting and measuring spliced nucleic acids
JOURNAL      Patent: JP 2002521037-A 15 16-JUL-2002;
COMMENT      OS      Artificial Sequence
PN      JP 2002521037-A/15
PD      16-JUL-2002
PF      23-JUL-1999 JP 2000561364
PR      23-JUL-1998 US 09/121239
PI      RICHARD C HARVEY, PAUL S EASTMAN
PC      C12Q1/68, C12N15/09, C12N15/00
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FH      Key      Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1 CAAAGGAGCAGGGAAGG 20
        |||||
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Db
RESULT 4
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LOCUS
DEFINITION      Methods for detecting and measuring spliced nucleic acids.
ACCESSION      BD222547
VERSION      BD222547.1 GI:33032317
KEYWORDS      JP 2002521037-A/25.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
REFERENCE      1 (bases 1 to 299)
AUTHORS      Harvey, R.C. and Eastman, P.S.
TITLE      Methods for detecting and measuring spliced nucleic acids
JOURNAL      Patent: JP 2002521037-A 25 16-JUL-2002;
COMMENT      OS      Homo sapiens (human)
PN      JP 2002521037-A/25
PD      16-JUL-2002
PF      23-JUL-1999 JP 2000561364
PR      23-JUL-1998 US 09/121239
PI      RICHARD C HARVEY, PAUL S EASTMAN
PC      C12Q1/68, C12N15/09, C12N15/00
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QY      1 CAAAGGAGCAGGGAAGG 20
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        20 CAAAGGAGCAGGGAAGG 1
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DEFINITION      Methods for detecting and measuring spliced nucleic acids.
ACCESSION      BD222537
VERSION      BD222537.1 GI:33032307
KEYWORDS      JP 2002521037-A/15.
SOURCE      synthetic construct
ORGANISM      artificial sequences.
REFERENCE      1 (bases 1 to 20)
AUTHORS      Harvey, R.C. and Eastman, P.S.
TITLE      Methods for detecting and measuring spliced nucleic acids
JOURNAL      Patent: JP 2002521037-A 15 16-JUL-2002;
COMMENT      OS      Artificial Sequence
PN      JP 2002521037-A/15
PD      16-JUL-2002
PF      23-JUL-1999 JP 2000561364
PR      23-JUL-1998 US 09/121239
PI      RICHARD C HARVEY, PAUL S EASTMAN
PC      C12Q1/68, C12N15/09, C12N15/00
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Db
RESULT 4
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LOCUS
DEFINITION      Methods for detecting and measuring spliced nucleic acids.
ACCESSION      BD222547
VERSION      BD222547.1 GI:33032317
KEYWORDS      JP 2002521037-A/25.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
REFERENCE      1 (bases 1 to 299)
AUTHORS      Harvey, R.C. and Eastman, P.S.
TITLE      Methods for detecting and measuring spliced nucleic acids
JOURNAL      Patent: JP 2002521037-A 25 16-JUL-2002;
COMMENT      OS      Homo sapiens (human)
PN      JP 2002521037-A/25
PD      16-JUL-2002
PF      23-JUL-1999 JP 2000561364
PR      23-JUL-1998 US 09/121239
PI      RICHARD C HARVEY, PAUL S EASTMAN
PC      C12Q1/68, C12N15/09, C12N15/00
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QY 1 CAAAGGAGCAGGAGGAGG 20
Db 84 CAAAGGAGCAGGAGGAGG 103

RESULT 5
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LOCUS          532 bp      mRNA      linear      PRI 30-OCT-1994
DEFINITION    Human abl mRNA containing alternative first exons.
ACCESSION     M14753
VERSION       M14753.1 GI:177945
KEYWORDS      c-myc proto-oncogene; protein kinase.
SOURCE        Homo sapiens (human)
ORGANISM      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE     1 (bases 1 to 532)
AUTHORS      Shtivelman,E., Lifshitz,B., Gale,R.P., Roe,B.A. and Canaani,E.
TITLE        Alternative splicing of RNAs transcribed from the human abl gene
              and from the bcr-abl fused gene
JOURNAL       Cell 47 (2), 277-284 (1986)
MEDLINE       87028219
PUBMED        3021337
COMMENT       Original source text: Human cDNA to mRNA, clone K8.
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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAAAGGAGCAGGAGGAGG 20
Db 409 CAAAGGAGCAGGAGGAGG 428

RESULT 6
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LOCUS          1346 bp      mRNA      linear      ROD 03-OCT-2003
DEFINITION    Mus musculus RIKEN cDNA 2310044P18 gene, mRNA (cDNA clone MGC:11770
IMAGE:3497962), complete cds.
ACCESSION     BC005711
VERSION       BC005711.1 GI:13543068
KEYWORDS      MGC.
SOURCE        Mus musculus (house mouse)
ORGANISM      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
              1 (bases 1 to 1346)
REFERENCE     Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
              Klausner,R.D., Collins,E.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
              Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,

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Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,P.,
Ditachenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
Scheetz,T.E., Brownstein,M.J., Ustin,T.B., Toshiyuki,S.,
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Abramson,R.D., Mullaly,S.J., Bosak,S.A., McEwan,P.J.,
McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
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Sanchez,A., Whitting,M., Madan,A., Young,A.C., Shevchenko,Y.,
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Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smalusz,D.E.,
Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
22388957
JOURNAL       2388957
MEDLINE       22388957
PUBMED        12477932
REFERENCE     2 (bases 1 to 1346)
AUTHORS      Strausberg,R.
TITLE        Direct Submission
JOURNAL       Submitted (02-APR-2001) National Institutes of Health, Mammalian
              Gene Collection (MGC), Cancer Genomics Office, National Cancer
              Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
              USA
REMARK        NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT       Contact: MGC help desk
              Email: cgapbs-remail.nih.gov
              Tissue Procurement: Jeffrey Green M.D.
              cDNA Library Preparation: Life Technologies, Inc.
              cDNA library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
              DNA Sequencing by: Baylor College of Medicine Human Genome
              Sequencing Center
              Center code: BCM-HGSC
              Web site: http://www.hgsc.bcm.tmc.edu/cdna/
              Contact: amg@bcm.tmc.edu
              Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulaeeg, H.,
              Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
              A.N., Gibbs, R.A.
Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAK Plate: 16 Row: n Column: 3
This clone was selected for full length sequencing because it
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## ORIGIN

Query Match 100.0%; Score 20; DB 10; Length 1346;  
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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAAAGGAGCAGGGAAGG 20

Db 1170 CAAAGGAGCAGGGAAGG 1189

## RESULT 7

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LOCUS Human c-abl gene, exon 1b.  
DEFINITION M17310  
ACCESSION M17310

VERSION M17310.1 GI:177941  
KEYWORDS abl proto-oncogene; c-myc proto-oncogene; cellular oncogene;  
proto-oncogene; translocation.

SOURCE Homo sapiens (human)

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 2278 to 2795)

## REFERENCE

1 (bases 2278 to 2795)

Unpublished (1987)

2 (bases 1 to 2277)

Bernards, A., Rubin, C.M., Westbrook, C.A., Paskind, M. and

Baltimore, D.

Baltimore, D.

The first intron in the human c-abl gene is at least 200 kilobases

long and is a target for translocations in chronic myelogenous

leukemia

Mol. Cell. Biol. 7 (9), 3231-3236 (1987)

88038877

3313010

Unpublished (1987)

Original source text: Human DNA, clone pHER7.5.

Draft entry and computer-readable sequence [2], [1] kindly submitted

by A. Bernards (23-OCT-1987).

Location/Qualifiers

1..2795

/organism="Homo sapiens"

/mol\_type="genomic DNA"

/db\_xref="taxon:9606"

/map="9q34.1"

repeat\_region 1..70

/notes="Alu repeat"

751..2795

/gene="ABL1"

751..2162

/gene="ABL1"

/notes="G00-119-640"

2027..2162

/gene="ABL1"

/notes="G00-119-640"

2163..>2795

/gene="ABL1"

/notes="intron A; G00-119-640"

About 0.1 kb downstream from XhoI site; chromosome 9q34.

ORIGIN

Query Match 100.0%; Score 20; DB 9; Length 2795;

Best Local Similarity 100.0%; Pred. No. 19;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAAAGGAGCAGGGAAGG 20

Db 2095 CAAAGGAGCAGGGAAGG 2114

## RESULT 8

AL732315/c

LOCUS

DEFINITION

Mouse DNA sequence from clone Rp23-124N11 on chromosome 11,

complete sequence.

ACCESSION

AL732315

VERSION

AL732315.7 GI:23337296

KEYWORDS

HTG.

SOURCE

Mus musculus (house mouse)

ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 35737)

Direct Submission

Submitted (26-SEP-2002) Wellcome Trust Sanger Institute, Hinxton,

Cambridgeshire, CB10 1SA, UK. E-mail enquiries:

humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk

On Sep 27, 2002 this sequence version replaced gi:22798063.

----- Genome Center

Center: Wellcome Trust Sanger Institute

Center code: SC

Web site: http://www.sanger.ac.uk

Contact: humquery@sanger.ac.uk

-----

During sequence assembly data is compared from overlapping clones.

Where differences are found these are annotated as variations

together with a note of the overlapping clone name. Note that the

variation annotation may not be found in the sequence submission

corresponding to the overlapping clone, as we submit sequences with

only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all

regions were either double-stranded or sequenced with an alternate

chemistry or covered by high quality data (i.e., phred quality >=

30); an attempt was made to resolve all sequencing problems, such

as compressions and repeats; all regions were covered by at least

one plasmid subclone or more than one M13 subclone; and the

assembly was confirmed by restriction digest. The following

abbreviations are used to associate primary accession numbers given

in the feature table with their source databases: Em: EMBL; Sw:

SWISSPROT; Tr: TrEMBL; Wp: WORMPEP; Information on the WORMPEP

database can be found at

http://www.sanger.ac.uk/Projects/C\_elegans/wormpep

from the RPCI-23 Mouse PAC Library

constructed by the group of Pieter de Jong.

For further details see http://www.chori.org/bacpac/home.htm

VECTOR: pBACE3.6.

Location/Qualifiers

1..35737

/organism="Mus musculus"

/mol\_type="genomic DNA"

/db\_xref="taxon:10090"

/chromosome="11"

/clone="RP23-124N11"

/clone\_lib="RPCI-23"

ORIGIN

Query Match 100.0%; Score 20; DB 10; Length 35737;

Best Local Similarity 100.0%; Pred. No. 7.6;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAAAGGAGCAGGGAAGG 20

Db 19478 CAAAGGAGCAGGGAAGG 19459

AX598662

RESULT 9

AX598662

LOCUS

35962 bp DNA linear PAT 14-FEB-2003



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DEFINITION      Sequence 2 from Patent WO02077272.
ACCESSION       AX598662
VERSION         AX598662.1  GI:28398798
KEYWORDS
SOURCE         Homo sapiens (human)
ORGANISM       Homo sapiens
REFERENCE      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS       Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
TITLE         Berlin,K., Braun,A., Distler,J., Guetig,D., Howe,A., Mueller,J.,
JOURNAL       Olek,A., Piepenbrock,C., Adorjan,P., Grabs,G., Lesche,R., Leu,E.,
MEDLINE      Lewin,A., Lipacher,E., Maier,S., Model,F., Mueller,V., Otto,T.,
PUBMED      Pellet,C. and Ziebarth,H.
REFERENCE      Methods and nucleic acids for the analysis of hematopoietic cell
AUTHORS       proliferative disorders
TITLE         Patent: WO 02077272-A 2 03-OCT-2002;
JOURNAL       Epigenomics AG (DE)
MEDLINE      Epigenomics AG (DE)
PUBMED      1. .35962
FEATURES       Location/Qualifiers
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              /mol_type="unassigned DNA"
              /db_xref="taxon:9606"
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Query Match      100.0%; Score 20; DB 6; Length 35962;
Best Local Similarity 100.0%; Pred. No. 7.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CAAAGGAGCAGGAGGAGG 20
Db 29200 CAAAGGAGCAGGAGGAGG 29219
RESULT 10
HSABLCR1
LOCUS           35962 bp DNA linear PRI 16-APR-2002
DEFINITION     Human ABL gene, exon 1b and intron 1b, and putative M8604 Met
ACCESSION      U07561
VERSION        U07561.1  GI:514262
KEYWORDS
SEGMENT
SOURCE         1 of 3
ORGANISM       Homo sapiens (human)
REFERENCE      Homo sapiens
AUTHORS       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
              1 (bases 1 to 35962)
              Chisoe,S.L., Bodenteich,A., Wang,Y., Jian,L., Burian,D.,
              Carbtree,J.S., Freeman,A., Hamed,O.S., McLaury,H., Pan,H., Toth,S.,
              Wang,Z., Zhang,G., Clifton,S., Groffen,J., Heisterkamp,N. and
              Roe,B.A.
              Sequence and analysis of the human ABL gene, the BCR gene, and
              regions involved in the Philadelphia chromosomal translocation
              Genomics 27 (1), 67-82 (1995)
              95394474
              PUBMED 7665185
REFERENCE      2 (bases 1 to 35962)
AUTHORS       Groffen,J., Heisterkamp,N., Grosveld,F., Van de Ven,W. and
              Stephenson,J.R.
              Isolation of human oncogene sequences (v-fes homolog) from a cosmid
              library
              Science 216 (4550), 1136-1138 (1982)
              82199444
              PUBMED 6281890
REFERENCE      3 (bases 1 to 35962)
AUTHORS       Morris,C.M., Heisterkamp,N., Groffen,J. and Fitzgerald,P.H.
              Entire ABL gene is joined with 5'-BCR in some patients with
              Philadelphia-positive leukemia
              Blood 78 (4), 1078-1084 (1991)
              91329820
              PUBMED 1868241
REFERENCE      4 (bases 27793 to 28338; 28792 to 29265)
AUTHORS       Shtivelman,E., Lifshitz,B., Gale,R.P., Roe,B.A. and Canaani,E.
Alternative splicing of RNAs transcribed from the human abl gene
and from the bcr-abl fused gene
Cell 47 (2), 277-284 (1986)
87028219
MEDLINE
PUBMED 3021337
REFERENCE 5 (bases 27108 to 29899)
AUTHORS       Bernard,A., Rubin,C.M., Westbrook,C.A., Paskind,M. and
              Baltimore,D.
              The first intron in the human c-abl gene is at least 200 kilobases
              long and is a target for translocations in chronic myelogenous
              leukemia
              Mol. Cell. Biol. 7 (9), 3231-3236 (1987)
              88038877
              PUBMED 3313010
REFERENCE 6 (bases 1 to 35962)
AUTHORS       Mount,S.M.
              A catalogue of splice junction sequences
              Nucleic Acids Res. 10 (2), 459-472 (1982)
              82150208
              PUBMED 7063411
REFERENCE 7 (bases 1 to 35962)
AUTHORS       Adams,M.D., Dubnick,M., Kerlavage,A.R., Moreno,R., Kelley,J.M.,
              Utterback,T.R., Nagle,J.W., Fields,C. and Venter,J.C.
              Sequence identification of 2,375 human brain genes
              Nature 355 (6361), 632-634 (1992)
              92168112
              PUBMED 1538749
REFERENCE 8 (bases 1 to 35962)
AUTHORS       Zhu,Q.S., Heisterkamp,N. and Groffen,J.
              Characterization of the human ABL promoter regions
              Oncogene 5 (6), 885-891 (1990)
              90295283
              PUBMED 2163052
REFERENCE 9 (bases 1 to 35962)
AUTHORS       Paskind,M.
              Personal communication
              Unpublished
              10 (bases 1 to 35962)
              Tatusov,R. and Lipman,D.J.
              Using local similarities for pattern detection in
              nucleotide/protein sequences
              Unpublished
              11 (bases 1 to 35962)
              Groffen,J., Stephenson,J.R., Heisterkamp,N., de Klein,A.,
              Bartram,C.R. and Grosveld,G.
              Philadelphia chromosomal breakpoints are clustered within a limited
              region, bcr, on chromosome 22
              Cell 36 (1), 93-99 (1984)
              84106827
              PUBMED 6319012
REFERENCE 12 (bases 1 to 35962)
AUTHORS       Chisoe,S.L.
              Sequence of the human abl and bcr genes
              Thesis (1994) University of Oklahoma
              13 (bases 1 to 35962)
              Roe,B.A.
              Direct Submission
              Submitted (08-MAR-1994) Bruce A. Roe, Dept. of Chem. and Biochem.,
              University of Oklahoma, 620 Parrington Oval, Rm 208, Norman, OK
              73019, USA
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              /rpt_family="Alu"
              repeat_region complement (478..>728)

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15672. .15740,16939. .17115,17862. .17990,18503. .18583)
/notes="putative 8604 MET gene, 5' to the ABL gene"
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/evidence=experimental
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LQEGDLISAEQAVFDGAVSLHTRSLKYLKGLGVQVSPSLVKRQKTHFDLPFG
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Best Local Similarity 100.0%; Pred. No. 7.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAAAGGAGGAGGAGGAGG 20
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Db 29200 CAAAGGAGGAGGAGGAGG 29219

RESULT 11
AC023898/c
LOCUS 79302 bp DNA linear HTG 16-OCT-2001
DEFINITION Mus musculus clone RP23-281H12, *** SEQUENCING IN PROGRESS ***, 27
unordered pieces.
ACCESSION AC023898
VERSION AC023898.7 GI:16118065
KEYWORDS HTG; HTGS PHASE1.
SOURCE Mus musculus
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 79302)
AUTHORS Metzker,M.L., Lewis,L.R., Hume,J., Edwards,C., Harris,C.,
Dederich,D., Thomas,S., Okwuonu,G., Carlock,C., Garner,T.,
Addison,S., Pace,A., Williams,G., Bonnin,D., Brooks,A., Brown,J.,
Buhay,C., Bunac,C., Burkett,C., Chacko,J., Chen,G., Chen,Z.,
Cox,C., Davis,C., Delgado,O., Ding,Y., Dugan-Rocha,S.,
Fernandez,C., Ferraguto,D., Forcum-Tansey,J., Gill,R.,
Correll,J.H., Gunaratne,P., Haller,G., Hernandez,J., Hogue,M.,
Hosak,H., Hou,X., Huber,J., Jackson,L., Jia,Y., Kelly,J., Kelly,S.,
Kovar,C., Liu,J., Liu,W., Loulseghe,H., Lozado,R.J., Martin,R.,
Massey,E., McLeod,M.P., Mei,G., Moore,S., Morgan,M., Morris,S.,
Neal,D., Nelson,A., Nguyen,R., Nguyen,N., Ogih,M., Parish,B.,
Perez,L., Reiter,D., Say,J., Shen,H., Vasquez,L., Watlington,S.,
Williamson,A., Wrensford,G., Zhou,X., Bouck,J., Hodgson,A.,
Muzny,D.M., Rives,M., Scherer,S., Sodergren,E., Weinstein,G.,
Worley,K. and Gibbs,R.
Direct Submission
Unpublished
2 (bases 1 to 79302)
Worley,K.C.
Direct Submission
Submitted (20-FEB-2000) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Oct 14, 2001 this sequence version replaced gi:11079363.
----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: MABD
Center clone name: RP23-281H12
----- Summary Statistics
Sequencing vector: M13; L08821
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FEATURES
source
Location/Qualifiers
1. .79302
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/clone="RP23-281H12"

ORIGIN

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Best Local Similarity 100.0%; Pred. NO. 5.7;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY    1   CAAAGGACGAGCGAAGAAG 20
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Db     58995 CAAAGGACGAGCGAAGAAG 58976

RESULT 12
AC015497
LOCUS
DEFINITION
piece.
Accession AC015497
Version AC015497.3 GI:75333974
Keywords HTG; HTGS_PHASE1; HTGS_DRAFT.
Source Homo sapiens (human)
Organism Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 158264)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens, clone RP11-21G10, WORKING DRAFT SEQUENCE, 27 unordered
pieces.
REFERENCE
1 (bases 1 to 158264)
Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M.,
Baldwin,J., Barna,N., Beckerly,R., Boguslavsky,I., Bouckhalter,B.,
Brown,A., Castle,A., Collinge,S., Collins,S., Collymore,A.,
Cooke,P., DeArrellano,K., Dewar,K., Domino,M., Donelan,L., Doyle,M.,
Ferreira,P., FitzHugh,W., Forrest,C., Funke,R., Gage,D.,
Galagan,J., Gardyna,S., Grant,G., Hagos,B., Heaford,A., Horton,L.,
Howland,J.C., Johnson,R., Jones,C., Kann,L., Karatas,A., Klein,J.,
Lehoczky,J., Lieu,C., Locke,K., Macdonald,P., Marquis,N.,
McSwan,P., McGurk,A., McKernan,K., McLaughlin,T., Meldrim,J.,
Morrow,J., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,
Peterson,K., Pollara,V., Riley,R., Roy,A., Santos,R., Severy,P.,
Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,
Tefaye,S., Tirrell,A., Vassiliev,H., Vo,A., Wheeler,J., Wu,X.,
Wyman,D., Ye,W.J., Zimmer,A. and Zody,M.
Direct Submission
Submitted (16-NOV-1999) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Apr 11, 2000 this sequence version replaced gi:6587901.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RW/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L4002
Center clone name: 21 G 10
----- Summary Statistics
Sequencing vector: M13; M7815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 118404 bases at least Q40
Consensus quality: 139706 bases at least Q30
Consensus quality: 149210 bases at least Q20
Insert size: 111000; agarose-fp
Insert size: 155664; sum-of-contigs
Quality coverage: 5.1 in Q20 bases; agarose-fp

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Quality coverage: 3.6 in Q20 bases; sum-of-contigs

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\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 27 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.

\* 1  
\* 1099: contig of 1099 bp in length  
\* 1199: gap of 100 bp  
\* 1200: contig of 1010 bp in length  
\* 2209: contig of 100 bp  
\* 2309: gap of 100 bp  
\* 2310: contig of 1015 bp in length  
\* 3234: gap of 100 bp  
\* 3425: contig of 100 bp  
\* 4909: contig of 1485 bp in length  
\* 5009: gap of 100 bp  
\* 6227: contig of 1218 bp in length  
\* 6328: gap of 100 bp  
\* 7565: contig of 1238 bp in length  
\* 7666: gap of 100 bp  
\* 7666: contig of 1130 bp in length  
\* 8895: gap of 100 bp  
\* 8896: contig of 1991 bp in length  
\* 10887: gap of 100 bp  
\* 10987: contig of 2269 bp in length  
\* 13256: gap of 100 bp  
\* 13356: contig of 3119 bp in length  
\* 16474: gap of 100 bp  
\* 16575: contig of 3262 bp in length  
\* 19837: gap of 100 bp  
\* 19837: contig of 3113 bp in length  
\* 23050: gap of 100 bp  
\* 23150: contig of 3479 bp in length  
\* 26629: gap of 100 bp  
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\* 30237: gap of 100 bp  
\* 30337: contig of 3651 bp in length  
\* 33988: gap of 100 bp  
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\* 39138: gap of 100 bp  
\* 39238: contig of 5714 bp in length  
\* 44951: gap of 100 bp  
\* 45052: contig of 5332 bp in length  
\* 50384: gap of 100 bp  
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\* 55556: gap of 100 bp  
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\* 61724: gap of 100 bp  
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\* 68825: gap of 100 bp  
\* 68925: contig of 8693 bp in length  
\* 77618: gap of 100 bp  
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\* 87000: gap of 100 bp  
\* 87100: contig of 13223 bp in length  
\* 100323: gap of 100 bp  
\* 100423: contig of 13123 bp in length  
\* 113546: gap of 100 bp  
\* 113646: contig of 12825 bp in length  
\* 126471: gap of 100 bp  
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FEATURES Location/Qualifiers

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1200. .2209

misc\_feature

misc\_feature

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5010. .6227  
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ORIGIN

Query Match 100.0%; Score 20; DB 2; Length 158264;  
Best Local Similarity 100.0%; Pred. No. 4.4;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAAAGGAGCAGGAGGAGG 20

Db 66359 CAAAGGAGCAGGAGGAGG 66378

RESULT 13

AL359092  
LOCUS AL359092 173463 bp DNA linear PRI 17-MAR-2001  
DEFINITION Human DNA sequence from clone RP11-57C19 on chromosome 9, complete  
sequence.  
ACCESSION AL359092  
VERSION AL359092.14 GI:13274746

HTG. Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 173463)  
Lloyd.D.  
REFERENCE Direct Submission  
AUTHORS Submitted (15-MAR-2001) Sanger Centre, Hinxton, Cambridgeshire,  
TITLE CB10 ISA, UK. E-mail enquiries: humquery@sanger.ac.uk  
JOURNAL requests: clonerequest@sanger.ac.uk  
COMMENT On Mar 12, 2001 this sequence version replaced gi:13273753.  
During sequence assembly data is compared from overlapping clones.  
Where differences are found these are annotated as variations  
together with a note of the overlapping clone name. Note that the  
variation annotation may not be found in the sequence submission  
corresponding to the overlapping clone, as we submit sequences with  
only a small overlap as described above.  
This sequence was finished as follows unless otherwise noted: all  
regions were either double-stranded or sequenced with an alternate  
chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such  
as compressions and repeats; all regions were covered by at least  
one plasmid subclone or more than one M13 subclone; and the  
assembly was confirmed by restriction digest. The following  
abbreviations are used to associate primary accession numbers given  
in the feature table with their source databases: Em, EMBL; Sw,  
SWISSPROT; Tr, TREMBL; Wp, WORMPEP; Information on the WORMPEP  
database can be found at  
http://www.sanger.ac.uk/Projects/C\_elegans/wormpep/ This sequence  
was generated from part of bacterial clone contigs of human  
chromosome 9, constructed by the Sanger Centre Chromosome 9 Mapping  
Group. Further information can be found at  
http://www.sanger.ac.uk/HGP/Chr9  
Rpl1-57C19 is from the library RBC1-11.1 constructed by the group  
of Pieter de Jong. For further details see  
http://www.chori.org/bacpac/home.htm  
VECTOR: pBACE3.6  
This sequence is the entire insert of clone Rpl1-57C19 The true  
left end of clone Rpl1-83J21 is at 160857 in this sequence. The  
true right end of clone Rpl1-17L7 is at 26509 in this sequence.  
FEATURES  
source  
1..173463  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"  
/chromosome="9"  
/clone="Rpl1-57C19"  
/clone\_lib="RBC1-11.1"  
misc\_feature  
1..183  
/note="match: GSS: Em:AQ035345"  
misc\_feature  
6..403  
/note="match: GSS: Em:AQ115418"  
repeat\_region  
90..213  
/note="L2 repeat: matches 2575..2708 of consensus"  
repeat\_region  
545..848  
/note="AluSx repeat: matches 1..304 of consensus"  
repeat\_region  
1382..1677  
/note="AluSp repeat: matches 1..297 of consensus"  
repeat\_region  
1845..2114  
/note="AluSx repeat: matches 1..269 of consensus"  
repeat\_region  
5671..5722  
/note="26 copies 2 mer tt 71% conserved"  
misc\_feature  
6481..6706  
/note="match: GSS: Em:AQ088691"  
misc\_feature  
complement(9530..10310)  
/note="match: GSS: Em:AQ740221"  
misc\_feature  
10440..10705  
/note="match: GSS: Em:AQ097316"  
repeat\_region  
10785..10968  
/note="L2 repeat: matches 2524..2707 of consensus"  
repeat\_region  
11894..11943  
/note="MER46C repeat: matches 284..333 of consensus"

complement(12898..13402)  
/note="match: GSS: Em:B71356"  
12899..13060  
/note="MER3 repeat: matches 33..208 of consensus"  
13559..13598  
/note="2 copies 20 mer 100% conserved"  
14220..14327  
/note="L1MC4 repeat: matches 7751..7885 of consensus"  
15419..15887  
/note="match: GSS: Em:AQ545312"  
15665..16010  
/note="L1MB4 repeat: matches 5817..6185 of consensus"  
16051..16318  
/note="AluJo repeat: matches 7..265 of consensus"  
16468..16770  
/note="AluSg repeat: matches 1..303 of consensus"  
16884..17185  
/note="AluSx repeat: matches 1..305 of consensus"  
17193..17488  
/note="AluSx repeat: matches 1..297 of consensus"  
19180..19344  
/note="MERSA repeat: matches 1..173 of consensus"  
19356..19597  
/note="MER30 repeat: matches 1..230 of consensus"  
19649..19778  
/note="AluSg/x repeat: matches 1..132 of consensus"  
19781..20059  
/note="AluSg repeat: matches 1..290 of consensus"  
22904..22983  
/note="4 copies 20 mer 76% conserved"  
23603..23911  
/note="AluSp repeat: matches 1..310 of consensus"  
complement(23996..24443)  
/note="match: GSS: Em:AQ239485"  
26524..26927  
/note="match: GSS: Em:AQ893594"  
26667..26930  
/note="match: GSS: Em:AQ083068"  
32584..32978  
/note="match: GSS: Em:AQ112811"  
34131..34553  
/note="match: GSS: Em:AQ763967"  
34143..34353  
/note="match: GSS: Em:AQ001150"  
35569..35654  
/note="MIR repeat: matches 81..172 of consensus"  
35847..36321  
/note="MER82 repeat: matches 160..653 of consensus"  
36322..36629  
/note="AluSx repeat: matches 1..309 of consensus"  
36630..36672  
/note="MER82 repeat: matches 117..160 of consensus"  
36673..36841  
/note="FAM repeat: matches 5..173 of consensus"  
36844..37154  
/note="AluSx repeat: matches 1..312 of consensus"  
37155..37312  
/note="MER82 repeat: matches 1..117 of consensus"  
37324..37374  
/note="MIR repeat: matches 122..170 of consensus"  
37375..37679  
/note="AluSg repeat: matches 1..305 of consensus"  
37680..37718  
/note="MIR repeat: matches 83..122 of consensus"  
37738..37817  
/note="MIR repeat: matches 81..170 of consensus"  
38230..38536  
/note="AluJo repeat: matches 1..300 of consensus"  
38537..38840  
/note="AluSx repeat: matches 1..302 of consensus"  
38841..39144  
/note="AluY repeat: matches 1..311 of consensus"  
39417..39697

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/note="AluSx repeat: matches 1. .298 of consensus"
39792. .40097
/note="AluSg repeat: matches 1. .304 of consensus"
40138. .40411
/note="AluY repeat: matches 39. .310 of consensus"
40416. .40636
/note="L1M4 repeat: matches 4539. .4769 of consensus"
40825. .41072
/note="L1 repeat: matches 3771. .4023 of consensus"
complement(40954. .41169)
/note="match: STS: Em:G08714"
complement(40988. .41142)
/note="match: GSS: Em:AZ640566"
40993. .41171
/note="match: GSS: Em:AZ040457"
complement(41024. .41169)
/note="match: STS: Em:G08716"
41025. .41164
/note="match: GSS: Em:AZ0407452"
41028. .41169
/note="match: GSS: Em:AZ020257"
complement(41028. .41163)
/note="match: GSS: Em:AZ056687"
complement(41028. .41155)
/note="match: GSS: Em:AZ179869"
complement(41038. .41160)
/note="match: GSS: Em:AZ838018 Em:AZ838106"
41040. .41151
/note="match: STS: Em:L30635"
41041. .41179
/note="match: GSS: Em:AZ921614"
complement(41041. .41171)
/note="match: GSS: Em:AZ035323"
41041. .41169
/note="match: STS: Em:L17666"
complement(41044. .41171)
/note="match: GSS: Em:AZ644560"
41052. .41170
/note="match: GSS: Em:AZ975962"
41059. .41222
/note="match: GSS: Em:AZ060388"
complement(41059. .41171)
/note="match: GSS: Em:AZ0881617"
complement(41068. .41175)
/note="match: GSS: Em:AZ640589"
complement(41068. .41171)
/note="match: STS: Em:G07990 Em:G07994 Em:G09150"
complement(41069. .41218)
/note="match: GSS: Em:AZ318431"

Query Match 100.0%; Score 20; DB 9; Length 173463;
Best Local Similarity 100.0%; Pred. No. 4.2;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAAAGGAGCAGGGAAGG 20
Db 109231 CAAAGGAGCAGGGAAGG 109250
|||||
|||||

RESULT 14
AL357893/c AL357893 235338 bp DNA linear HTG 10-JUL-2001
LOCUS Homo sapiens chromosome 9 clone RP11-253A1, 29 unordered pieces.
DEFINITION AL357893
ACCESSION AL357893
VERSION AL357893.8 GI:14586541
KEYWORDS HTG; HTGS_PHASE1; HTGS_CANCELLED.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Plumb,B.
TITLE Direct Submission

```

JOURNAL

COMMENT

Submitted (09-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk

On Jul 3, 2001 this sequence version replaced gi:14575206.

----- Genome Center

Center: Sanger Centre

Center code: SC

Web site: http://www.sanger.ac.uk

Contact: humquery@sanger.ac.uk

----- Project information

Center project name: bA253A1

----- Summary Statistics

Assembly program: XGAP4; version 4.5

Sequencing vector: plasmid; L08752; 100% of reads

Chemistry: Dye-terminator Big Dye; 100% of reads

Consensus quality: 113075 bases at least Q40

Consensus quality: 120255 bases at least Q30

Consensus quality: 124314 bases at least Q20

Insert size: 232538; sum-of-contigs

Insert size: 166097; 3.1% error; agarose-fp

Quality coverage: 1.72x in Q20 bases; sum-of-contigs Quality coverage: 2.59x in Q20 bases; agarose-fp

-----

\* NOTE: This is a 'working draft' sequence. It currently consists of 29 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

*	1	5789:	contig of 5789 bp in length
*	5790	5889:	gap of 100 bp
*	5890	9227:	contig of 3338 bp in length
*	9228	9327:	gap of 100 bp
*	9328	15450:	contig of 6123 bp in length
*	15451	15550:	gap of 100 bp
*	15551	24512:	contig of 8962 bp in length
*	24513	24612:	gap of 100 bp
*	24613	33557:	contig of 8745 bp in length
*	33558	33457:	gap of 100 bp
*	33458	45426:	contig of 11969 bp in length
*	45427	45526:	gap of 100 bp
*	45527	48337:	contig of 2811 bp in length
*	48338	48437:	gap of 100 bp
*	48438	51040:	contig of 2603 bp in length
*	51041	51140:	gap of 100 bp
*	51141	53592:	contig of 2452 bp in length
*	53593	53692:	gap of 100 bp
*	53693	56386:	contig of 2694 bp in length
*	56387	56486:	gap of 100 bp
*	56487	62895:	contig of 6509 bp in length
*	62896	63095:	gap of 100 bp
*	63096	66159:	contig of 3064 bp in length
*	66160	66259:	gap of 100 bp
*	66260	69523:	contig of 3264 bp in length
*	69524	69623:	gap of 100 bp
*	69624	74715:	contig of 5092 bp in length
*	74716	74815:	gap of 100 bp
*	74816	83734:	contig of 8919 bp in length
*	83735	83834:	gap of 100 bp
*	83835	87461:	contig of 3627 bp in length
*	87462	87561:	gap of 100 bp
*	87562	119073:	contig of 31512 bp in length
*	119074	119173:	gap of 100 bp
*	119174	123743:	contig of 4570 bp in length
*	123744	123843:	gap of 100 bp
*	123844	129766:	contig of 5923 bp in length
*	129767	129866:	gap of 100 bp
*	129867	142567:	contig of 12701 bp in length
*	142568	142667:	gap of 100 bp
*	142668	151783:	contig of 9116 bp in length
*	151784	151883:	gap of 100 bp

```

* 151884 165129: contig of 13246 bp in length
* 165130 165229: gap of 100 bp
* 165230 169016: contig of 3787 bp in length
* 169017 169116: gap of 100 bp
* 169117 172815: contig of 3699 bp in length
* 172816 172915: gap of 100 bp
* 172916 178100: contig of 5185 bp in length
* 178101 178200: gap of 100 bp
* 178201 186238: contig of 8038 bp in length
* 186239 186338: gap of 100 bp
* 186339 189386: contig of 3048 bp in length
* 189387 189486: gap of 100 bp
* 189487 217139: contig of 27653 bp in length
* 217140 217240 235338: contig of 18099 bp in length.
FEATURES
    source
        1. .235338
            /organism="Homo sapiens"
            /mol_type="genomic DNA"
            /db_xref="taxon:9606"
            /chromosome="9"
            /clone="RP11-253A1"
            /clone_lib="RPC1-11.1"
            1. .5789
            /note="assembly_fragment:01637"
            clone_end:17
            vector_side:left
            5890. .9227
            /note="assembly_fragment:00699"
            fragment_chain:1
            9328. .15450
            /note="assembly_fragment:00899"
            fragment_chain:1
            15551. .24512
            /note="assembly_fragment:01643"
            fragment_chain:2
            24613. .33357
            /note="assembly_fragment:01662"
            fragment_chain:2
            33458. .45426
            /note="assembly_fragment:01699"
            fragment_chain:3
            45527. .48337
            /note="assembly_fragment:01712"
            fragment_chain:3
            48438. .51040
            /note="assembly_fragment:00070"
            51141. .53592
            /note="assembly_fragment:00277"
            53693. .56386
            /note="assembly_fragment:00560"
            56487. .62995
            /note="assembly_fragment:00561.0"
            63096. .66159
            /note="assembly_fragment:00630"
            66260. .69523
            /note="assembly_fragment:00835"
            69624. .74715
            /note="assembly_fragment:00836"
            74816. .83734
            /note="assembly_fragment:01652"
            83835. .87461
            /note="assembly_fragment:01659"
            87562. .119073
            /note="assembly_fragment:01666"
            119174. .123743
            /note="assembly_fragment:01715"
            123844. .129766
            /note="assembly_fragment:01719"
            129867. .142567
            /note="assembly_fragment:01724"
            142688. .151783
            /note="assembly_fragment:01746"

```

```

misc_feature 151884. .165129
/note="assembly_fragment:01756"
misc_feature 165230. .169016
/note="assembly_fragment:01773"
misc_feature 169117. .172815
/note="assembly_fragment:01777"
misc_feature 172916. .178100
/note="assembly_fragment:01781"
misc_feature 178201. .186238
/note="assembly_fragment:01788"
misc_feature 186339. .189386
/note="assembly_fragment:01796"
misc_feature 189487. .217139
/note="assembly_fragment:01799.0"
misc_feature 217240. .235338
/note="assembly_fragment:01800"
ORIGIN
Query Match 100.0%; Score 20; DB 2; Length 235338;
Best Local Similarity 100.0%; Pred. No. 3.8;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CAACGAGCAGCGGAGGAGG 20
|||||
Db 41885 CAACGAGCAGCGGAGGAGG 41866
|||||
RESULT 15
AC114327 136641 bp DNA linear HTG 07-MAR-2002
LOCUS Canis familiaris clone RP81-158C13, WORKING DRAFT SEQUENCE, 2
DEFINITION unordered pieces.
ACCESSION AC114327.1 GI:19224976
VERSION HTG; HTGS PHASE1; HTGS DRAFT.
KEYWORDS Canis familiaris (dog)_DRAFT.
SOURCE Canis familiaris
ORGANISM Canis familiaris
REFERENCE 1 (bases 1 to 136641)
AUTHORS Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G., Breen,K., Brinkley,C., Brooks,S.,
Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
Ho,S.-L., Idol,J.R., Karlins,E., Laric,P., Lee-Lin,S.-O.,
Legaspi,R., Maduro,Q.L., Maduro,V.B., Masiello,C., Maskeri,B.,
Mastrian,S.D., McCloskey,J.C., McDowell,J., Pearson,R., Prasad,A.,
Stantripop,S., Thomas,J.W., Thomas,P.J., Touchman,J.W.,
Tsurgenev,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
Young,A., Zhang,L.-H. and Green,E.D.
NISC Comparative Sequencing Initiative
Unpublished
REFERENCE 2 (bases 1 to 136641)
AUTHORS Green,E.D.
TITLE Direct Submission
JOURNAL Submitted (07-MAR-2002) NIH Intramural Sequencing Center, 8717
Grovemont Circle, Gaithersburg, MD 20877, USA
COMMENT
Center: NIH Intramural Sequencing Center
Center code: NISC
Web site: http://www.nisc.nih.gov
Contact: nisc_mouse@nigri.nih.gov
----- Project Information
Center project name: cin
Center clone name: 158C13
----- Summary Statistics
Sequencing vector: plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 136372 bases at least Q40
Consensus quality: 136409 bases at least Q30
Consensus quality: 136413 bases at least Q20
Insert size: 109000; agarose-fp
Insert size: 136541; sum-of-contigs

```

Quality coverage: 12.91x in Q20 bases; agarose-fp  
Quality coverage: 10.31x in Q20 bases; sum-of-contigs

-----  
\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 2 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.

\* 1 49995: contig of 49995 bp in length  
\* 49996 50095: gap of unknown length  
\* 50096 136641: contig of 86546 bp in length.

FEATURES

source

1..136641  
/organism="Canis familiaris"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9615"  
/clone="RP81-158C13"  
/clone\_lib="RP81"

misc\_feature

1..49995  
/note="assembly\_fragment"  
clone\_end:SP6  
vector\_side:right  
50096..136641  
/note="assembly\_fragment"  
clone\_end:T7  
vector\_side:right"

misc\_feature

ORIGIN

Query Match 95.0%; Score 19; DB 2; Length 136641;  
Best Local Similarity 100.0%; Pred. No. 13;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAAAGGAGCAGGAGGAAG 19

Db 18197 CAAAGGAGCAGGAGGAAG 18215  
|||||

Search completed: May 27, 2004, 02:16:44  
Job time : 430.652 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 26, 2004, 14:55:11 ; Search time 89.1973 Seconds  
(without alignments)  
952.539 Million cell updates/sec

Title: US-09-121-239-13

Perfect score: 20  
Sequence: 1 CAACGAGCAGGGAAGAGG 20

Scoring table: OLIGO NUC  
Gapop 60.0 , Gapext 60.0

Searched: 3373863 seqs, 2124099041 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : N Geneseq\_29Jan04:\*  
1: Geneseqn1980s:\*  
2: Geneseqn1990s:\*  
3: Geneseqn2000s:\*  
4: Geneseqn2001as:\*  
5: Geneseqn2001bs:\*  
6: Geneseqn2002s:\*  
7: Geneseqn2003as:\*  
8: Geneseqn2003bs:\*  
9: Geneseqn2003cs:\*  
10: Geneseqn2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	3	Aaz60852 Oligonucle
C 2	20	100.0	20	3	Aaz60854 Oligonucle
C 3	20	100.0	20	3	Aaz60853 Oligonucle
4	20	100.0	299	3	Aaz60854 Region su
5	20	100.0	530	5	Aad08655 Mouse can
6	20	100.0	1538	7	Abx05481 Human nov
7	20	100.0	5434	6	Abv77964 Hypoxia-r
8	20	100.0	35962	7	Abz09862 Human 5'
C 9	18	90.0	396	6	AbL69622 Prostate
10	18	90.0	474	8	Ach32870 Human end
11	18	90.0	543	2	Aat19863 Human gen
12	18	90.0	1345	6	Aba94712 Human ani
13	18	90.0	1390	4	Aas41347 cDNA enco
C 14	18	90.0	1611	4	Aal06632 Human rep
C 15	18	90.0	1611	5	Aas40715 DNA enco
16	18	90.0	1859	4	Aak55488 Human imm
17	18	90.0	1869	4	Aai58813 Human pol
18	18	90.0	1869	8	Adb48794 Human hum
19	18	90.0	2177	4	Aai60599 Human pol
20	18	90.0	3380	7	Abz18520 Group III
21	17	85.0	416	6	Abn96456 Gene #295
C 22	17	85.0	36305	6	Abk22783 Human hlg
C 23	17	85.0	39729	9	Adc86832 Human gpc

C 24	17	85.0	55795	6	ABL68242	AbL68242 Kidney ca
C 25	17	85.0	55795	6	ABL68863	AbL68863 Kidney ca
C 26	17	85.0	55795	6	ABL68484	AbL68484 Kidney ca
C 27	17	85.0	55795	6	ABN95045	Abn95045 Gene #154
C 28	17	85.0	57273	6	ABK22784	Abk22784 Human hlg
C 29	17	85.0	66933	5	ABA82625	ABA82625 Human HBM
C 30	17	85.0	66933	7	ACC45366	Acc45366 Human HBM
C 31	17	85.0	66933	9	ADB98066	ADB98066 HBM-relat
C 32	17	85.0	66933	9	ADE82435	AdE82435 Human DNA
C 33	17	85.0	72049	5	ABR82623	ABa82623 Human HBM
C 34	17	85.0	72049	7	ACC45364	Acc45364 Human HBM
C 35	17	85.0	72049	9	ADB98064	AdB98064 HBM-relat
C 36	17	85.0	72049	9	ABE82433	Ade82433 Human DNA
C 37	16	80.0	444	4	AAD05102	Aad05102 Human sec
38	16	80.0	621	5	AAS84646	Aas84646 DNA enco
39	16	80.0	1763	5	AAD07934	Aad07934 Human TDC
C 40	16	80.0	1876	4	AAD05101	Aad05101 Human sec
41	16	80.0	2162	9	ADC32407	Adc32407 Human nov
C 42	16	80.0	2307	4	AAD05064	Aad05064 Human sec
43	16	80.0	2491	4	AAH15154	Aah15154 Human cDN
C 44	16	80.0	3598	7	ADA57705	Ada57705 BAC fragm
C 45	16	80.0	3598	7	ADA41572	Ada41572 Human sec

## ALIGNMENTS

RESULT 1  
AAZ60852  
ID AAZ60852 standard; DNA; 20 BP.  
XX  
AC AAZ60852;  
XX  
DT 16-MAY-2000 (first entry)  
DE  
DE  
XX  
XX  
KW Oligonucleotide used to detect bcr b3-abl fusion transcripts.  
KW Fusion transcript; translocation; bcr b3 region; abl gene;  
KW amplification assay; detection assay; medical diagnosis;  
KW clinical monitoring; chimeric RNA; fusion RNA; condition marker;  
KW disease marker; cancer; leukemia; ss.  
XX  
OS Synthetic.  
XX  
PN WO200005418-A1.  
XX  
XX  
PD 03-FEB-2000.  
XX  
PF 23-JUL-1999; 99WO-US016832.  
XX  
PR 23-JUL-1998; 98US-00121239.  
XX  
PA (GENP-) GEN-PROBE INC.  
XX  
PI Harvey RC, Eastman PS;  
XX  
DR WPI; 2000-182730/16.  
XX  
PT Novel methods for preparing RNA from biological samples, used for the  
PT detection and measurement of nucleic acids and fusion nucleic acids.  
XX  
XX  
PS Claim 19; Page 42; 49pp; English.  
XX  
XX  
CC Oligonucleotides AAZ60840-62 and AAZ60865-66 are used in the method of  
CC the invention to detect fusion transcripts produced from a translocation  
CC between the bcr b3 region and the abl gene. The specification describes a  
CC method for detecting a fusion nucleic acid (particularly chimeric mRNA  
CC species), in a biological sample. The method comprises contacting a  
CC sample of fusion nucleic acid with primers, amplifying the hybridized  
CC fusion nucleic acid, and detecting the target hybrid. The method is used  
CC for the sample and rapid preparation of RNA from a biological sample,  
CC particularly from the cytoplasm of eukaryotic cells, which is suitable  
CC for use in an amplification and detection assay. The methods are used for

CC the analysis and detection of nucleic acids in biological samples. The  
CC methods are useful in the human medical and veterinary fields, for  
CC medical diagnoses and clinical monitoring of a patient's response to  
CC therapy where a disease or medical condition is associated with a  
CC particular type and/or level of mRNA present in the sample. The methods  
CC are also useful for detecting or quantifying fusion or chimeric RNA  
CC species, and for detecting a translocation as a marker for a given  
CC condition or disease, e.g. translocations associate with cancers,  
CC particularly forms of leukemia

XX Sequence 20 BP; 9 A; 2 C; 9 G; 0 T; 0 U; 0 Other;  
SQ

Query Match 100.0%; Score 20; DB 3; Length 20;  
Best Local Similarity 100.0%; Pred. No. 0.73;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAAAGGAGCAGGGAAGG 20  
Db 1 CAAAGGAGCAGGGAAGG 20  
|||||

RESULT 2  
AAZ60854/c  
ID AAZ60854 standard; RNA; 20 BP.  
XX  
AC AAZ60854;  
XX  
XX  
DT 16-MAY-2000 (first entry)  
XX  
DE Oligonucleotide used to detect bcr b3-abl fusion transcripts.  
XX  
KW Fusion transcript; translocation; bcr b3 region; abl gene;  
KW amplification assay; detection assay; medical diagnosis;  
KW clinical monitoring; chimeric RNA; fusion RNA; condition marker;  
KW disease marker; cancer; leukemia; ss.  
XX  
OS Synthetic.  
XX  
XX WO200005418-A1.  
XX  
PD 03-FEB-2000.  
XX  
PF 23-JUL-1999; 99WO-US016832.  
XX  
PR 23-JUL-1998; 98US-00121239.  
XX  
PA (GENP-) GEN-PROBE INC.  
XX  
PI Harvey RC, Eastman PS;  
XX  
XX WPI; 2000-182730/16.  
XX  
XX Novel methods for preparing RNA from biological samples, used for the  
XX detection and measurement of nucleic acids and fusion nucleic acids.  
XX  
XX Claim 19; Page 42; 49pp; English.  
XX  
XX Oligonucleotides AAZ60840-62 and AAZ60865-66 are used in the method of  
XX the invention to detect fusion transcripts produced from a translocation  
XX between the bcr b3 region and the abl gene. The specification describes a  
XX method for detecting a fusion nucleic acid (particularly chimeric mRNA  
XX species), in a biological sample. The method comprises contacting a  
XX sample of fusion nucleic acid with primers, amplifying the hybridized  
XX fusion nucleic acid, and detecting the target hybrid. The method is used  
XX for the simple and rapid preparation of RNA from a biological sample,  
XX particularly from the cytoplasm of eukaryotic cells, which is suitable  
XX for use in an amplification and detection assay. The methods are used for  
XX the analysis and detection of nucleic acids in biological samples. The  
XX methods are useful in the human medical and veterinary fields, for  
XX medical diagnoses and clinical monitoring of a patient's response to  
XX therapy where a disease or medical condition is associated with a  
XX particular type and/or level of mRNA present in the sample. The methods  
XX are also useful for detecting or quantifying fusion or chimeric RNA

CC species, and for detecting a translocation as a marker for a given  
CC condition or disease, e.g. translocations associate with cancers,  
CC particularly forms of leukemia

XX Sequence 20 BP; 0 A; 9 C; 2 G; 0 T; 9 U; 0 Other;  
SQ

Query Match 100.0%; Score 20; DB 3; Length 20;  
Best Local Similarity 100.0%; Pred. No. 0.73;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAAAGGAGCAGGGAAGG 20  
Db 20 CAAAGGAGCAGGGAAGG 1  
|||||

RESULT 3  
AAZ60853/c  
ID AAZ60853 standard; DNA; 20 BP.  
XX  
XX AAZ60853;  
XX  
XX  
DT 16-MAY-2000 (first entry)  
XX  
DE Oligonucleotide used to detect bcr b3-abl fusion transcripts.  
XX  
KW Fusion transcript; translocation; bcr b3 region; abl gene;  
KW amplification assay; detection assay; medical diagnosis;  
KW clinical monitoring; chimeric RNA; fusion RNA; condition marker;  
KW disease marker; cancer; leukemia; ss.  
XX  
OS Synthetic.  
XX  
XX WO200005418-A1.  
XX  
PD 03-FEB-2000.  
XX  
PF 23-JUL-1999; 99WO-US016832.  
XX  
PR 23-JUL-1998; 98US-00121239.  
XX  
XX (GENP-) GEN-PROBE INC.  
XX  
PI Harvey RC, Eastman PS;  
XX  
XX WPI; 2000-182730/16.  
XX  
XX Novel methods for preparing RNA from biological samples, used for the  
XX detection and measurement of nucleic acids and fusion nucleic acids.  
XX  
XX Claim 19; Page 42; 49pp; English.  
XX  
XX Oligonucleotides AAZ60840-62 and AAZ60865-66 are used in the method of  
XX the invention to detect fusion transcripts produced from a translocation  
XX between the bcr b3 region and the abl gene. The specification describes a  
XX method for detecting a fusion nucleic acid (particularly chimeric mRNA  
XX species), in a biological sample. The method comprises contacting a  
XX sample of fusion nucleic acid with primers, amplifying the hybridized  
XX fusion nucleic acid, and detecting the target hybrid. The method is used  
XX for the simple and rapid preparation of RNA from a biological sample,  
XX particularly from the cytoplasm of eukaryotic cells, which is suitable  
XX for use in an amplification and detection assay. The methods are used for  
XX the analysis and detection of nucleic acids in biological samples. The  
XX methods are useful in the human medical and veterinary fields, for  
XX medical diagnoses and clinical monitoring of a patient's response to  
XX therapy where a disease or medical condition is associated with a  
XX particular type and/or level of mRNA present in the sample. The methods  
XX are also useful for detecting or quantifying fusion or chimeric RNA  
XX species, and for detecting a translocation as a marker for a given  
XX condition or disease, e.g. translocations associate with cancers,  
XX particularly forms of leukemia

XX Sequence 20 BP; 0 A; 9 C; 2 G; 9 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 3; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 0.73;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CAAGGAGCAGGGAAGAAGG 20  
 DB 20 CAAGGAGCAGGGAAGAAGG 1

RESULT 4  
 AAZ60864  
 ID AAZ60864 standard; DNA; 299 BP.  
 XX  
 AC AAZ60864;  
 XX  
 DT 16-MAY-2000 (first entry)  
 XX  
 DE Region surrounding a splice junction in a normal abl transcript.  
 XX  
 KW Fusion transcript; translocation; bcr b3 region; abl gene;  
 KW amplification assay; detection assay; medical diagnosis;  
 KW clinical monitoring; chimeric RNA; fusion RNA; condition marker;  
 KW disease marker; cancer; leukemia; ss.  
 XX  
 OS Unidentified.  
 XX  
 FN WO200005418-A1.  
 XX  
 PD 03-FEB-2000.  
 XX  
 PF 23-JUL-1999; 99WO-US016832.  
 XX  
 PR 23-JUL-1998; 98US-00121239.  
 XX  
 PA (GENP-) GEN-PROBE INC.  
 XX  
 PI Harvey RC, Eastman PS;  
 XX  
 DR WPI; 2000-182730/16.  
 XX  
 PT Novel methods for preparing RNA from biological samples, used for the  
 PT detection and measurement of nucleic acids and fusion nucleic acids.  
 XX  
 PS Disclosure; Fig 3; 49pp; English.  
 CC  
 CC The present sequence represents a region surrounding a potential splice  
 CC junction in a normal abl transcript. The specification describes  
 CC oligonucleotides which are used to detect fusion transcripts produced  
 CC from a translocation between the bcr b3 region and the abl gene. The  
 CC specification also describes a method for detecting a fusion nucleic acid  
 CC (particularly chimeric mRNA species), in a biological sample. The method  
 CC comprises contacting a sample of fusion nucleic acid with primers,  
 CC amplifying the hybridized fusion nucleic acid, and detecting the target  
 CC hybrid. The method is used for the simple and rapid preparation of RNA  
 CC from a biological sample, particularly from the cytoplasm of eukaryotic  
 CC cells, which is suitable for use in an amplification and detection assay.  
 CC The methods are used for the analysis and detection of nucleic acids in  
 CC biological samples. The methods are useful in the human medical and  
 CC veterinary fields, for medical diagnoses and clinical monitoring of a  
 CC patients response to therapy where a disease or medical condition is  
 CC associated with a particular type and/or level of mRNA present in the  
 CC sample. The methods are also useful for detecting or quantifying fusion  
 CC or chimeric RNA species, and for detecting a translocation as a marker  
 CC for a given condition or disease, e.g. translocations associate with  
 CC cancers, particularly forms of leukemia  
 XX  
 SQ Sequence 299 BP; 77 A; 70 C; 81 G; 71 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 20; DB 3; Length 299;  
 Best Local Similarity 100.0%; Pred. No. 0.67;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CAAGGAGCAGGGAAGAAGG 20

Db 84 CAAGGAGCAGGGAAGAAGG 103  
 RESULT 5  
 AAD08655  
 ID AAD08655 standard; cDNA; 530 BP.  
 XX  
 AC AAD08655;  
 XX  
 DT 04-SEP-2001 (first entry)  
 XX  
 DE Mouse cancer associated antigen OY-MC-10 cDNA.  
 XX  
 KW Mouse; OY-MC-10; cytostatic; gene therapy; vaccine; fibrosarcoma cancer;  
 KW cancer associated antigen; ss.  
 XX  
 OS Mus musculus.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 2..484  
 FT /\*tag= a  
 FT /product= "Mouse OY-MC-10 protein"  
 FT /note= "CDS does not include start codon"  
 FT /partial  
 XX  
 XX WO200140271-A2.  
 XX  
 PD 07-JUN-2001.  
 XX  
 PF 01-DEC-2000; 2000WO-US032750.  
 XX  
 PR 01-DEC-1999; 99US-0168353P.  
 PR 26-APR-2000; 2000US-00559013.  
 XX  
 PA (LUDW-) LUDWIG INST CANCER RES.  
 XX  
 PI Ono T, Nakayama E;  
 XX  
 DR WPI; 2001-397941/42.  
 DR P-PSDB; AAE04381.  
 XX  
 PT Isolated polypeptide, useful in treating disorders such as cancer, is  
 PT encoded by a nucleic acid (NA) Group 3 or 4 molecule.  
 XX  
 PS Claim 56; Page 117; 127pp; English.  
 CC  
 CC The invention relates to cancer associated antigens and their nucleic  
 CC acids which are expressed in methylcholanthrene-induced fibrosarcoma  
 CC cancer cells from mice. Cancer associated antigens and a pharmaceutical  
 CC composition containing nucleic acid molecules encoding cancer associated  
 CC antigens are used to treat a condition e.g. cancer. Cancer associated  
 CC antigens, the nucleotides encoding them, antibodies against them and the  
 CC pharmaceutical compositions comprising them are useful for diagnosing,  
 CC monitoring and treating the diseases characterised by the expression of  
 CC one or more cancer associated antigens, e.g. fibrosarcoma cancer, and for  
 CC research purposes. Cancer associated antigens DNA is also useful in gene  
 CC therapy. The present sequence is a cDNA encoding mouse cancer associated  
 CC antigen OY-MC-10  
 XX  
 SQ Sequence 530 BP; 138 A; 125 C; 169 G; 98 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 20; DB 5; Length 530;  
 Best Local Similarity 100.0%; Pred. No. 0.66;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CAAGGAGCAGGGAAGAAGG 20  
 DB 370 CAAGGAGCAGGGAAGAAGG 389  
 RESULT 6  
 ABX05481



DT 16-JAN-2003 (first entry)  
DE Human 5' and/or regulatory region of ABL1 DNA SEQ ID NO:2.  
XX  
XX Human; haematopoietic cell proliferation disorder; cytostatic;  
KW gene therapy; lymphocytic leukaemia; acute myelogenous leukaemia;  
KW cytosine methylation state; gene; ds.  
XX  
OS Homo sapiens.  
XX  
XX WO200277272-A2.  
XX  
XX 03-OCT-2002.  
PD  
XX  
XX 26-MAR-2002; 2002WO-EP003401.  
PF  
XX  
XX 26-MAR-2001; 2001US-0278333P.  
PR  
XX  
XX (EPIG-) EPIGENOMICS AG.  
XX  
XX Berlin K, Braun A, Distler J, Guetig D, Howe A, Mueller J;  
PI Olek A, Piepenbrock C, Adorjan P, Grabs G, Lesche R, Leu E;  
PI Lewin A, Lipscher E, Maier S, Model F, Mueller V, Otto T, Pelet C;  
PI Schwöpe I, Ziebarth H;  
XX  
XX WPI; 2003-018942/01.  
DR  
XX  
XX Detecting and differentiating between hematopoietic cell proliferative  
PT disorders, comprising a target nucleic acid with a reagent that  
PT distinguishes between methylated and non-methylated CpG dinucleotides.  
XX  
XX Claim 38; SEQ ID NO 2; 117pp; English.  
XX  
XX The present invention describes a method for detecting and  
CC differentiating between haematopoietic cell proliferative disorders  
CC associated with at least 1 gene and/or their regulatory regions in a  
CC subject. The method comprises contacting a target nucleic acid in a  
CC biological sample obtained from the subject with at least 1 reagent,  
CC which distinguishes between methylated and non-methylated CpG  
CC dinucleotides within the target nucleic acid. ABZ09861 to ABZ11118  
CC represent specifically claimed nucleotide sequences from the present  
CC invention. Oligonucleotides from the present invention can be used: for  
CC differentiating between healthy haematopoietic cells and proliferative  
CC disorder haematopoietic cells; for differentiating between acute  
CC lymphocytic leukaemia and acute myelogenous leukaemia; as probes for  
CC determining the cytosine methylation state and/or single nucleotide  
CC polymorphisms (SNPs) of haematopoietic cell proliferation disorder  
CC related sequences and their complements; and as primers for the  
CC amplification of haematopoietic cell proliferation disorder related DNA  
CC sequences. The nucleotide sequences from the present invention can also  
CC be used for detecting a predisposition to, differentiation between  
CC subclasses, diagnosis, prognosis, treatment and/or monitoring of  
CC haematopoietic cell proliferative disorders. The present method enables a  
CC highly specific classification of haematopoietic cell proliferative  
CC disorders allowing for improved and informed treatment of patients  
XX  
SQ Sequence 35962 BP; 9078 A; 7926 C; 9130 G; 9828 T; 0 U; 0 Other;  
Query Match 100.0%; Score 20; DB 7; Length 35962;  
Best Local Similarity 100.0%; Pred. No. 0.58;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CAAAGGAGCAGGAGAGAGG 20  
Db 29200 CAAAGGAGCAGGAGAGAGG 29219  
|||||  
RESULT 9  
ABL69622/c  
ID ABL69622 standard; DNA; 396 BP.  
XX  
XX ABL69622;  
AC  
XX

DT 15-MAY-2002 (first entry)  
DE Prostate cancer related gene sequence SEQ ID NO:7959.  
XX  
XX Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;  
KW stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;  
KW cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;  
KW gene; ds.  
XX  
OS Homo sapiens.  
XX  
XX WO200194629-A2.  
XX  
XX 13-DEC-2001.  
PD  
XX  
XX 30-MAY-2001; 2001WO-US010838.  
PF  
XX  
XX 05-JUN-2000; 2000US-0209473P.  
PR  
XX 05-JUN-2000; 2000US-0209531P.  
PR  
XX 18-SEP-2000; 2000US-0233133P.  
PR  
XX 18-SEP-2000; 2000US-0233617P.  
PR  
XX 20-SEP-2000; 2000US-0234009P.  
PR  
XX 20-SEP-2000; 2000US-0234034P.  
PR  
XX 20-SEP-2000; 2000US-0234052P.  
PR  
XX 22-SEP-2000; 2000US-0234509P.  
PR  
XX 22-SEP-2000; 2000US-0234567P.  
PR  
XX 25-SEP-2000; 2000US-0234923P.  
PR  
XX 25-SEP-2000; 2000US-0234924P.  
PR  
XX 25-SEP-2000; 2000US-0235077P.  
PR  
XX 25-SEP-2000; 2000US-0235082P.  
PR  
XX 25-SEP-2000; 2000US-0235134P.  
PR  
XX 25-SEP-2000; 2000US-0235280P.  
PR  
XX 26-SEP-2000; 2000US-0235637P.  
PR  
XX 26-SEP-2000; 2000US-0235638P.  
PR  
XX 27-SEP-2000; 2000US-0235711P.  
PR  
XX 27-SEP-2000; 2000US-0235720P.  
PR  
XX 27-SEP-2000; 2000US-0235840P.  
PR  
XX 28-SEP-2000; 2000US-0235863P.  
PR  
XX 28-SEP-2000; 2000US-0236028P.  
PR  
XX 28-SEP-2000; 2000US-0236032P.  
PR  
XX 28-SEP-2000; 2000US-0236033P.  
PR  
XX 28-SEP-2000; 2000US-0236034P.  
PR  
XX 28-SEP-2000; 2000US-0236109P.  
PR  
XX 28-SEP-2000; 2000US-0236111P.  
PR  
XX 29-SEP-2000; 2000US-0236842P.  
PR  
XX 29-SEP-2000; 2000US-0236891P.  
PR  
XX 02-OCT-2000; 2000US-0237172P.  
PR  
XX 02-OCT-2000; 2000US-0237173P.  
PR  
XX 02-OCT-2000; 2000US-0237278P.  
PR  
XX 02-OCT-2000; 2000US-0237294P.  
PR  
XX 02-OCT-2000; 2000US-0237295P.  
PR  
XX 03-OCT-2000; 2000US-0237316P.  
PR  
XX 03-OCT-2000; 2000US-0237425P.  
PR  
XX 03-OCT-2000; 2000US-0237598P.  
PR  
XX 03-OCT-2000; 2000US-0237604P.  
PR  
XX 03-OCT-2000; 2000US-0237606P.  
PR  
XX 03-OCT-2000; 2000US-0237608P.  
PR  
XX 01-NOV-2000; 2000US-0244867P.  
PR  
XX 01-NOV-2000; 2000US-0245084P.  
XX  
XX (AVAL-) AVALON PHARM.  
XX  
XX Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;  
PI Soppet DR, Weaver Z;  
XX  
XX WPI; 2002-188264/24.  
DR  
XX  
XX Screening for anti-neoplastic agent involves exposing cells to a chemical  
PT agent to be tested for anti-neoplastic activity, and determining a change  
PT in expression of a gene of a signature gene set.  
XX  
XX Claim 1; SEQ ID NO 7959; 44pp; English.  
XX

CC The present invention describes a method (M1) for screening for an anti-neoplastic agent. The method involves exposing cells to a chemical agent CC to be tested for anti-neoplastic activity, determining a change in CC expression of at least one gene (I) of a signature gene set, where (I) CC comprises a sequence (S) selected from 8447 sequences (given in ABL1664 CC to ABL70110), or is at least 95% identical to (S), where a change in CC expression is indicative of anti-neoplastic activity. (I) has cytostatic CC activity and can be used in gene therapy. M1 can be used for screening an CC anti-neoplastic agent, and can be used for producing a product which is CC the data collected with respect to the anti-neoplastic agent as a result CC of M1, and the data is sufficient to convey the chemical structure and/or CC properties of the agent. M1 can be used in the treatment of cancer such CC as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney, CC prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell CC cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous CC cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilm's CC tumour CC

SQ Sequence 396 BP; 82 A; 129 C; 85 G; 100 T; 0 U; 0 Other;

Query Match 90.0%; Score 18; DB 6; Length 396;  
Best Local Similarity 100.0%; Pred. No. 6.7;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAAAGGAGCAGGAGAGAA 18  
Db 181 CAAAGGAGCAGGAGAGAA 164

RESULT 10  
ACH32870  
ID ACH32870 standard; cDNA; 474 BP.

AC ACH32870;  
XX  
XX  
DT 13-OCT-2003 (first entry)  
DE Human endothelial cell cDNA #1003.

KW Human; ss; sequencing by hybridisation; SBH; expressed sequence tag; EST;  
KW Genome mapping; biodiversity; genetic disorder.

OS Homo sapiens.

PN US2003073623-A1.

XX 17-APR-2003.

PF 30-JUL-2001; 2001US-00918995.

XX 30-JUL-2001; 2001US-00918995.

PA (DRMA/) DRMANAC R T.

PA (LABA/) LABAT I.

PA (STAC/) STACHE-CRAIN B.

PA (DICK/) DICKSON M C.

PA (JONE/) JONES L W.

XX Drmanac RT, Labat I, Stache-Crain B, Dickson MC, Jones LW;

XX WPI; 2003-615964/59.

XX New polynucleotide sequences obtained from various cDNA libraries, useful  
PT as hybridization probes, as oligomers for PCR, for chromosome and gene  
PT mapping, in the recombinant production of protein, or in generating  
PT antisense DNA or RNA.

PS Claim 1; SEQ ID NO 20082; 44pp; English.

XX The invention relates to an isolated polynucleotide comprising any one of  
CC 38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence was  
CC determined by the technique of SBH (sequencing by hybridisation). Also  
CC included is a purified polypeptide comprising a sequence corresponding to

CC a reading frame of the novel polynucleotide. The nucleic acid sequences  
CC are useful in diagnostics as expressed sequence tags (EST) for  
CC identifying expressed genes or for physical mapping of the human genome,  
CC in forensics, in assessing biodiversity, or in identifying mutations  
CC responsible for genetic disorders and other traits. The nucleotide  
CC sequences are also useful as hybridisation probes, as oligomers for PCR,  
CC for chromosome and gene mapping, in the recombinant production of  
CC protein, or in generating antisense DNA or RNA. The purified polypeptide  
CC is useful for generating antibodies specific for it. The present sequence  
CC is one of the 38043 isolated cDNA/EST sequences. Note: The sequence data  
CC for this patent did not form part of the printed specification, but was  
CC obtained in electronic format directly from USPTO at  
CC seqdata.uspto.gov/sequence.html?DocID=20030073623

SQ Sequence 474 BP; 118 A; 117 C; 145 G; 92 T; 0 U; 2 Other;

Query Match 90.0%; Score 18; DB 8; Length 474;  
Best Local Similarity 100.0%; Pred. No. 6.7;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAAAGGAGCAGGAGAGAA 18  
Db 331 CAAAGGAGCAGGAGAGAA 348

RESULT 11  
AAT19863  
ID AAT19863 standard; cDNA to mRNA; 543 BP.

XX AAT19863;

DT 26-JUL-1996 (first entry)

XX Human gene signature HUMGS00986.

KW Gene signature; messenger RNA; mRNA; relative abundance; frequency;  
KW human; cloning; mapping; non-biased library; diagnosis; detection;  
KW cell typing; abnormal cell function; ss.

OS Homo sapiens.

PN WO9514772-A1.

XX 01-JUN-1995.

PF 11-NOV-1994; 94WO-JP001916.

XX 12-NOV-1993; 93JP-00355504.

PA (MATS/) MATSUBARA K.

PA (OKUB/) OKUBO K.

XX Matsubara K, Okubo K;

XX WPI; 1995-206931/27.

PT Single-stranded DNA for identifying gene signatures - isolated from 3'-  
PT directed human cDNA library that reflects relative abundance of corresp.  
PT mRNA in specific human tissues.

PS Claim 1; Page 489; 2245pp; Japanese.

XX A single-stranded DNA (or its complementary strand or the corresp. double  
CC -stranded DNA) which comprises one of the 7837 "GS" sequences given in  
CC AAT19001-T36837 and which is able to hybridise to part of human genomic  
CC DNA, cDNA or mRNA is claimed. The GS (Gene Signature) sequences were  
CC obtained from 3'-directed cDNA libraries prepared from various human  
CC tissues; synthesis of cDNA was initiated from the 3'-end of mRNA by using  
CC poly(T) as the sole primer. Since the 3'- untranslated sequence is unique  
CC to a particular mRNA species, almost all the 3'-oriented cDNAs hybridise  
CC with specific mRNAs. Each library is constructed so as to reflect  
CC accurately the relative abundance of different mRNAs in the particular  
CC tissue from which it was derived. The appearance frequency of a given GS

CC in a cDNA library can be determined (esp. using primers and probes  
 CC derived from the GS sequences) as a means of diagnosing abnormal cell  
 CC function or for recognising different cell types

XX  
 SQ Sequence 543 BP; 119 A; 115 C; 153 G; 142 T; 0 U; 14 Other;

Query Match 90.0%; Score 18; DB 2; Length 543;  
 Best Local Similarity 100.0%; Pred. No. 6.6;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAAAGGAGCAGGGAAGAA 18

DB 354 CAAAGGAGCAGGGAAGAA 371

RESULT 12

ABA94712

ID ABA94712 standard; cDNA; 1345 BP.

XX ABA94712;

XX 23-APR-2002 (first entry)

XX Human aminoacyl tRNA synthetase (ATRS) encoding cDNA (ID: 1554103CB1).

XX Aminoacyl tRNA synthetase; ATRS; anti-allergic; antianemic; antiasthmatic;  
 KW osteopathic; antirheumatic; antiarthritic; dermatological; nephrotropic;  
 KW antiinflammatory; vulnery; antibacterial; viricide; antiparasitic;  
 KW protozoacide; fungicide; antihelminthic; cytostatic; human; enzyme;  
 KW antiarteriosclerotic; hepatotropic; gene therapy; vaccine; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

FT CDS 1..1269

FT /\*tag= a

FT /product= "ATRS"

XX WO200204611-A2.

XX 17-JAN-2002.

XX 29-JUN-2001; 2001WO-US020723.

XX 07-JUL-2000; 2000US-0216748P.

XX 18-JUL-2000; 2000US-0219019P.

XX 04-AUG-2000; 2000US-023058P.

XX 21-SEP-2000; 2000US-0234693P.

XX 11-OCT-2000; 2000US-0239797P.

XX (INCY-) INCYTE GENOMICS INC.

XX Lee EA, Tang YT, Lu DAM, Tribouley CM, Gandhi AR, Lu Y;

PI Baughn MR, Warren BA, Thornton M, Yue H, Hillman JL, Patterson C;

PI Elliott VS, Thangavelu K, Ramkumar J, Wallia NK, Yao MG;

XX WPI; 2002-164640/21.

XX P-PSDB; ABB07509.

XX Novel human aminoacyl tRNA synthetases and polynucleotides encoding the  
 PT enzymes, useful for treating, diagnosing or preventing  
 PT autoimmune/inflammatory and cell proliferative disorders.

XX Claim 5; Page 105; 107pp; English.

XX The invention provides human aminoacyl tRNA synthetase (ATRS)  
 CC polypeptides and polynucleotides. The ATRS polypeptides can be expressed  
 CC by standard recombinant methodology. Compositions comprising the  
 CC polypeptide or its modulators are useful for treating a disease or  
 CC condition associated with decreased or increased expression of functional  
 CC ATRS. Compositions comprising antibodies specific for ATRS is useful for  
 CC diagnosing a condition or disease associated with the expression of ATRS  
 CC in a subject. The ATRS polypeptides and polynucleotides are useful for

CC diagnosing, treating and preventing autoimmune/inflammatory (allergies,  
 CC anemia, asthma, osteoporosis, rheumatoid arthritis, atopic dermatitis,  
 CC glomerulonephritis and irritable bowel syndrome, trauma, and bacterial,  
 CC viral, parasitic, protozoal, fungal or helminthic infections), and cell  
 CC proliferative (e.g. cancer, atherosclerosis, and hepatitis). The ATRS  
 CC polypeptides are useful in drug screening techniques, and to analyse the  
 CC proteome of a tissue or cell type. The present sequence represents a  
 XX human ATRS polynucleotide sequence

SQ Sequence 1345 BP; 349 A; 300 C; 410 G; 286 T; 0 U; 0 Other;

Query Match 90.0%; Score 18; DB 6; Length 1345;

Best Local Similarity 100.0%; Pred. No. 6.4;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAAAGGAGCAGGGAAGAA 18

DB 1155 CAAAGGAGCAGGGAAGAA 1172

RESULT 13

AAS41347

ID AAS41347 standard; cDNA; 1390 BP.

XX AAS41347;

XX 17-DEC-2001 (first entry)

XX cDNA encoding novel human enzyme polypeptide #563.

XX Human; oxidoreductase enzyme; transferase; hydrolase; lyase; isomerase;  
 KW ligase; hyperproliferative disorder; immunodeficiency disorder;  
 KW autoimmune disorder; neurological disorder; metabolic disorder;  
 KW inflammatory disorder; cardiovascular disorder; reproductive disorder;  
 KW blood-related disorder; infectious disorder; gene therapy; cytostatic;  
 KW anti arthritic; nephrotropic; anticoagulant; ss.

XX Homo sapiens.

XX WO200155301-A2.

XX 02-AUG-2001.

XX 17-JAN-2001; 2001WO-US001239.

XX 31-JAN-2000; 2000US-0179065P.

XX 04-FEB-2000; 2000US-0180628P.

XX 24-FEB-2000; 2000US-0184664P.

XX 02-MAR-2000; 2000US-0186350P.

XX 16-MAR-2000; 2000US-0189874P.

XX 17-MAR-2000; 2000US-0190076P.

XX 18-APR-2000; 2000US-0198123P.

XX 19-MAY-2000; 2000US-0205515P.

XX 07-JUN-2000; 2000US-0209467P.

XX 28-JUN-2000; 2000US-0214886P.

XX 30-JUN-2000; 2000US-0215135P.

XX 07-JUL-2000; 2000US-0216647P.

XX 07-JUL-2000; 2000US-0216880P.

XX 11-JUL-2000; 2000US-0217487P.

XX 11-JUL-2000; 2000US-0217496P.

XX 14-JUL-2000; 2000US-0218290P.

XX 26-JUL-2000; 2000US-0220963P.

XX 26-JUL-2000; 2000US-0220964P.

XX 14-AUG-2000; 2000US-0224518P.

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XX 14-AUG-2000; 2000US-0225214P.

XX 14-AUG-2000; 2000US-0225266P.

XX 14-AUG-2000; 2000US-0225267P.

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XX 14-AUG-2000; 2000US-0225270P.

XX 14-AUG-2000; 2000US-0225447P.

XX 14-AUG-2000; 2000US-0225757P.

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 PR 05-JAN-2001; 2001US-0259678P.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 PI Rosen CA, Barash SC, Ruben SM;  
 XX  
 PI WPI; 2001-465566/50.  
 XX P-PSDB; AAU23477.  
 DR  
 XX  
 PT Novel polypeptides and polynucleotides useful for diagnosing, preventing,  
 PT treating neural, immune system, muscular, reproductive, pulmonary,  
 PT cardiovascular, renal, proliferative disorders and cancerous diseases.  
 XX  
 PS Claim 4; SEQ ID NO 573; 1180pp; English.  
 XX  
 CC The present invention relates to the isolation of novel human enzyme  
 CC polypeptides (AAU22915-AAU23814), and the cDNA and genomic sequences  
 CC encoding them. The enzyme polypeptides of the invention may comprise the  
 CC functional classes of oxidoreductases, transferases, hydrolases, lyases,  
 CC isomerases or ligases. The sequences of the invention are useful in the  
 CC diagnosis, treatment, prevention and/or prognosis of a wide range of  
 CC disorders including hyperproliferative disorders (e.g. cancer),  
 CC immunodeficiency disorders (e.g. AIDS) autoimmune disorders (e.g.  
 CC arthritis), neurological disorders (e.g. Alzheimer's disease), metabolic  
 CC disorders (e.g. phenylketonuria), inflammatory disorders (e.g. asthma),  
 CC cardiovascular disorders (e.g. atherosclerosis), blood-related disorders  
 CC (e.g. haemophilia), reproductive disorders (e.g. infertility) and  
 CC infectious disorders (e.g. Influenza). The polynucleotides of the  
 CC invention can also be used in gene therapy. AAU20785-AAU241684 represent  
 CC cDNA sequences encoding for the novel human enzyme polypeptides of the  
 CC invention. Note: The sequence data for this patent did not form part of  
 CC the printed specification, but was obtained in electronic format directly  
 CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 1390 BP; 364 A; 312 C; 427 G; 285 T; 0 U; 2 Other;  
 Query Match 90.0%; Score 18; DB 4; Length 1390;  
 Best Local Similarity 100.0%; Pred. No. 6.4;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;





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 PR 05-JAN-2001; 2001US-0259678P.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 PI Rosen CA, Barash SC, Ruben SM;  
 XX  
 DR WPI; 2001-465570/50.  
 XX  
 PT Isolated nucleic acid molecule encoding a reproductive system antigen is  
 used in preventing, treating or ameliorating a medical condition.  
 XX  
 PS Disclosure; SEQ ID NO 9320; 1297pp + Sequence Listing; English.  
 XX  
 CC The present invention provides the protein and coding sequences of a  
 number of human reproductive system related antigens. These can be used  
 in the prevention and treatment of reproductive system disorders,  
 CC including cancer. The present sequence is a genomic sequence encoding a  
 protein of the invention  
 XX  
 SQ Sequence 1611 BP; 491 A; 377 C; 391 G; 352 T; 0 U; 0 Other;  
 Query Match 90.0%; Score 18; DB 4; Length 1611;  
 Best Local Similarity 100.0%; Pred. No. 6.4;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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 Db 183 CAAAGGAGCAGGGAAGAA 166  
 RESULT 15  
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 ID AAS40715 standard; DNA; 1611 BP.  
 XX  
 AC AAS40715;  
 XX  
 DT 17-DEC-2001 (first entry)  
 XX  
 DE DNA encoding human prostate cancer antigen, Seq ID No 867.  
 XX  
 KW Human; prostate cancer antigen; cytostatic; uropathic; diagnostic;  
 KW reproductive system; chromosomal marker; forensic; urinary disorder;  
 KW chronic nephritis; blood-related disorder; thrombosis; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO20015316-A2.  
 XX  
 PD 02-AUG-2001.  
 XX  
 PF 17-JAN-2001; 2001WO-US001328.  
 XX  
 PR 31-JAN-2000; 2000US-0179065P.  
 PR 04-FEB-2000; 2000US-0180628P.  
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 PR 02-MAR-2000; 2000US-0186350P.  
 PR 16-MAR-2000; 2000US-0189874P.  
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PR 17-MAR-2000; 2000US-0190076P.  
 PR 18-APR-2000; 2000US-0198123P.  
 PR 19-MAY-2000; 2000US-0205515P.  
 PR 07-JUN-2000; 2000US-0209467P.  
 PR 28-JUN-2000; 2000US-0214886P.  
 PR 30-JUN-2000; 2000US-0215135P.  
 PR 07-JUL-2000; 2000US-0216647P.  
 PR 07-JUL-2000; 2000US-0216880P.  
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 PR 05-JAN-2001; 2001US-0259678P.  
 (HUMA-) HUMAN GENOME SCI INC.

PI Rosen CA, Barash SC, Ruben SM;  
 WPI; 2001-451929/48.

PT Isolated polypeptide for treating, preventing and/ or prognosing  
 PT disorders related to the reproductive system including prostate cancer  
 PT and also for testing and detection e.g. diagnosis.  
 XX  
 PS Disclosure; SEQ ID NO 867; 546pp; English.  
 XX  
 CC The invention relates to novel isolated human prostate cancer antigen  
 CC polynucleotides (I) and polypeptides (II). (I) and (II) are useful for

CC preventing, treating or ameliorating a medical condition when  
 CC administered. (I), (II) and the antibody to (II) are useful for treating,  
 CC preventing and/ or prognosing disorders related to the reproductive  
 CC system including prostate cancers; urinary disorders e.g. chronic  
 CC nephritis; and blood-related disorders e.g. thrombosis. (II) can be used  
 CC for testing and detection e.g. as a chromosomal marker and in forensics.  
 CC (I) and the anti-(II) antibody can be used in testing and detection in  
 CC immunoassays. AAS40061-AAS40775 represent the human prostate cancer  
 CC antigen coding sequences, and related PCR primers and sequences of the  
 CC invention. Note: The sequence data for this patent did not form part of  
 CC the printed specification, but was obtained in electronic format directly  
 CC from WIPO at: ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 1611 BP; 491 A; 377 C; 391 G; 352 T; 0 U; 0 Other;  
 Query Match 90.0%; Score 18; DB 5; Length 1611;  
 Best Local Similarity 100.0%; Pred. No. 6.4;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 183 CAAGGAGCAGGGAAGAA 166

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Title: US-09-121-239-13

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Searched: 682709 seqs, 277475446 residues

Word size : 0

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Minimum DB seq length: 0

Maximum DB seq length: 2000000000

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 2	16	80.0	16998	4	US-09-676-610B-24
C 3	16	80.0	197496	4	US-09-877-177A-10
4	15	75.0	533	4	US-09-621-976-159
5	15	75.0	9217	4	US-09-634-238-402
6	14	70.0	303	4	US-09-313-294A-6758
C 7	14	70.0	418	2	US-08-691-814B-105
C 8	14	70.0	440	4	US-09-621-976-14605
9	14	70.0	673	3	US-09-040-984-33
10	14	70.0	673	4	US-09-123-912-33
11	14	70.0	673	4	US-09-643-597-33
12	14	70.0	673	4	US-09-480-884A-33
13	14	70.0	673	4	US-09-542-615A-33
14	14	70.0	673	4	US-09-606-421B-33
15	14	70.0	673	4	US-09-221-107-33
C 16	14	70.0	1350	4	US-09-149-476-248
C 17	14	70.0	1503	4	US-09-254-465A-5
C 18	14	70.0	1521	2	US-09-004-502-2
C 19	14	70.0	1521	3	US-09-360-125-2
C 20	14	70.0	1590	4	US-09-369-247-14
C 21	14	70.0	1744	4	US-09-484-970B-83
C 22	14	70.0	2181	4	US-09-254-465A-7
C 23	14	70.0	2181	4	US-09-254-465A-11
24	14	70.0	41100	4	US-09-755-665-46
25	14	70.0	62804	4	US-09-800-960-3
26	14	70.0	62804	4	US-10-096-960-3
C 27	13	65.0	249	4	US-09-107-532A-2549

28	13	65.0	287	4	US-09-313-294A-1166	Sequence 1166, Ap
C 29	13	65.0	302	4	US-09-313-294A-1121	Sequence 1121, Ap
C 30	13	65.0	333	4	US-09-621-976-16174	Sequence 16174, A
C 31	13	65.0	352	4	US-09-621-976-1644	Sequence 1644, Ap
C 32	13	65.0	387	4	US-09-489-039A-6598	Sequence 6598, Ap
C 33	13	65.0	400	4	US-09-621-976-16175	Sequence 16175, A
C 34	13	65.0	404	4	US-09-539-333D-202	Sequence 202, App
C 35	13	65.0	418	4	US-09-621-976-16177	Sequence 16177, A
C 36	13	65.0	438	4	US-09-621-976-1841	Sequence 1841, Ap
C 37	13	65.0	447	4	US-09-621-976-8713	Sequence 8713, Ap
C 38	13	65.0	462	4	US-09-104-308-3	Sequence 15146, A
C 39	13	65.0	463	3	US-09-321-981-3	Sequence 3, Appli
C 40	13	65.0	463	3	US-09-739-861A-3	Sequence 3, Appli
C 41	13	65.0	463	4	US-09-795-583-3	Sequence 3, Appli
C 42	13	65.0	511	4	US-09-404-879A-70	Sequence 70, Appl
C 43	13	65.0	511	4	US-09-338-933-70	Sequence 70, Appl
C 44	13	65.0	511	4	US-09-215-681-70	Sequence 70, Appl
C 45	13	65.0	511	4	US-09-215-681-70	Sequence 70, Appl

ALIGNMENTS

RESULT 1  
US-09-620-312D-704  
; Sequence 704, Application US/09620312D  
; Patent No. 6569662  
; GENERAL INFORMATION:  
; APPLICANT: Tang, Y. Tom  
; APPLICANT: Liu, Chenghua  
; APPLICANT: Asundi, Vinod  
; APPLICANT: Zhang, Jie  
; APPLICANT: Ren, Feiyan  
; APPLICANT: Chen, Rui-hong  
; APPLICANT: Zhao, Qing A.  
; APPLICANT: Wehrman, Tom  
; APPLICANT: Xue, Aidong J.  
; APPLICANT: Yang, Yonghong  
; APPLICANT: Wang, Jian-Rui  
; APPLICANT: Zhou, Ping  
; APPLICANT: Ma, Yunqing  
; APPLICANT: Wang, Dunrui  
; APPLICANT: Wang, Zhiwei  
; APPLICANT: John Tillinghast  
; APPLICANT: Drmanac, Radoje T.  
; TITLE OF INVENTION: No. 6569662el Nucleic Acids and  
; FILE REFERENCE: 784CIP2B  
; CURRENT APPLICATION NUMBER: US/09/620,312D  
; CURRENT FILING DATE: 2000-07-19  
; PRIOR APPLICATION NUMBER: 09/552,317  
; PRIOR FILING DATE: 2000-04-25  
; PRIOR APPLICATION NUMBER: 09/488,725  
; PRIOR FILING DATE: 2000-01-21  
; NUMBER OF SEQ ID NOS: 1105  
; SOFTWARE: pc FL genes Version 1.0  
; SEQ ID NO 704  
; LENGTH: 1869  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (161)..(1792)  
US-09-620-312D-704

Query Match 90.0%; Score 18; DB 4; Length 1869;  
Best Local Similarity 100.0%; Pred.No. 0.4;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CAAGGACGAGGAGAGAA 18  
DB 1678 CAAGGACGAGGAGAGAA 1695

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RESULT 2
US-09-676-610B-24/c
; Sequence 24, Application US/09676610B
; Patent No. 644465
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Jacqueline Wyatt
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: OLIGONUCLEOTIDE INHIBITION OF HER-1 EXPRESSION
; FILE REFERENCE: RTS-0138
; CURRENT APPLICATION NUMBER: US/09/676,610B
; CURRENT FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 182
; SEQ ID NO 24
; LENGTH: 169998
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: exon
; LOCATION: (1208)...(1472)
; NAME/KEY: intron
; LOCATION: (1473)...(124390)
; NAME/KEY: exon
; LOCATION: (124391)...(124544)
; NAME/KEY: intron
; LOCATION: (124545)...(125409)
; NAME/KEY: exon
; LOCATION: (125410)...(125595)
; NAME/KEY: intron
; LOCATION: (125596)...(128711)
; NAME/KEY: exon
; LOCATION: (128712)...(128848)
; NAME/KEY: intron
; LOCATION: (128849)...(133400)
; NAME/KEY: exon
; LOCATION: (133401)...(133469)
; NAME/KEY: intron
; LOCATION: (133470)...(134652)
; NAME/KEY: exon
; LOCATION: (134653)...(134773)
; NAME/KEY: intron
; LOCATION: (134774)...(136116)
; NAME/KEY: exon
; LOCATION: (136117)...(136261)
; NAME/KEY: intron
; LOCATION: (136262)...(137936)
; NAME/KEY: exon
; LOCATION: (137937)...(138053)
; NAME/KEY: intron
; LOCATION: (138054)...(138637)
; NAME/KEY: exon
; LOCATION: (138638)...(138766)
; NAME/KEY: intron
; LOCATION: (138767)...(138864)
; NAME/KEY: exon
; LOCATION: (138865)...(138940)
; NAME/KEY: intron
; LOCATION: (138941)...(139765)
; NAME/KEY: exon
; LOCATION: (139766)...(139860)
; NAME/KEY: intron
; LOCATION: (139861)...(142245)
; NAME/KEY: exon
; LOCATION: (142246)...(142445)
; NAME/KEY: intron
; LOCATION: (142446)...(143605)
; NAME/KEY: exon
; LOCATION: (143606)...(143738)
; NAME/KEY: intron
; LOCATION: (143739)...(145838)
; NAME/KEY: exon
; LOCATION: (145839)...(145931)

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; NAME/KEY: intron
; LOCATION: (145932)...(147385)
; NAME/KEY: exon
; LOCATION: (147386)...(147544)
; NAME/KEY: intron
; LOCATION: (147545)...(153274)
; NAME/KEY: exon
; LOCATION: (153275)...(153321)
; NAME/KEY: intron
; LOCATION: (153322)...(155088)
; NAME/KEY: exon
; LOCATION: (155089)...(155231)
; NAME/KEY: intron
; LOCATION: (155232)...(156025)
; NAME/KEY: exon
; LOCATION: (156026)...(156151)
; NAME/KEY: intron
; LOCATION: (156152)...(156826)
; NAME/KEY: exon
; LOCATION: (156827)...(156928)
; NAME/KEY: intron
; LOCATION: (156929)...(163399)
; NAME/KEY: exon
; LOCATION: (163400)...(163586)
; US-09-676-610B-24
Query Match      80.0%; Score 16; DB 4; Length 169998;
Best Local Similarity 100.0%; Pred. No. 5.1;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 AAGGAGCAGGGAAGAA 18
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Db      89323 AAGGAGCAGGGAAGAA 89308

RESULT 3
US-09-877-177A-10/c
; Sequence 10, Application US/09877177A
; Patent No. 6582919
; GENERAL INFORMATION:
; APPLICANT: K. Danenberg
; TITLE OF INVENTION: Method of determining Epidermal Growth
; TITLE OF INVENTION: Factor Receptor and HER2-Neu Gene Expression
; TITLE OF INVENTION: and Correlation of Levels Thereof With Survival
; FILE REFERENCE: 11220/120
; CURRENT APPLICATION NUMBER: US/09/877,177A
; CURRENT FILING DATE: 2001-06-11
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 197496
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-877-177A-10
Query Match      80.0%; Score 16; DB 4; Length 197496;
Best Local Similarity 100.0%; Pred. No. 5.1;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 AAGGAGCAGGGAAGAA 18
      |||||
Db      97323 AAGGAGCAGGGAAGAA 97308

RESULT 4
US-09-621-976-159
; Sequence 159, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.

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; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 159
; LENGTH: 533
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: CDS
; LOCATION: 55..531
; NAME/KEY: sig_peptide
; LOCATION: 55..378
; OTHER INFORMATION: Von Heijne matrix
; OTHER INFORMATION: score 5.5
; OTHER INFORMATION: seq RFECLSLSPGVRG/LK
US-09-621-976-159

Query Match      75.0%; Score 15; DB 4; Length 533;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 GCAGCAGGGAAG 19
DB      203 GCAGCAGGGAAG 217

RESULT 5
US-09-634-238-402
; Sequence 402, Application US/09634238
; Patent No. 6544772
; GENERAL INFORMATION:
; APPLICANT: Glenn, Matthew
; APPLICANT: Havukkala, Ilkka J.
; APPLICANT: Bloksberg, Leonard, N.
; APPLICANT: Lubbers, Mark W.
; APPLICANT: Dekker, James
; APPLICANT: Christensson, Anna C.
; APPLICANT: Holland, Ross
; APPLICANT: O'Toole, Paul W.
; APPLICANT: Reid, Julian R.
; APPLICANT: Coolbear, Timothy
; TITLE OF INVENTION: Polynucleotides, materials incorporating
; TITLE OF INVENTION: them and methods for using them.
; FILE REFERENCE: 11000.1043U1
; CURRENT APPLICATION NUMBER: US/09/634,238
; CURRENT FILING DATE: 2000-08-08
; NUMBER OF SEQ ID NOS: 422
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 402
; LENGTH: 9217
; TYPE: DNA
; ORGANISM: Lactobacillus rhamnosus
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(9217)
; OTHER INFORMATION: n = A,T,C or G
US-09-634-238-402

Query Match      75.0%; Score 15; DB 4; Length 9217;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 AAAGGAGCAGGAAG 16
DB      166 AAAGGAGCAGGAAG 180

RESULT 6
US-09-313-294A-6758
; Sequence 6758, Application US/09313294A
; Patent No. 6476212
```

```
; GENERAL INFORMATION:
; APPLICANT: Lalgudi, Raghunath V.
; APPLICANT: Ito, Laura Y.
; APPLICANT: Sherman, Bradley K.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
; FILE REFERENCE: PL-0017 US
; CURRENT APPLICATION NUMBER: US/09/313,294A
; CURRENT FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 7600
; SOFTWARE: PERL Program
; SEQ ID NO 6758
; LENGTH: 303
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6476212 700352349H1
; NAME/KEY: unsure
; LOCATION: 164-165, 169, 179, 189-190, 200, 206, 209, 221, 262
; OTHER INFORMATION: a, t, c, g, or other
US-09-313-294A-6758

Query Match      70.0%; Score 14; DB 4; Length 303;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 AGCAGGGAAGG 20
DB      103 AGCAGGGAAGG 116

RESULT 7
US-08-691-814B-105/c
; Sequence 105, Application US/08691814B
; Patent No. 5981218
; GENERAL INFORMATION:
; APPLICANT: Rio, Marie-Christine
; APPLICANT: Tomasetto, Catherine
; APPLICANT: Basset, Paul
; APPLICANT: Byrne, Jennifer
; TITLE OF INVENTION: Isolated Nucleic Acid Molecules Useful
; TITLE OF INVENTION: as Leukemia Markers and in Breast Cancer Prognosis
; NUMBER OF SEQUENCES: 124
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
; STREET: 1100 New York Ave, NW, Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/691,814B
; FILING DATE: 31-JUL-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/002,183
; FILING DATE: 09-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Steffe, Eric K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1383.0090001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2543
; INFORMATION FOR SEQ ID NO: 105:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 418 base pairs
; TYPE: nucleic acid
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; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: CDNA
US-08-691-814B-105

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Query Match 70.0%; Score 14; DB 2; Length 418;  
Best Local Similarity 100.0%; Pred. No. 51;  
Matches 14; Conservative 0; Mismatches 0; Gaps 0;

QY 7 AGCAGGGAAGAAGG 20  
          |||||  
Db 361 AGCAGGGAAGAAGG 348

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RESULT 8
US-09-621-976-14605/c
; Sequence 14605, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621.976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 14605
; LENGTH: 440
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-621-976-14605

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Query Match 70.0%; Score 14; DB 4; Length 440;  
Best Local Similarity 100.0%; Pred. No. 51;  
Matches 14; Conservative 0; Mismatches 0; Indels

Qy 3 AAGAGCAGGGAAG 16  
Db 314 AAGAGCAGGGAAG 301

RESULT 9  
 US-09-040-984-33  
 ; Sequence 33, Application US/09040984  
 ; Patent No. 6210883  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Reed, Steven G.  
 ; APPLICANT: Wang, Tongtong  
 ; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS  
 ; TITLE OF INVENTION: OF LUNG CANCER  
 ; NUMBER OF SEQUENCES: 86  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: SEED AND BERRY LLP  
 ; STREET: 6300 Columbia Center, 701 Fifth Avenue  
 ; CITY: Seattle  
 ; STATE: WA  
 ; COUNTRY: USA  
 ; ZIP: 98104  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Diskette  
 ; COMPUTER: IBM Compatible  
 ; OPERATING SYSTEM: DOS  
 ; SOFTWARE: FASCSEQ for Windows Version 2.0  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/040,984  
 ; FILING DATE: 18-MAR-1998  
 ; CLASSIFICATION:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Makl, David J.  
 ; REGISTRATION NUMBER: 31,392  
 ; REFERENCE/DOCKET NUMBER: 210121.456

TELECOMMUNICATION INFORMATION:  
TELEPHONE: 206-622-4900  
TELEFAX: 206-282-6031  
TELEX:

Query Match 70.0%; Score 14; DB 3; Length 673;  
Best Local Similarity 100.0%; Pred.No. 51;  
Matches 14; Conservative 0; Mismatches 0; Indels

Qy 2 AAAGGAGCAGGGAA 15  
Db 129 AAAGGAGCAGGGAA 142

RESULT 10  
US-09-123-912-33  
; Sequence 33, Application US/09123912A  
; Patent No. 6312695  
; GENERAL INFORMATION:  
; APPLICANT: Reed, Steven G.  
; APPLICANT: Wang, Tongcong  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY OF LUNG CANCER  
; FILE REFERENCE: 210121.455C1  
; CURRENT APPLICATION NUMBER: US/09/123,912A  
; CURRENT FILING DATE: 1998-07-27  
; PRIOR APPLICATION NUMBER: 09/040,802  
; PRIOR FILING DATE: 1998-03-18  
; NUMBER OF SEQ ID NOS: 114  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 33  
; LENGTH: 673  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: modified\_base  
; LOCATION: (325)  
; OTHER INFORMATION: Where n is a, c, g or t  
; NAME/KEY: modified\_base  
; LOCATION: (419)  
; OTHER INFORMATION: Where n is a, c, g or t  
; NAME/KEY: modified\_base  
; LOCATION: (452)  
; OTHER INFORMATION: Where n is a, c, g or t  
; NAME/KEY: modified\_base  
; LOCATION: (532)  
; OTHER INFORMATION: Where n is a, c, g or t  
; NAME/KEY: modified\_base  
; LOCATION: (538)  
; OTHER INFORMATION: Where n is a, c, g or t  
; NAME/KEY: modified\_base  
; LOCATION: (542)  
; OTHER INFORMATION: Where n is a, c, g or t  
; NAME/KEY: modified\_base  
; LOCATION: (571)  
; OTHER INFORMATION: Where n is a, c, g or t  
; NAME/KEY: modified\_base  
; LOCATION: (600)  
; OTHER INFORMATION: Where n is a, c, g or t  
; NAME/KEY: modified\_base  
; LOCATION: (616)  
; OTHER INFORMATION: Where n is a, c, g or t  
; NAME/KEY: modified\_base  
; LOCATION: (651)  
; OTHER INFORMATION: Where n is a, c, g or t  
; NAME/KEY: modified\_base  
; LOCATION: (653)



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; OTHER INFORMATION: Where n is a, c, g or t
; NAME/KEY: modified_base
; LOCATION: (672)
; OTHER INFORMATION: Where n is a, c, g or t
US-09-123-912-33

Query Match      70.0%; Score 14; DB 4; Length 673;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AAAGGAGCAGGGAA 15
   |||||
Db 129 AAAGGAGCAGGGAA 142

RESULT 11
US-09-643-597-33
; Sequence 33, Application US/09643597
; Patent No. 6426072
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C11
; CURRENT APPLICATION NUMBER: US/09/643,597
; CURRENT FILING DATE: 2000-08-21
; NUMBER OF SEQ ID NOS: 369
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 33
; LENGTH: 673
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(673)
; OTHER INFORMATION: n = A,T,C or G
US-09-643-597-33

Query Match      70.0%; Score 14; DB 4; Length 673;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AAAGGAGCAGGGAA 15
   |||||
Db 129 AAAGGAGCAGGGAA 142

RESULT 12
US-09-480-884A-33
; Sequence 33, Application US/09480884A
; Patent No. 6482597
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Hosken, Nancy A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY
; FILE REFERENCE: 210121.455C6
; CURRENT APPLICATION NUMBER: US/09/480,884A
; CURRENT FILING DATE: 2001-08-27
; NUMBER OF SEQ ID NOS: 330

; OTHER INFORMATION: Where n is a, c, g or t
; NAME/KEY: modified_base
; LOCATION: (672)
; OTHER INFORMATION: Where n is a, c, g or t
US-09-123-912-33

Query Match      70.0%; Score 14; DB 4; Length 673;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AAAGGAGCAGGGAA 15
   |||||
Db 129 AAAGGAGCAGGGAA 142

RESULT 13
US-09-542-615A-33
; Sequence 33, Application US/09542615A
; Patent No. 6518256
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy A.
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY
; FILE REFERENCE: 210121.455C8
; CURRENT APPLICATION NUMBER: US/09/542,615A
; CURRENT FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 33
; LENGTH: 673
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(673)
; OTHER INFORMATION: n = A,T,C or G
US-09-542-615A-33

Query Match      70.0%; Score 14; DB 4; Length 673;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AAAGGAGCAGGGAA 15
   |||||
Db 129 AAAGGAGCAGGGAA 142

RESULT 14
US-09-606-421B-33
; Sequence 33, Application US/09606421B
; Patent No. 6531315
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C6
; CURRENT APPLICATION NUMBER: US/09/606,421B
; CURRENT FILING DATE: 2001-08-27
; NUMBER OF SEQ ID NOS: 330
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; FILE REFERENCE: 210121.455C9
; CURRENT APPLICATION NUMBER: US/09/606,421B
; CURRENT FILING DATE: 2000-06-28
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 33
; LENGTH: 673
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(673)
; OTHER INFORMATION: n = A,T,C or G
US-09-606-421B-33

Query Match 70.0%; Score 14; DB 4; Length 673;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AAAGGAGCAGGGAA 15
|||
Db 129 AAAGGAGCAGGGAA 142

RESULT 15
US-09-221-107-33
; Sequence 33, Application US/09221107
; Patent No. 6660839
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY OF LUNG CANCER
; FILE REFERENCE: 210121.455C2
; CURRENT APPLICATION NUMBER: US/09/221,107
; CURRENT FILING DATE: 1998-12-22
; NUMBER OF SEQ ID NOS: 161
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 33
; LENGTH: 673
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (325)
; OTHER INFORMATION: Where n is a, c, g or t
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (419)
; OTHER INFORMATION: Where n is a, c, g or t
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (452)
; OTHER INFORMATION: Where n is a, c, g or t
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (532)
; OTHER INFORMATION: Where n is a, c, g or t
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (538)
; OTHER INFORMATION: Where n is a, c, g or t
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (542)
; OTHER INFORMATION: Where n is a, c, g or t
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (571)
; OTHER INFORMATION: Where n is a, c, g or t
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (600)
; OTHER INFORMATION: Where n is a, c, g or t
; FEATURE:

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: May 27, 2004, 11:30:47 ; Search time 105.251 Seconds  
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Title: US-09-121-239-13

Perfect score: 20

Sequence: 1 CAAGGACGAGGAGG 20

Scoring table:

OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 2960401 seqs, 2274450654 residues

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Minimum DB seq length: 0

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- 10: /cgn2\_6/ptodata/2/pubpna/US09B\_PUBCOMB.seq.\*
- 11: /cgn2\_6/ptodata/2/pubpna/US09C\_PUBCOMB.seq.\*
- 12: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq.\*
- 13: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq.\*
- 14: /cgn2\_6/ptodata/2/pubpna/US10A\_PUBCOMB.seq.\*
- 15: /cgn2\_6/ptodata/2/pubpna/US10B\_PUBCOMB.seq.\*
- 16: /cgn2\_6/ptodata/2/pubpna/US10C\_PUBCOMB.seq.\*
- 17: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq.\*
- 18: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq.\*
- 19: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	ID	Description
1	20	100.0	186 15	US-10-029-386-23233
2	20	100.0	530 17	US-10-148-641A-19
3	20	100.0	551 15	US-10-029-386-9533
4	20	100.0	3450 16	US-10-457-954-5
5	20	100.0	5434 13	US-10-170-385-182
6	18	90.0	396 9	US-09-969-708-488
7	18	90.0	474 10	US-09-918-995-20082
8	18	90.0	620 13	US-10-027-632-278076
9	18	90.0	620 16	US-10-027-632-278076
10	18	90.0	1345 16	US-10-332-424-9
11	18	90.0	1611 10	US-09-764-891-9320
12	18	90.0	1611 15	US-10-091-572-867
13	18	90.0	1726 16	US-10-108-260A-1
14	18	90.0	1869 15	US-10-037-270-704

15	18	90.0	1869	16	US-10-117-722-704	Sequence 704, Appl
16	17	85.0	416	9	US-09-880-107-2953	Sequence 2953, Ap
c 17	17	85.0	965	13	US-10-027-632-323768	Sequence 323768,
c 18	17	85.0	965	16	US-10-027-632-323768	Sequence 323768,
19	17	85.0	2564	13	US-10-027-632-111606	Sequence 111606,
20	17	85.0	2564	16	US-10-027-632-111606	Sequence 111606,
c 21	17	85.0	39725	15	US-10-017-161-1611	Sequence 111606,
c 22	17	85.0	39725	16	US-10-292-798-1285	Sequence 1285, Ap
c 23	17	85.0	57953	9	US-09-880-107-1543	Sequence 1543, Ap
c 24	17	85.0	66933	13	US-10-182-936A-11	Sequence 11, Appl
c 25	17	85.0	66933	16	US-10-374-979-11	Sequence 11, Appl
c 26	17	85.0	72049	13	US-10-182-936A-9	Sequence 9, Appli
c 27	17	85.0	72049	16	US-10-374-979-9	Sequence 9, Appli
c 28	17	85.0	156843	13	US-10-087-192-1408	Sequence 1408, Ap
c 29	16	80.0	320	13	US-10-085-783A-13435	Sequence 13435, A
c 30	16	80.0	320	16	US-10-242-535A-13435	Sequence 13435, A
c 31	16	80.0	822	13	US-10-027-632-125717	Sequence 125717,
c 32	16	80.0	822	16	US-10-027-632-125717	Sequence 125717,
c 33	16	80.0	1763	9	US-09-891-171-3	Sequence 3, Appli
c 34	16	80.0	1763	15	US-10-266-767-3	Sequence 3, Appli
c 35	16	80.0	2059	13	US-10-027-632-99852	Sequence 99852, A
c 36	16	80.0	2059	16	US-10-027-632-99852	Sequence 99852, A
c 37	16	80.0	5086	16	US-10-062-674-1873	Sequence 1873, Ap
c 38	16	80.0	54929	13	US-10-087-192-823	Sequence 823, Ap
c 39	16	80.0	163998	16	US-10-380-931-24	Sequence 24, Appl
c 40	16	80.0	197496	9	US-09-877-177-10	Sequence 10, Appl
c 41	16	80.0	197496	13	US-10-426-836-10	Sequence 10, Appl
c 42	15	75.0	321	11	US-09-864-408A-1461	Sequence 1461, Ap
c 43	15	75.0	410	10	US-09-918-995-8043	Sequence 8043, Ap
c 44	15	75.0	486	9	US-09-924-401-61	Sequence 61, Appl
c 45	15	75.0	550	10	US-09-918-995-11063	Sequence 11063, A

ALIGNMENTS

RESULT 1

- US-10-029-386-23233
- Sequence 23233, Application US/10029386
- Publication No. US20030194704A1
- GENERAL INFORMATION:
- APPLICANT: Penn, Sharon G.
- APPLICANT: Rank, David R.
- APPLICANT: Hanzel, David K.
- TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G
- FILE REFERENCE: AOMICA-X-2
- CURRENT APPLICATION NUMBER: US/10/029,386
- CURRENT FILING DATE: 2001-12-20
- NUMBER OF SEQ ID NOS: 34288
- SOFTWARE: Annonax Sequence Listing Engine vers. 1.1
- SEQ ID NO 23233
- LENGTH: 186
- TYPE: DNA
- ORGANISM: Homo sapiens
- FEATURE:
- OTHER INFORMATION: MAP TO CHR9.3
- OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.3
- OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.4
- OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.5
- OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.8
- OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.3
- OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.1
- OTHER INFORMATION: SWISSPROT HIT: P38571, EVALUE 1.50e+00
- OTHER INFORMATION: NT HIT: M17310.1, EVALUE 1.00e-100
- OTHER INFORMATION: EST\_HUMAN HIT: H81820.1, EVALUE 5.00e-95
- US-10-029-386-23233

Query Match 100.0%; Score 20; DB 15; Length 186;  
Best Local Similarity 100.0%; Pred. No. 0.2;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAAGGACGAGGAGGAGG 20

Db 110 CAAAGGAGCAGGGAAGG 129  
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## RESULT 2

US-10-148-641A-19  
; Sequence 19, Application US/10148641A  
; Publication No. US20040086852A1  
; GENERAL INFORMATION:  
; APPLICANT: Ono, Toshiro and Nakayama, Eiichi  
; TITLE OF INVENTION: CANCER ASSOCIATED ANTIGENS AND USES  
; FILE OF INVENTION: THEREFOR  
; FILE REFERENCE: L00461.70132.US  
; CURRENT APPLICATION NUMBER: US/10/148,641A  
; CURRENT FILING DATE: 2003-03-18  
; PRIOR APPLICATION NUMBER: US 09/559,013  
; PRIOR FILING DATE: 2000-04-26  
; PRIOR APPLICATION NUMBER: US 60/168,353  
; PRIOR FILING DATE: 1999-12-01  
; NUMBER OF SEQ ID NOS: 39  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 19  
; LENGTH: 530  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-10-148-641A-19

Query Match 100.0%; Score 20; DB 17; Length 530;  
Best Local Similarity 100.0%; Pred. No. 0.17;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAAAGGAGCAGGGAAGG 20  
Db 370 CAAAGGAGCAGGGAAGG 389  
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## RESULT 3

US-10-029-386-9533  
; Sequence 9533, Application US/10029386  
; Publication No. US20030194704A1  
; GENERAL INFORMATION:  
; APPLICANT: Penn, Sharron G.  
; APPLICANT: Rank, David R.  
; APPLICANT: Hanzel, David K.  
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
; FILE OF INVENTION: EXPRESSION ANALYSIS TWO  
; FILE REFERENCE: AEOMICA-X-2  
; CURRENT APPLICATION NUMBER: US/10/029,386  
; CURRENT FILING DATE: 2001-12-20  
; NUMBER OF SEQ ID NOS: 34288  
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1  
; SEQ ID NO 9533  
; LENGTH: 551  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: MAP TO CHR9.3  
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.3  
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.4  
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.5  
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.8  
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.3  
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.1  
; OTHER INFORMATION: NT HIT: M7310.1, EVALUE 0.00e+00  
; OTHER INFORMATION: SWISSPROT HIT: O05974, EVALUE 3.00e+00  
; OTHER INFORMATION: EST\_HUMAN HIT: A1025543.1, EVALUE 0.00e+00  
US-10-029-386-9533

Query Match 100.0%; Score 20; DB 15; Length 551;  
Best Local Similarity 100.0%; Pred. No. 0.17;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAAAGGAGCAGGGAAGG 20

Db 192 CAAAGGAGCAGGGAAGG 211  
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## RESULT 4

US-10-457-954-5  
; Sequence 5, Application US/10457954  
; Publication No. US20040005623A1  
; GENERAL INFORMATION:  
; APPLICANT: Longley, B. Jack  
; TITLE OF INVENTION: Method of determining tumor sensitivities to therapeutic drugs  
; FILE REFERENCE: 960296.98890  
; CURRENT APPLICATION NUMBER: US/10/457,954  
; CURRENT FILING DATE: 2003-06-10  
; PRIOR APPLICATION NUMBER: 60/387,370  
; PRIOR FILING DATE: 2002-06-10  
; PRIOR APPLICATION NUMBER: 60/387,406  
; PRIOR FILING DATE: 2002-06-10  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 5  
; LENGTH: 3450  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(3447)  
; FEATURE:  
; NAME/KEY: misc\_structure  
; LOCATION: (730)..(765)  
; OTHER INFORMATION: encode amino acids 244-255 for forming the sides of the enzymatic  
; OTHER INFORMATION: pocket  
; FEATURE:  
; NAME/KEY: misc\_structure  
; LOCATION: (931)..(1077)  
; OTHER INFORMATION: encode amino acids 311-359 for forming the sides of the enzymatic  
; OTHER INFORMATION: pocket  
; FEATURE:  
; NAME/KEY: misc\_structure  
; LOCATION: (1141)..(1206)  
; OTHER INFORMATION: encode amino acids 381-402 for forming the enzymatic pocket's  
; OTHER INFORMATION: activation loop  
US-10-457-954-5

Query Match 100.0%; Score 20; DB 16; Length 3450;  
Best Local Similarity 100.0%; Pred. No. 0.13;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAAAGGAGCAGGGAAGG 20  
Db 69 CAAAGGAGCAGGGAAGG 88  
|||||

## RESULT 5

US-10-170-385-182  
; Sequence 182, Application US/10170385  
; Publication No. US20030203372A1  
; GENERAL INFORMATION:  
; APPLICANT: Ward, Neil Raymond  
; APPLICANT: Mundy, Christopher Robert  
; APPLICANT: Kan, On  
; APPLICANT: Harris, Robert Alan  
; APPLICANT: White, Jonathan  
; APPLICANT: Binley, Katie Mary  
; APPLICANT: Rayner, William Nigel  
; APPLICANT: Naylor, Stuart  
; APPLICANT: Kingman, Susan Mary  
; APPLICANT: Krige, David  
; TITLE OF INVENTION: ANALYSIS METHOD  
; FILE REFERENCE: 532682000100  
; CURRENT APPLICATION NUMBER: US/10/170,385  
; CURRENT FILING DATE: 2002-06-12  
; PRIOR APPLICATION NUMBER: PCT/GB02/01662

; PRIOR FILING DATE: 2002-04-08  
 ; PRIOR APPLICATION NUMBER: PCT/GB01/05458  
 ; PRIOR FILING DATE: 2001-12-10  
 ; NUMBER OF SEQ ID NOS: 549  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 182  
 ; LENGTH: 5434  
 ; TYPE: DNA  
 ; ORGANISM: Homo Sapiens  
 US-10-170-385-182

Query Match 100.0%; Score 20; DB 13; Length 5434;  
 Best Local Similarity 100.0%; Pred. No. 0.12; Indels 0; Gaps 0;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAAAGGAGCAGGGAAGG 20  
 Db 69 CAAAGGAGCAGGGAAGG 88

RESULT 6  
 US-09-969-708-488/c  
 ; Sequence 488, Application US/09969708  
 ; Patent No. US20020102532A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Augustus, Meena  
 ; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu  
 ; FILE OF INVENTION: Sets  
 ; FILE REFERENCE: 689290-70  
 ; CURRENT APPLICATION NUMBER: US/09/969,708  
 ; PRIOR FILING DATE: 2001-10-03  
 ; PRIOR APPLICATION NUMBER: US/60/237,606  
 ; PRIOR FILING DATE: 2000-10-03  
 ; PRIOR APPLICATION NUMBER: US/60/237,608  
 ; PRIOR FILING DATE: 2000-10-03  
 ; PRIOR APPLICATION NUMBER: US/60/237,425  
 ; PRIOR FILING DATE: 2000-10-03  
 ; NUMBER OF SEQ ID NOS: 658  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 488  
 ; LENGTH: 396  
 ; TYPE: DNA  
 ; ORGANISM: Homosapiens  
 US-09-969-708-488

Query Match 90.0%; Score 18; DB 9; Length 396;  
 Best Local Similarity 100.0%; Pred. No. 2.1; Indels 0; Gaps 0;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAAAGGAGCAGGGAAGG 18  
 Db 181 CAAAGGAGCAGGGAAGG 164

RESULT 7  
 US-09-918-995-20082  
 ; Sequence 20082, Application US/09918995  
 ; Publication No. US20030073623A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Hyseq, Inc.  
 ; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED  
 ; FILE OF INVENTION: FROM VARIOUS CDNA LIBRARIES  
 ; FILE REFERENCE: 20411-756  
 ; CURRENT APPLICATION NUMBER: US/09/918,995  
 ; PRIOR FILING DATE: 2001-07-30  
 ; PRIOR APPLICATION NUMBER: US/09/235,076  
 ; PRIOR FILING DATE: 1999-01-20  
 ; NUMBER OF SEQ ID NOS: 38054  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 20082  
 ; LENGTH: 474  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens

; FEATURE:  
 ; NAME/KEY: misc feature  
 ; LOCATION: (1)...(474)  
 ; OTHER INFORMATION: n = A,T,C or G  
 US-09-918-995-20082

Query Match 90.0%; Score 18; DB 10; Length 474;  
 Best Local Similarity 100.0%; Pred. No. 2;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAAAGGAGCAGGGAAGG 18  
 Db 331 CAAAGGAGCAGGGAAGG 348

RESULT 8  
 US-10-027-632-278076  
 ; Sequence 278076, Application US/10027632  
 ; Publication No. US20020198371A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Wang, David G.  
 ; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
 ; FILE OF INVENTION: Polymorphisms in the Human Genome  
 ; FILE REFERENCE: 108827.129  
 ; CURRENT APPLICATION NUMBER: US/10/027,632  
 ; CURRENT FILING DATE: 2002-04-30  
 ; PRIOR FILING DATE: 2000-07-12  
 ; PRIOR APPLICATION NUMBER: US 60/218,006  
 ; PRIOR FILING DATE: 2000-07-12  
 ; PRIOR APPLICATION NUMBER: US 60/198,676  
 ; PRIOR FILING DATE: 2000-04-20  
 ; PRIOR APPLICATION NUMBER: US 60/193,483  
 ; PRIOR FILING DATE: 2000-03-29  
 ; PRIOR APPLICATION NUMBER: US 60/185,218  
 ; PRIOR FILING DATE: 2000-02-24  
 ; PRIOR APPLICATION NUMBER: US 60/167,363  
 ; PRIOR FILING DATE: 1999-11-23  
 ; PRIOR APPLICATION NUMBER: US 60/156,358  
 ; PRIOR FILING DATE: 1999-09-28  
 ; PRIOR APPLICATION NUMBER: US 60/146,002  
 ; PRIOR FILING DATE: 1999-08-09  
 ; NUMBER OF SEQ ID NOS: 325720  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 278076  
 ; LENGTH: 620  
 ; TYPE: DNA  
 ; ORGANISM: Human  
 US-10-027-632-278076

Query Match 90.0%; Score 18; DB 13; Length 620;  
 Best Local Similarity 100.0%; Pred. No. 2;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAAAGGAGCAGGGAAGG 18  
 Db 43 CAAAGGAGCAGGGAAGG 60

RESULT 9  
 US-10-027-632-278076  
 ; Sequence 278076, Application US/10027632  
 ; Publication No. US20030204075A9  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Wang, David G.  
 ; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
 ; FILE OF INVENTION: Polymorphisms in the Human Genome  
 ; FILE REFERENCE: 108827.129  
 ; CURRENT APPLICATION NUMBER: US/10/027,632  
 ; CURRENT FILING DATE: 2002-04-30  
 ; PRIOR FILING DATE: 2000-07-12  
 ; PRIOR APPLICATION NUMBER: US 60/218,006  
 ; PRIOR FILING DATE: 2000-07-12  
 ; PRIOR APPLICATION NUMBER: US 60/198,676  
 ; PRIOR FILING DATE: 2000-04-20  
 ; PRIOR APPLICATION NUMBER: US 60/193,483

; PRIOR FILING DATE: 2000-03-29  
 ; PRIOR APPLICATION NUMBER: US 60/185,218  
 ; PRIOR FILING DATE: 2000-02-24  
 ; PRIOR APPLICATION NUMBER: US 60/167,363  
 ; PRIOR FILING DATE: 1999-11-23  
 ; PRIOR APPLICATION NUMBER: US 60/156,358  
 ; PRIOR FILING DATE: 1999-09-28  
 ; PRIOR APPLICATION NUMBER: US 60/146,002  
 ; PRIOR FILING DATE: 1999-08-09  
 ; NUMBER OF SEQ ID NOS: 325720  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 278076  
 ; LENGTH: 620  
 ; TYPE: DNA  
 ; ORGANISM: Human  
 US-10-027-632-278076

Query Match 90.0%; Score 18; DB 16; Length 620;  
 Best Local Similarity 100.0%; Pred. No. 2;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAAAGGAGCAGGGAAGAA 18  
 Db 43 CAAAGGAGCAGGGAAGAA 60

RESULT 10  
 US-10-332-424-9  
 ; Sequence 9, Application US/10332424  
 ; Publication No. US20040018505A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: INCYTE GENOMICS, INC.; LEE, Ernestine A.  
 ; APPLICANT: TANG, Y. Ton; LU, Dying Aina M.  
 ; APPLICANT: TRIBOULEY, Catherine M.; GANDHI, Ameena R.  
 ; APPLICANT: LU, Yan; BAUGHN, Mariah R.  
 ; APPLICANT: WARREN, Bridget A.; THORNTON, Michael  
 ; APPLICANT: YUE, Henry; JACKSON, Jennifer L.  
 ; APPLICANT: ARVIZU, Chandra S.; ELLIOTT, Vicki S.  
 ; APPLICANT: THANGAVELU, Kavitha; RAMKUMAR, Jayalaxmi  
 ; APPLICANT: CHAWLA, Narinder K.; YAO, Monique G.  
 ; APPLICANT: GANDHI, Ameena R.  
 ; TITLE OF INVENTION: AMINOACYL TRNA SYNTHETASES  
 ; FILE REFERENCE: PI-0153 USN  
 ; CURRENT APPLICATION NUMBER: US/10/332,424  
 ; CURRENT FILING DATE: 2002-01-06  
 ; PRIOR APPLICATION NUMBER: US 60/216,748  
 ; PRIOR FILING DATE: 2000-07-07  
 ; PRIOR APPLICATION NUMBER: US 60/219,019  
 ; PRIOR FILING DATE: 2000-07-18  
 ; PRIOR APPLICATION NUMBER: US 60/223,058  
 ; PRIOR FILING DATE: 2000-08-04  
 ; PRIOR APPLICATION NUMBER: US 60/234,593  
 ; PRIOR FILING DATE: 2000-09-21  
 ; PRIOR APPLICATION NUMBER: US 60/239,797  
 ; PRIOR FILING DATE: 2000-10-11  
 ; NUMBER OF SEQ ID NOS: 12  
 ; SOFTWARE: PERL Program  
 ; SEQ ID NO 9  
 ; LENGTH: 1345  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
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 ; NAME/KEY: misc feature  
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 US-10-332-424-9

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 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 ; Sequence 9320, Application US/09764891  
 ; Publication No. US20030077808A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Rosen et al.  
 ; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
 ; FILE REFERENCE: PC006  
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 ; CURRENT FILING DATE: 2001-01-17  
 ; Prior application data removed - consult PALM or file wrapper  
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 US-09-764-891-9320

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 Best Local Similarity 100.0%; Pred. No. 1.7;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAAAGGAGCAGGGAAGAA 18  
 Db 183 CAAAGGAGCAGGGAAGAA 166

RESULT 12  
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 ; Sequence 867, Application US/10091572  
 ; Publication No. US20030054373A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Rosen et al.  
 ; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
 ; FILE REFERENCE: P118C1  
 ; CURRENT APPLICATION NUMBER: US/10/091,572  
 ; CURRENT FILING DATE: 2002-03-07  
 ; PRIOR APPLICATION NUMBER: 09/764,850  
 ; PRIOR FILING DATE: 2001-01-17  
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 ; PRIOR APPLICATION NUMBER: 60/239,937  
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 ; PRIOR APPLICATION NUMBER: 60/241,787  
 ; PRIOR FILING DATE: 2000-10-20

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 ; PRIOR APPLICATION NUMBER: 60/235,836  
 ; PRIOR FILING DATE: 2000-09-27  
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 ; PRIOR FILING DATE: 2000-09-06  
 ; PRIOR APPLICATION NUMBER: 60/215,135  
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 ; PRIOR APPLICATION NUMBER: 60/225,266  
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; PRIOR FILING DATE: 2000-09-14
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Query Match          90.0%; Score 18; DB 15; Length 1611;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 CAAAGGAGCAGCGAAGAA 18
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Db      183 CAAAGGAGCAGCGAAGAA 166

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RESULT 13
US-10-108-260A-1
; Sequence 1, Application US/10108260A
; Publication No. US20040005560A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. US20040005560A1 full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/10/108,260A
; CURRENT FILING DATE: 2002-03-27
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1726
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-108-260A-1

```

```

Query Match          90.0%; Score 18; DB 16; Length 1726;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

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QY      1 CAAAGGAGCAGCGAAGAA 18
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```

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RESULT 14
US-10-037-270-704
; Sequence 704, Application US/10037270
; Publication No. US20030104529A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyun
; APPLICANT: Chen, Rui-hong
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wehrman, Tom
; APPLICANT: Xue, Aidong J.
; APPLICANT: Yang, Yonghong
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Zhou, Ping
; APPLICANT: Ma, Yunging
; APPLICANT: Wang, Dunrui
; APPLICANT: Wang, Zhiwei
; APPLICANT: Tillinghast, John
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. US20030104529A1el Nucleic Acids and

```

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; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 784CIP2B
; CURRENT APPLICATION NUMBER: US/10/037,270
; CURRENT FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 1104
; SOFTWARE: pt_FL_genes Version 1.0
; SEQ ID NO 704
; LENGTH: 1869
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (161)..(1792)
US-10-037-270-704

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Query Match          90.0%; Score 18; DB 15; Length 1869;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 CAAAGGAGCAGCGAAGAA 18
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Db      1678 CAAAGGAGCAGCGAAGAA 1695

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RESULT 15
US-10-117-722-704
; Sequence 704, Application US/10117722
; Publication No. US20030219744A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Zhang, Jie
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. US20030219744A1el Nucleic Acids and
; FILE REFERENCE: 784CIP2B
; CURRENT APPLICATION NUMBER: US/10/117,722
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: 09/620,312
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 1104
; SOFTWARE: pt_FL_genes Version 1.0
; SEQ ID NO 704
; LENGTH: 1869
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (161)..(1792)
US-10-117-722-704

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Query Match          90.0%; Score 18; DB 16; Length 1869;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 CAAAGGAGCAGCGAAGAA 18
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Db      1678 CAAAGGAGCAGCGAAGAA 1695

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Job time : 106.251 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 26, 2004, 15:22:41 ; Search time 706.154 Seconds  
(without alignments)  
845.770 Million cell updates/sec

Title: US-09-121-239-13

Perfect score: 20

Sequence: 1 CAAGGACGAGGAGAGAGG 20

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 27513289 seqs, 14931090276 residues

Word size : 0

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

EST:

1: em\_estba:\*

2: em\_esthum:\*

3: em\_estin:\*

4: em\_estmu:\*

5: em\_estov:\*

6: em\_estpl:\*

7: em\_estro:\*

8: em\_htc:\*

9: gb\_est1:\*

10: gb\_est2:\*

11: gb\_hcc:\*

12: gb\_est3:\*

13: gb\_est4:\*

14: gb\_est5:\*

15: em\_estfun:\*

16: em\_estom:\*

17: em\_gss\_hum:\*

18: em\_gss\_inv:\*

19: em\_gss\_pln:\*

20: em\_gss\_vrt:\*

21: em\_gss\_fun:\*

22: em\_gss\_nam:\*

23: em\_gss\_mus:\*

24: em\_gss\_pro:\*

25: em\_gss\_rod:\*

26: em\_gss\_phg:\*

27: em\_gss\_vrl:\*

28: gb\_gss1:\*

29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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3	20	100.0	196	10	BB047102	BB047102 BB047102
4	20	100.0	198	29	CG636709	CG636709 OST361614

5	20	100.0	209	9	AV173479	AV173479 AV173479
6	20	100.0	220	10	BB132800	BB132800 BB132800
7	20	100.0	233	9	AV104236	AV104236 AV104236
8	20	100.0	237	9	AV323022	AV323022 AV323022
9	20	100.0	245	10	BB047117	BB047117 BB047117
10	20	100.0	249	13	BY371403	BY371403 BY371403
11	20	100.0	250	9	AV136928	AV136928 AV136928
12	20	100.0	250	9	AV215533	AV215533 AV215533
13	20	100.0	250	9	AV346046	AV346046 AV346046
14	20	100.0	253	9	AV296437	AV296437 AV296437
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16	20	100.0	254	9	AV338176	AV338176 AV338176
17	20	100.0	256	9	AV218421	AV218421 AV218421
18	20	100.0	258	9	AV134910	AV134910 AV134910
19	20	100.0	258	9	AV339053	AV339053 AV339053
20	20	100.0	262	10	BE916612	BE916612 601667217
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22	20	100.0	282	9	AV055312	AV055312 AV055312
c 23	20	100.0	295	12	BM122590	BM122590 L0512C06-
24	20	100.0	296	9	AV147138	AV147138 AV147138
25	20	100.0	297	9	AV100468	AV100468 AV100468
c 26	20	100.0	298	9	AI025543	AI025543 ov87a04.s
27	20	100.0	305	9	AA415759	AA415759 va32d09.r
28	20	100.0	311	9	AI100354	AI100354 AV100354
c 29	20	100.0	319	10	BF456747	BF456747 UI-M-BZ1-
30	20	100.0	321	10	BB026196	BB026196 BB026196
31	20	100.0	324	9	AV095169	AV095169 AV095169
c 32	20	100.0	326	13	B0842273	B0842273 AGENCOURT
c 33	20	100.0	332	12	BG796781	BG796781 UTWS SM5C
c 34	20	100.0	333	9	AI838832	AI838832 UI-M-AL0-
c 35	20	100.0	340	12	BM115670	BM115670 L0824A07-
c 36	20	100.0	344	9	AI553501	AI553501 vw37602.x
37	20	100.0	344	13	BK099890	BK099890 BX099890
38	20	100.0	344	13	BY709426	BY709426 BY709426
39	20	100.0	346	10	BB793854	BB793854 BB793854
40	20	100.0	348	11	AK009808	AK009808 Mus muscu
41	20	100.0	352	9	AI154779	AI154779 ud59g05.r
42	20	100.0	358	13	BY409310	BY409310 BY409310
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45	20	100.0	369	13	BY408267	BY408267 BY408267

#### ALIGNMENTS

RESULT 1  
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LOCUS ov87a03.s1 Soares testis NHT Homo sapiens cDNA clone IMAGE:1644268  
DEFINITION 3' similar to TR:Q13688 Q13688 ABL ; mRNA sequence.  
ACCESSION AI025542  
VERSION AI025542.1 GI:3241155  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 115)  
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index  
JOURNAL Unpublished (1997)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.  
CDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html







RIKEN Mouse ESTs  
Unpublished (1999)  
Contact: Chie Owa  
Genome Science Laboratory  
RIKEN  
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan  
Tel: 81-298-36-9145  
Fax: 81-298-36-9098  
Email: genome-res@gs.riken.go.jp  
Thermolabile and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA (Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))  
Transcriptional sequencing: A method for DNA sequencing using RNA polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))  
Please visit our web site (<http://genome.rtc.riken.go.jp>) for further details.

FEATURES  
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QY 1 CAAAGGAGCAGGAGGAGG 20  
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DB 70 CAAAGGAGCAGGAGGAGG 89  
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RESULT 8  
AV323022  
LOCUS  
DEFINITION  
AV323022  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
1 (bases 1 to 237)  
Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
Konno, H., Aizawa, K., Akahira, S., Akiyama, J., Carninci, P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., Hirozane, T., Hori, F., Ishii, Y., Ishikawa, T., Itoh, M., Izawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N., Kojima, Y., Koya, S., Kusakabe, M., Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y., Owa, C., Ozawa, Y., Saito, H., Sano, M., Sato, K., Shibata, K., Shibata, Y., Shigemoto, Y., Shiraki, T., Sogabe, Y., Sugahara, Y., Suzuki, H., Suzuki, H., Takahashi, F., Tateno, M., Tominaga, N., Tsunoda, Y., Watahiki, A., Watanabe, S., Yamamura, T., Yasunishi, A., Yokota, T., Yoshiki, A., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.  
RIKEN Mouse ESTs (Konno, H., et al. 1999)  
Unpublished (1999)  
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Fax: 81-45-503-9216  
Email: genome-res@gs.riken.go.jp  
URL: <http://genome.gsc.riken.go.jp/>  
Sasaki, N., Izawa, M., Watahiki, M., Ozawa, K., Tanaka, T., Yoneda, Y.,

Matsura, S., Carninci, P., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y.  
Transcriptional sequencing: A method for DNA sequencing using RNA polymerase. Proc. Natl. Acad. Sci. U.S.A. 95 (7), 3455-3460 (1998)  
Itoh, M., Kiteunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J., Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y.  
Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)  
Carninci, P. and Hayashizaki, Y.  
High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)  
Please visit our web site (<http://genome.rtc.riken.go.jp>) for further details.

FEATURES  
source  
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/mol\_type="mRNA"  
/strain="C57BL/6J"  
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/clone="6230405E19"  
/sex="mixed"  
/tissue\_type="head"  
/dev\_stage="11 days embryo"  
/lab\_host="DH10B"  
/clone\_lib="RIKEN full-length enriched, 11 days embryo head"  
/note="Site 1: SalI; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGGATCCAGAGCTCTTTTCTTTTCTTNN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 10.0 and subtraction to Rot = 100.0. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGATTCGAGTAAATTAATATCCCTCCCCCCCC 3']. cDNA was cloned into the XhoI and BamHI sites. Vector: a modified phagescript KS(+) after bulk excision from Lambda FLC I. Cloning sites, 5' end: SalI; 3' end: BamHI."

ORIGIN  
Query Match 100.0%; Score 20; DB 9; Length 237;  
Best Local Similarity 100.0%; Pred. No. 11;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CAAAGGAGCAGGAGGAGG 20  
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DB 73 CAAAGGAGCAGGAGGAGG 92  
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RESULT 9  
BB047117  
LOCUS  
DEFINITION  
BB047117  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
245 bp mRNA linear EST 25-JUN-2000  
Mus musculus cDNA clone 6330581P16 3', mRNA sequence.  
BB047117.1 GI:8454293  
Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 245)  
Konno, H., Aizawa, K., Akahira, S., Akiyama, J., Arakawa, T., Carninci, P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., Hirozane, T., Hori, F., Ishii, Y., Ishikawa, J., Ishikawa, T., Itoh, M., Izawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N.,



encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)  
 cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.  
 Please visit our web site (<http://genome.gsc.riken.go.jp>) for further details.

#### FEATURES

source

Location/Qualifiers  
 1..249  
 /organism="Mus musculus"  
 /mol\_type="mRNA"  
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 /db\_xref="taxon:10090"  
 /clone="G430078A20"  
 /sex="female"  
 /tissue\_type="mammary gland"  
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 /dev\_stage="1.5 years"  
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#### ORIGIN

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 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAAAGGACGAGGAGAAGG 20  
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 Db 89 CAAAGGACGAGGAGAAGG 108

#### RESULT 11

AV136928

LOCUS

AV136928 Mus musculus C57BL/6J 10-11 day embryo Mus musculus cDNA  
 clone 2810029G21, mRNA sequence.

#### ACCESSION

AV136928

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

1 (bases 1 to 250)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 Carninci, P., Shibata, K., Ozawa, Y., Konno, H., Itoh, M., Aizawa, K., Akahira, S., Akiyama, J., Fukuda, S., Fukunishi, Y., Funayama, T., Hara, A., Hayatsu, N., Hori, F., Ishikawa, T., Itoh, M., Izawa, M., Kawai, J., Kikuchi, N., Kojima, Y., Matsuyama, T., Nitsuuma, H., Oda, H., Owa, C., Sato, K., Shibata, Y., Shigemoto, Y., Shiraki, T., Sogabe, Y., Sugahara, Y., Suzuki, H., Suzuki, H., Tateno, M., Tomaru, Y., Tominaga, N., Watanabe, S., Yagane, M., Yamamura, T., Yokota, T., Yoshino, M., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y.  
 RIKEN Mouse ESTs  
 Unpublished (1999)  
 Contact: Chie Owa  
 Genome Science Laboratory  
 RIKEN  
 3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan  
 Tel: 81-298-36-9145  
 Fax: 81-298-36-9098  
 Email: genome-res@rtc.riken.go.jp  
 Thermotabilization and thermoactivation of thermostable enzymes by trehalose and its application for the synthesis of full length cDNA (Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))  
 Transcriptional sequencing: A method for DNA sequencing using RNA polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))  
 Please visit our web site (<http://genome.rtc.riken.go.jp>) for further details.

#### FEATURES

source

Location/Qualifiers  
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QY 1 CAAAGGACGAGGAGAAGG 20  
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 Db 90 CAAAGGACGAGGAGAAGG 109

#### RESULT 12

AV215533

LOCUS

AV215533 RIKEN full-length enriched, ES cells Mus musculus cDNA  
 clone 2410149G15 3', mRNA sequence.

#### ACCESSION

AV215533

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

1 (bases 1 to 250)  
 Mus musculus (house mouse)  
 Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 Konno, H., Aizawa, K., Akahira, S., Akiyama, J., Carninci, P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., Hirozane, T., Hori, F., Ishii, Y., Ishikawa, T., Itoh, M., Izawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N., Kojima, Y., Koya, S., Kusakabe, M., Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y., Owa, C., Ozawa, Y., Saito, H., Sano, M., Sato, K., Shibata, K., Shibata, Y., Shigemoto, Y., Shiraki, T., Sogabe, Y., Sugahara, Y., Suzuki, H., Suzuki, H., Takahashi, F., Tateno, M., Tominaga, N., Tsunoda, Y., Watahiki, A., Watanabe, S., Yamamura, T., Yasunishi, A., Yokota, T., Yoshiki, A., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.  
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 1-7-22 Saito-cho, Tsukuba, Ibaraki 305-0045, Japan  
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 Sasaki, N., Izawa, M., Watahiki, M., Ozawa, K., Tanaka, T., Yoneda, Y., Matsumura, S., Carninci, P., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y.

#### TITLE

JOURNAL

COMMENT

Transcriptional sequencing: A method for DNA sequencing using RNA polymerase. Proc. Natl. Acad. Sci. U.S.A. 95 (7), 3455-3460 (1998)  
 Itoh, M., Kitsuunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J., Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y.  
 Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)  
 Carninci, P. and Hayashizaki, Y.  
 High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)  
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#### FEATURES

source

Location/Qualifiers  
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 /organism="Mus musculus"  
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/lab host="SOLR"
/clone lib="RIKEN full-length enriched, ES cells"
/note="Site 1: XhoI; Site 2: BamHI; cDNA library was
prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN, Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. 1st strand cDNA was
primed with a primer [5'
GAGAGGAGAGATTCGAGTCTTTTAAATTAATTCCTTTTNN 3'], cDNA was
prepared by using trehalose thermo-activated reverse
transcriptase and subsequently enriched for full-length by
cap-trapper. cDNA went through one round of normalization
to Rot = 5.0 and subtraction to Rot = 25.0. Second strand
cDNA was prepared with the primer adapter of sequence [5'
GAGAGGAGATTCGAGTCTTTTAAATTAATTCCTTTTNN 3']."

ORIGIN
Query Match 100.0%; Score 20; DB 9; Length 250;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAAAGGAGCAGGGAAGAAG 20
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Db 88 CAAAGGAGCAGGGAAGAAG 107

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LOCUS AV346046 RIKEN full-length enriched, adult male olfactory bulb Mus
DEFINITION musculus cDNA clone 6430567L23 3', mRNA sequence.
ACCESSION AV346046
VERSION AV346046.1 GI:6387105
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 250)
Konno, H., Aizawa, K., Akahira, S., Akiyama, J., Carninci, P., Endo, T.,
Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., Hirozane, T., Hori, F.,
Ishii, Y., Ishikawa, T., Itoh, M., Izawa, M., Kadota, K., Kagawa, I.,
Kai, C., Kawai, J., Kikuchi, N., Kojima, Y., Koya, S., Kusakabe, M.,
Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y.,
Owa, C., Ozawa, Y., Saito, H., Sano, M., Sato, K., Shibata, K.,
Shibata, Y., Shigenoto, Y., Shiraki, T., Sogabe, Y., Sugahara, Y.,
Suzuki, H., Suzuki, H., Takahashi, F., Tateno, M., Tominaga, N.,
Tsunoda, Y., Watahiki, A., Watanabe, S., Yamamura, T., Yasunishi, A.,
Yokota, T., Yoshiki, A., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.
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Unpublished (1999)
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URL: http://genome.gsc.riken.go.jp/
Sasaki, N., Izawa, M., Watahiki, M., Ozawa, K., Tanaka, T., Yoneda, Y.,
Matsura, S., Carninci, P., Muramatsu, M., Okazaki, Y. and
Hayashizaki, Y.
Transcriptional sequencing: A method for DNA sequencing using RNA
polymerase. Proc. Natl. Acad. Sci. U.S.A. 95 (7), 3455-3460 (1998)
Itoh, M., Kitsuai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J.,
Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M.,
Okazaki, Y. and Hayashizaki, Y.
Automated filtration-based high-throughput plasmid preparation
system. Genome Res. 9 (5), 463-470 (1999)
Carninci, P. and Hayashizaki, Y.

```

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FEATURES
source
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/clone_lib="RIKEN full-length enriched, adult male
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/note="Site 1: SalI; Site 2: BamHI; cDNA library was
prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN, Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. 1st strand cDNA was
primed with a primer [5'
GAGAGGAGAGATTCGAGTCTTTTAAATTAATTCCTTTTNN 3'], cDNA was
prepared by using trehalose thermo-activated reverse
transcriptase and subsequently enriched for full-length by
cap-trapper. cDNA went through one round of normalization
to Rot = 10.0 and subtraction to Rot = 100.0. Second
strand cDNA was prepared with the primer adapter of
sequence [5' GAGAGGAGATTCGAGTCTTTTAAATTAATTCCTTTTNN 3']. cDNA was
cloned into the XhoI and BamHI sites.
Vector: a modified pBluescript KS(+) after bulk excision
from Lambda FLC I. Cloning sites, 5' end: SalI; 3' end:
BamHI"

ORIGIN
Query Match 100.0%; Score 20; DB 9; Length 250;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAAAGGAGCAGGGAAGAAG 20
|||||
Db 88 CAAAGGAGCAGGGAAGAAG 107

RESULT 14
AV296437
LOCUS AV296437 RIKEN full-length enriched, 8 days embryo Mus musculus
DEFINITION cDNA clone 5730441L12 3', mRNA sequence.
ACCESSION AV296437
VERSION AV296437.1 GI:6328456
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 253)
Konno, H., Aizawa, K., Akahira, S., Akiyama, J., Carninci, P., Endo, T.,
Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., Hirozane, T., Hori, F.,
Ishii, Y., Ishikawa, T., Itoh, M., Izawa, M., Kadota, K., Kagawa, I.,
Kai, C., Kawai, J., Kikuchi, N., Kojima, Y., Koya, S., Kusakabe, M.,
Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y.,
Owa, C., Ozawa, Y., Saito, H., Sano, M., Sato, K., Shibata, K.,
Shibata, Y., Shigenoto, Y., Shiraki, T., Sogabe, Y., Sugahara, Y.,
Suzuki, H., Suzuki, H., Takahashi, F., Tateno, M., Tominaga, N.,
Tsunoda, Y., Watahiki, A., Watanabe, S., Yamamura, T., Yasunishi, A.,
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Hayashizaki, Y.
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Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M.,
Okazaki, Y. and Hayashizaki, Y.
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Carninci, P. and Hayashizaki, Y.

```

High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)  
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Email: genome-res@gsc.riken.go.jp,  
URI: <http://genome.gsc.riken.go.jp/>  
Sasaki, N., Izawa, M., Wataniki, M., Ozawa, K., Tanaka, T., Yoneda, Y.,  
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Hayashizaki, Y.  
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Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M.,  
Okazaki, Y. and Hayashizaki, Y.  
Automated filtration-based high-throughput plasmid preparation  
system. *Genome Res.* 9 (5), 463-470 (1999)  
Carninci, P. and Hayashizaki, Y.  
High-efficiency full-length cDNA cloning. *Methods Enzymol.* 303,  
19-44 (1999)  
Please visit our web site (<http://genome.rtc.riken.go.jp>) for  
further details.

## FEATURES

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1. 253
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/clonene="5730441112"
/sex="mixed"
/dev_stage="8 days embryo"
/lab_host="DH10B"
/clonelib="RIKEN full-length enriched, 8 days embryo"
/notes="Site 1: Sali; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN, Division of Experimental Animal Research in Riken contributed to prepare mouse tissues, 1st strand cDNA was primed with a primer [5' GAGAGAGAGAGATCAGAGCTCTTTTCTTTTCTTTT 3'], cDNA was prepared by using trihalose thermo-activated reverse transcriptase and subsequently enriched for full-length cDNA-cap-trapper. cDNA went through one round of subtraction to Rot = 100.0 Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGATTCGAGTTAATTAATTAATTAATTCCTCCCCCCCC 3']. cDNA was cloned into the XhoI and BamHI sites. Vector: a modified pBluescript KS(+) after bulk excision from LambdaFLC 1. Cloning sites. 5' end: BamHI. 3' end: BamHI."

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## ORIGIN

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Query Match      100.0%; Score 20; DB 9; Length 253;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 CAAAGGAGCAGGGAAGAAGG 20  
Db 92 CAAAGGAGCAGGGAAGAAGG 111

## RESULT 15

BB467544

LOCUS	BB467544	253 bp	linear	EST 22-JUL-2000
DEFINITION	RIKEN full-length enriched, 12 days embryo eyeball Mus musculus			
	CDNA clone D23001SD20 3'			
	musculus			
				mRNA sequence.

ACCESSION BB467544

VERSION BB467544.1 GI:9384733

**KEYWORDS** EST.

**SOURCE** *Mus musculus* (house mouse)

ORGANISM	Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	

## REFERENCE

Kono, H., Aizawa, K., Akahira, S., Akiyama, J., Arakawa, T.,  
Carninci, P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N.,  
Hirozane, T., Horii, F., Ishikawa, J., Ishikawa, T., Itoh, M.,  
Izawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N.,  
Kiyosawa, H., Kojima, Y., Kondo, S., Koya, S., Kurihara, C.,  
Kusakabe, M., Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H.,  
Okazaki, Y., Ono, T., Owa, C., Saito, H., Sakai, C., Sato, K.,  
Shibata, K., Shibata, Y., Shigenoto, Y., Shinagawa, A., Shiraki, T.,  
Sogabe, Y., Sugahara, Y., Suzuki, H., Suzuki, H., Tagawa, A.,  
Takahashi, F., Tominaga, N., Toya, T., Tsunoda, Y., Watahiki, A.,  
Watanabe, S., Yamamura, T., Yamanaka, I., Yano, K., Yasunishi, A.,  
Yokota, T., Yoshida, K., Yoshiki, A., Yoshino, M., Muramatsu, M. and  
Havashizaki, Y.

**TITLE**

Unpublished (2000)  
Contact: Yoshihide Hayashizaki  
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Sciences Center (GSC), Yokohama Institute  
The Institute of Physical and Chemical Research (RIKEN)  
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan  
Tel: 81-45-503-9222  
Fax: 81-45-503-9216  
Email: genome-res@gsc.riken.go.jp,  
URL: <http://genome.gsc.riken.go.jp/>  
Carninci, P., Nishiyama, Y., Westover, A., Itoh, M., Nagaoka, S.,  
Sasaki, N., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.  
Thermotranscription and thermotranscription of thermolabile enzymes by  
trichloroacetic acid and its application for the synthesis of full length  
cDNA. *Proc. Natl. Acad. Sci. U.S.A.* 95 (2), 520-524 (1998)  
Itoh, M., Kutsuna, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J.,  
Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M.,  
Okazaki, Y. and Hayashizaki, Y.  
Automated filtration-based high-throughput plasmid preparation  
system. *Genome Res.* 9 (5), 463-470 (1999)  
Carninci, P. and Hayashizaki, Y.  
High-efficiency full-length cDNA cloning. *Methods Enzymol.* 303,  
19-44 (1999)  
Please visit our web site (<http://genome.rtc.riken.go.jp/>) for  
further details.

## FEATURES

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1. .253
location/Qualifiers
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="D230015D20"
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/dev_stage="12 days embryo"
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/note="Site 1: Sali; Site 2: BamHI; cDNA library was
prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN, Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. 1st strand cDNA was
primed with a primer [5'.
GAGAGAGAGAGCGCGCACTCGAGTTTTTTTTTTTTTTTTTTT 3']. cDNA was
prepared by using trihalose thermo-activated reverse
transcriptase and subsequently enriched for full-length by the
cap-trapper. Second strand cDNA was prepared with the
primer adapter of sequence [5'.
GAGAGAGAGATCTCGAGTTAAATTAATTCCTCCCCCCCCCCC 3']. cDNA
was cleaved with BamHI and XhoI. Vector: a modified
pBluescript KS(+) after bulk excision from Lambda FLC I."

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## ORIGIN

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QY      1 CAAAGGAGCAGGGAAGAAGG 20

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Db 92 CAAAGGAGCAGGAGGAGG 111  
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Search completed: May 26, 2004, 22:44:29  
Job time : 711.154 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 26, 2004, 16:00:31 ; Search time 425.652 Seconds  
(without alignments)  
2036.547 Million cell updates/sec

Title: US-09-121-239-14

Perfect score: 20

Sequence: 1 CCTTCTTCCTGCTCCTTTG 20

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 3470272 seqs, 21671516995 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

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1: gb\_ba.\*

2: gb\_hg.\*

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4: gb\_om.\*

5: gb\_ov.\*

6: gb\_pat.\*

7: gb\_ph.\*

8: gb\_pl.\*

9: gb\_pr.\*

10: gb\_ro.\*

11: gb\_sta.\*

12: gb\_sy.\*

13: gb\_un.\*

14: gb\_vi.\*

15: em\_ba.\*

16: em\_fun.\*

17: em\_hum.\*

18: em\_in.\*

19: em\_mu.\*

20: em\_om.\*

21: em\_or.\*

22: em\_ov.\*

23: em\_pat.\*

24: em\_ph.\*

25: em\_pl.\*

26: em\_ro.\*

27: em\_sta.\*

28: em\_un.\*

29: em\_vi.\*

30: em\_hg\_hum.\*

31: em\_hg\_inv.\*

32: em\_hg\_other.\*

33: em\_hg\_mus.\*

34: em\_hg\_pln.\*

35: em\_hg\_rod.\*

36: em\_hg\_mam.\*

37: em\_hg\_vrt.\*

38: em\_sy.\*

39: em\_hgo\_hum.\*

40: em\_hgo\_mus.\*

41: em\_hgo\_other.\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
C 1	20	100.0	20	6	BD222535	BD222535 Methods f
C 2	20	100.0	20	6	BD222536	BD222536 Methods f
C 3	20	100.0	20	6	BD222537	BD222537 Methods f
C 4	20	100.0	299	6	BD222547	BD222547 Methods f
C 5	20	100.0	532	9	HUMABEBA	M14753 Human abl m
C 6	20	100.0	1346	10	BC005711	BC005711 Mus muscu
C 7	20	100.0	2795	9	HUMABL1B	M17310 Human c-abl
C 8	20	100.0	35737	10	AL732315	AL732315 Mouse DNA
C 9	20	100.0	35962	6	AX598662	AX598662 Sequence
C 10	20	100.0	35962	9	HSABLGR1	U07561 Human ABL g
C 11	20	100.0	79302	2	AC023898	AC023898 Mus muscu
C 12	20	100.0	158264	2	AC015497	AC015497 Homo sapi
C 13	20	100.0	173463	9	AL359092	AL359092 Human DNA
C 14	20	100.0	235338	2	AL357893	AL357893 Homo sapi
C 15	19	95.0	136641	2	AC114327	AC114327 Canis fam
C 16	19	95.0	171026	9	AL590416	AL590416 Human DNA
C 17	19	95.0	184509	2	AC113237	AC113237 Canis fam
C 18	18	90.0	396	6	AX337450	AX337450 Sequence
C 19	18	90.0	543	11	G28197	G28197 human STS S
C 20	18	90.0	1345	6	AX380370	AX380370 Sequence
C 21	18	90.0	1726	6	AX832877	AX832877 Sequence
C 22	18	90.0	1726	9	AK094084	AK094084 Homo sapi
C 23	18	90.0	1835	9	BC004172	BC004172 Homo sapi
C 24	18	90.0	1835	9	BC019324	BC019324 Homo sapi
C 25	18	90.0	1869	6	AR339213	AR339213 Sequence
C 26	18	90.0	3868	9	AL627389	AL627389 Human DNA
C 27	18	90.0	3994	10	AL714015	AL714015 Mouse DNA
C 28	18	90.0	87430	9	AL139400	AL139400 Human DNA
C 29	18	90.0	142422	9	AC113935	AC113935 Homo sapi
C 30	18	90.0	158911	2	AC113803	AC113803 Rattus no
C 31	18	90.0	161692	2	AL138797	AL138797 Homo sapi
C 32	18	90.0	172613	9	AC093433	AC093433 Homo sapi
C 33	18	90.0	173995	2	AC073027	AC073027 Homo sapi
C 34	18	90.0	184660	2	AC123734	AC123734 Mus muscu
C 35	18	90.0	189149	2	AC046171	AC046171 Homo sapi
C 36	18	90.0	189616	2	AC128538	AC128538 Rattus no
C 37	18	90.0	203295	10	AL663049	AL663049 Mouse DNA
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C 40	18	90.0	209083	10	AC113999	AC113999 Mus muscu
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C 42	18	90.0	218127	2	AC132713	AC132713 Rattus no
C 43	18	90.0	218800	2	AC094410	AC094410 Rattus no
C 44	18	90.0	237998	2	BX544886	BX544886 Mus muscu
C 45	18	90.0	238075	2	AC127907	AC127907 Rattus no

ALIGNMENTS

RESULT 1  
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LOCUS BD222535 20 bp DNA linear PAT 17-JUL-2003  
DEFINITION Methods for detecting and measuring spliced nucleic acids.  
ACCESSION BD222535  
VERSION BD222535.1 GI:33032305  
KEYWORDS JP 2002521037-A/13.  
SOURCE synthetic construct  
ORGANISM artificial sequences.  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Harvey, R.C. and Eastman, P.S.  
TITLE Methods for detecting and measuring spliced nucleic acids  
JOURNAL Patent: JP 2002521037-A 13 16-JUL-2002;  
GEN PROBE INC

```

COMMENT      OS      Artificial Sequence
PN      JP 2002521037-A/13
PD      16-JUL-2002
PF      23-JUL-1999 JP 2000561364
PR      23-JUL-1998 US 09/121239
PI      RICHARD C HARVEY,PAUL S EASTMAN
PC      C12Q1/68,C12N15/09,C12N15/00
CC      Description of Artificial Sequence: Primer sequence for abl-1
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source      Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1 CCTCTTCCTCGTCTCCTTTG 20
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LOCUS      20 bp      DNA      linear      PAT 17-JUL-2003
DEFINITION      Methods for detecting and measuring spliced nucleic acids.
ACCESSION      BD222536
VERSION      BD222536.1 GI:33032306
KEYWORDS      JP 2002521037-A/14.
SOURCE      synthetic construct
            artificial sequences.
ORGANISM      1 (bases 1 to 20)
REFERENCE      Harvey,R.C. and Eastman,P.S.
AUTHORS      Methods for detecting and measuring spliced nucleic acids
TITLE      Patent: JP 2002521037-A 14 16-JUL-2002;
JOURNAL      GEN PROBE INC
COMMENT      OS      Artificial Sequence
PN      JP 2002521037-A/14
PD      16-JUL-2002
PF      23-JUL-1999 JP 2000561364
PR      23-JUL-1998 US 09/121239
PI      RICHARD C HARVEY,PAUL S EASTMAN
PC      C12Q1/68,C12N15/09,C12N15/00
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Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db      1 CCTCTTCCTCGTCTCCTTTG 20
RESULT 3
BD222537
LOCUS      20 bp      RNA      linear      PAT 17-JUL-2003

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DEFINITION      Methods for detecting and measuring spliced nucleic acids.
ACCESSION      BD222537
VERSION      BD222537.1 GI:33032307
KEYWORDS      JP 2002521037-A/15.
SOURCE      synthetic construct
            artificial sequences.
ORGANISM      1 (bases 1 to 20)
REFERENCE      Harvey,R.C. and Eastman,P.S.
AUTHORS      Methods for detecting and measuring spliced nucleic acids
TITLE      Patent: JP 2002521037-A 15 16-JUL-2002;
JOURNAL      GEN PROBE INC
COMMENT      OS      Artificial Sequence
PN      JP 2002521037-A/15
PD      16-JUL-2002
PF      23-JUL-1999 JP 2000561364
PR      23-JUL-1998 US 09/121239
PI      RICHARD C HARVEY,PAUL S EASTMAN
PC      C12Q1/68,C12N15/09,C12N15/00
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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1 CCTCTTCCTCGTCTCCTTTG 20
Db      1 CCTCTTCCTCGTCTCCTTTG 20
RESULT 4
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LOCUS      299 bp      DNA      linear      PAT 17-JUL-2003
DEFINITION      Methods for detecting and measuring spliced nucleic acids.
ACCESSION      BD222547
VERSION      BD222547.1 GI:33032317
KEYWORDS      JP 2002521037-A/25.
SOURCE      Homo sapiens
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
ORGANISM      1 (bases 1 to 299)
REFERENCE      Harvey,R.C. and Eastman,P.S.
AUTHORS      Methods for detecting and measuring spliced nucleic acids
TITLE      Patent: JP 2002521037-A 25 16-JUL-2002;
JOURNAL      GEN PROBE INC
COMMENT      OS      Homo sapiens (human)
PN      JP 2002521037-A/25
PD      16-JUL-2002
PF      23-JUL-1999 JP 2000561364
PR      23-JUL-1998 US 09/121239
PI      RICHARD C HARVEY,PAUL S EASTMAN
PC      C12Q1/68,C12N15/09,C12N15/00
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Best Local Similarity 100.0%; Pred. No. 43;
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QY 1 CCTTCTCCCTGCTCTCTTG 20
Db 103 CCTTCTCCCTGCTCTCTTG 84

RESULT 5
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LOCUS HUMABLA 532 bp mRNA linear PRI 30-OCT-1994
DEFINITION Human abl mRNA containing alternative first exons.
ACCESSION M14753
VERSION M14753.1 GI:177945
KEYWORDS c-myc proto-oncogene; protein kinase.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
1 (bases 1 to 532)
AUTHORS Shtivelman, E., Lifshitz, B., Gale, R.P., Roe, B.A. and Canaani, E.
TITLE Alternative splicing of RNAs transcribed from the human abl gene
and from the bcr-abl fused gene
JOURNAL Cell 47 (2), 277-284 (1986)
MEDLINE 87028219
PUBMED 3021337
COMMENT Original source text: Human cDNA to mRNA, clone K8.
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Best Local Similarity 100.0%; Pred. No. 35;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCCCTGCTCTCTTG 20
Db 428 CCTTCTCCCTGCTCTCTTG 409

RESULT 6
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LOCUS BC005711 1346 bp mRNA linear ROD 03-OCT-2003
DEFINITION Mus musculus RIKEN cDNA 2310044P18 gene, mRNA (cDNA clone MGC:11770
IMAGE:3497962), complete cds.
ACCESSION BC005711
VERSION BC005711.1 GI:13543068
KEYWORDS MGC.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 1346)
AUTHORS Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.P., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, P.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Kettelman, M., Madan, A., Rodriguez, S.,
Sanchez, A., Whitting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smalusz, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
22388257
JOURNAL
MEDLINE
PUBMED
REFERENCE
2 (bases 1 to 1346)
AUTHORS Strausberg, R.
TITLE Direct Submission
JOURNAL Submitted (02-APR-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
REMARK
NIN-MGC Project URL: http://mgc.nci.nih.gov
COMMENT Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulaeged, H.,
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
A.N., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAK Plate: 16 Row: n Column: 3
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 21450212.

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## ORIGIN

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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1189 CCTTCTTCCCTGCTCCTTTG 1170

## RESULT 7

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LOCUS HUMABLIB 2795 bp DNA linear PRI 30-OCT-1994  
DEFINITION Human c-abl gene, exon 1b.  
ACCESSION M17310  
VERSION M17310.1 GI:177941

KEYWORDS  
abl proto-oncogene; c-myc proto-oncogene; cellular oncogene;  
proto-oncogene; translocation.

SOURCE  
Homo sapiens (human)

REFERENCE  
1 (bases 2778 to 2795)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS  
Paskind,M.

JOURNAL  
Unpublished (1987)

REFERENCE  
2 (bases 1 to 2777)

AUTHORS  
Bernards,A., Rubin,C.M., Westbrook,C.A., Paskind,M. and  
Baltimore,D.

TITLE  
The first intron in the human c-abl gene is at least 200 kilobases  
long and is a target for translocations in chronic myelogenous  
leukemia

JOURNAL  
Mol. Cell. Biol. 7 (9), 3231-3236 (1987)

MEDLINE  
88038877

PUBMED  
3313010

COMMENT  
Original source text: Human DNA, clone pHER7.5.  
Draft entry and computer-readable sequence [2],[1] kindly submitted  
by A. Bernards (23-OCT-1987).

## FEATURES

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751..2162

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intron  
2163..>2795

intron  
/notes="ABL1"

ORIGIN  
About 0.1 kb downstream from XhoI site; chromosome 9q34.

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Best Local Similarity 100.0%; Pred. No. 19;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTTCCCTGCTCCTTTG 20

Db 2114 CCTTCTTCCCTGCTCCTTTG 2095

## RESULT 8

AL732315

LOCUS

DEFINITION

Mouse DNA sequence from clone RP23-124N11 on chromosome 11,

complete sequence.

ACCESSION

AL732315

VERSION

AL732315.7 GI:23337296

KEYWORDS

HTG.

SOURCE

Mus musculus (house mouse)

ORGANISM

Mus musculus

REFERENCE

1 (bases 1 to 35737)

AUTHORS

Phillimore,B.

TITLE

Direct Submission

JOURNAL

Submitted (26-SEP-2002) Wellcome Trust Sanger Institute, Hinxton,

Cambridgeshire, CB10 1SA, UK. E-mail enquiries:

humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk

On Sep 27, 2002 this sequence version replaced gi:22798063.

----- Genome Center

Center: Wellcome Trust Sanger Institute

Center code: SC

Web site: http://www.sanger.ac.uk

Contact: humquery@sanger.ac.uk

-----

During sequence assembly data is compared from overlapping clones.  
Where differences are found these are annotated as variations  
together with a note of the overlapping clone name. Note that the  
variation annotation may not be found in the sequence submission  
corresponding to the overlapping clone, as we submit sequences with  
only a small overlap as described above.  
This sequence was finished as follows unless otherwise noted: all  
regions were either double-stranded or sequenced with an alternate  
chemistry or covered by high quality data (i.e., phred quality >=  
30); an attempt was made to resolve all sequencing problems, such  
as compressions and repeats; all regions were covered by at least  
one plasmid subclone or more than one M13 subclone; and the  
assembly was confirmed by restriction digest. The following  
abbreviations are used to associate primary accession numbers given  
in the feature table with their source databases: Em:, EMBL; Sw:,  
SWISSPROT; Tr:, TrEMBL; Wp:, WORMPEP; Information on the WORMPEP  
database can be found at  
http://www.sanger.ac.uk/Projects/C\_elegans/wormpep RP23-124N11 is  
from the RPCI-23 Mouse PAC Library  
constructed by the group of Pieter de Jong.  
For further details see http://www.chori.org/bacpac/home.htm  
VECTOR: pBACE3.6.

## FEATURES

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1..35737  
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## ORIGIN

Query Match 100.0%; Score 20; DB 10; Length 35737;  
Best Local Similarity 100.0%; Pred. No. 7; 6;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTTCCCTGCTCCTTTG 20

DB 19459 CCTTCTTCCCTGCTCCTTTG 19478

## RESULT 9

AX598662/c

LOCUS

AX598662 35962 bp DNA linear PAT 14-FEB-2003

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DEFINITION Sequence 2 from Patent WO02077272.
ACCESSION AX598662
VERSION AX598662.1 GI:28398798
KEYWORDS Homo sapiens (human)
SOURCE ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Berlin,K., Braun,A., Distler,J., Guetig,D., Howe,A., Mueller,J.,
Olek,A., Piepenbrock,C., Adorjan,P., Grabs,G., Lesche,R., Leu,E.,
Lewin,A., Lipscher,E., Maier,S., Model,F., Mueller,V., Otto,T.,
Pellet,C. and Ziebarth,H.
TITLE Methods and nucleic acids for the analysis of hematopoietic cell
proliferative disorders
JOURNAL Patent: WO 02077272-A 2 03-OCT-2002;
FEATURES source
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ORIGIN
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Best Local Similarity 100.0%; Pred. No. 7.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCTCTCCCTCCTCTCTTG 20
Db 29219 CCTCTCTCCCTCCTCTTG 29200

RESULT 10
HSABLGR1/c
LOCUS 35962 bp DNA linear PRI 16-APR-2002
DEFINITION Human ABL gene, exon 1b and intron 1b, and putative M8604 Met
protein (M8604 Met) gene, complete cds.
ACCESSION U07561
VERSION U07561.1 GI:514262
KEYWORDS
SEGMENT 1 of 3
SOURCE ORGANISM
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 35962)
AUTHORS Chisoe,S.L., Bodenteich,A., Wang,Y., Jian,L., Burian,D.,
Carttree,J.S., Freeman,A., Hamed,O.S., McLaury,H., Pan,H., Toth,S.,
Wang,Z., Zhang,G., Clifton,S., Groffen,J., Heisterkamp,N. and
Roe,B.A.
TITLE Sequence and analysis of the human ABL gene, the BCR gene, and
regions involved in the Philadelphia chromosome translocation
JOURNAL Genomics 27 (1), 67-82 (1995)
MEDLINE 95394474
PUBMED 7665185
REFERENCE 2 (bases 1 to 35962)
AUTHORS Groffen,J., Heisterkamp,N., Grosveld,P., Van de Ven,W. and
Stephenson,J.R.
TITLE Isolation of human oncogene sequences (v-fes homolog) from a cosmid
library
JOURNAL Science 216 (4550), 1136-1138 (1982)
MEDLINE 82199444
PUBMED 6281890
REFERENCE 3 (bases 1 to 35962)
AUTHORS Morris,C.M., Heisterkamp,N., Groffen,J. and Fitzgerald,P.H.
TITLE Entire ABL gene is joined with 5'-BCR in some patients with
Philadelphia-positive leukemia
JOURNAL Blood 78 (4), 1078-1084 (1991)
MEDLINE 91329820
PUBMED 1868241
REFERENCE 4 (bases 27793 to 28338; 28792 to 29265)
AUTHORS Shiveimean,E., Lifshitz,B., Gale,R.P., Roe,B.A. and Canaani,B.

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TITLE Alternative splicing of RNAs transcribed from the human abl gene
and from the bcr-abl fused gene
JOURNAL Cell 47 (2), 277-284 (1986)
MEDLINE 87028219
PUBMED 3021337
REFERENCE 5 (bases 27108 to 29899)
AUTHORS Bernards,A., Rubin,C.M., Westbrook,C.A., Paskind,M. and
Baltimore,D.
TITLE The first intron in the human c-abl gene is at least 200 kilobases
long and is a target for translocations in chronic myelogenous
leukemia
JOURNAL Mol. Cell. Biol. 7 (9), 3231-3236 (1987)
MEDLINE 88038877
PUBMED 3313010
REFERENCE 6 (bases 1 to 35962)
AUTHORS Mount,S.M.
TITLE A catalogue of splice junction sequences
JOURNAL Nucleic Acids Res. 10 (2), 459-472 (1982)
MEDLINE 82150208
PUBMED 7063411
REFERENCE 7 (bases 1 to 35962)
AUTHORS Adams,M.D., Dubnick,M., Kervage,A.R., Moreno,R., Kelley,J.M.,
Utterback,T.R., Nagle,J.W., Fields,C. and Venter,J.C.
TITLE Sequence identification of 2,375 human brain genes
JOURNAL Nature 355 (6361), 632-634 (1992)
MEDLINE 92168112
PUBMED 1538749
REFERENCE 8 (bases 1 to 35962)
AUTHORS Zhu,Q.S., Heisterkamp,N. and Groffen,J.
TITLE Characterization of the human ABL promoter regions
JOURNAL Oncogene 5 (6), 885-891 (1990)
MEDLINE 90295283
PUBMED 2163052
REFERENCE 9 (bases 1 to 35962)
AUTHORS Paskind,M.
TITLE Personal communication
JOURNAL Unpublished
REFERENCE 10 (bases 1 to 35962)
AUTHORS Tatusov,R. and Lipman,D.J.
TITLE Using local similarities for pattern detection in
nucleotide/protein sequences
JOURNAL Unpublished
REFERENCE 11 (bases 1 to 35962)
AUTHORS Groffen,J., Stephenson,J.R., Heisterkamp,N., de Klein,A.,
Bartram,C.R. and Grosveld,G.
TITLE Philadelphia chromosome breakpoints are clustered within a limited
region, bcr, on chromosome 22
JOURNAL Cell 36 (1), 93-99 (1984)
MEDLINE 84106827
PUBMED 6319012
REFERENCE 12 (bases 1 to 35962)
AUTHORS Chisoe,S.L.
TITLE Sequence of the human abl and bcr genes
JOURNAL Thesis (1994) University of Oklahoma
REFERENCE 13 (bases 1 to 35962)
AUTHORS Roe,B.A.
TITLE Direct Submission
JOURNAL Submitted (08-MAR-1994) Bruce A. Roe, Dept. of Chem. and Biochem.,
University of Oklahoma, 620 Parrington Oval, Rm 208, Norman, OK
73019, USA
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Best Local Similarity 100.0%; Pred. No. 7.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTTCCTGCTCTTTG 20
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Db 29219 CCTTCTTCCTGCTCTTTG 29200

RESULT 11
AC023898 79302 bp DNA linear HTG 16-OCT-2001
LOCUS Mus musculus clone RP23-281H12, *** SEQUENCING IN PROGRESS ***, 27
DEFINITION unorderd pieces.
ACCESSION AC023898
VERSION AC023898.7 GI:16118065
KEYWORDS HTG; HTGS_PHASE1.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 79302)
AUTHORS Metzker,M.L., Lewis,L.R., Hume,J., Edwards,C., Harris,C.,
Dederich,D., Thomas,S., Okwuonu,G., Carlock,C., Garner,T.,
Addison,S., Pace,A., Williams,G., Bonnin,D., Brooks,A., Brown,J.,
Buhay,C., Bunac,C., Burkett,C., Chacko,J., Chen,G., Chen,Z.,
Cox,C., Davis,C., Delgado,O., Ding,Y., Dugan-Rocha,S.,
Fernandez,C., Ferraguto,D., Forcum-Tansey,J., Gill,R.,
Gorrell,J.H., Gunaratne,P., Haller,G., Hernandez,J., Hogues,M.,
Kovar,H., Hou,X., Huber,J., Jackson,L., Jia,Y., Kelly,J., Kelly,S.,
Kovak,C., Liu,J., Liu,W., Louissegh,H., Lozado,R.J., Martin,R.,
Massey,E., McLeod,M.P., Mei,G., Moore,S., Morgan,M., Morris,S.,
Neal,D., Nelson,A., Nguyen,R., Nguyen,N., Oguh,M., Parish,B.,
Perez,L., Reiter,D., Say,J., Shen,H., Vasquez,L., Watlington,S.,
Williamson,A., Wrensford,G., Zhou,X., Bouck,J., Hodgson,A.,
Muzny,D.M., Rives,M., Scherer,S., Sodergren,E., Weinstock,G.,
Worley,K. and Gibbs,R.
Direct Submission
Unpublished
REFERENCE 2 (bases 1 to 79302)
Worley,K.C.
Direct Submission
Submitted (20-FEB-2000) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Oct 14, 2001 this sequence version replaced gi:11079363.

----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: MABD
Center clone name: RP23-281H12
----- Summary Statistics
Sequencing vector: M13; L08821
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Chemistry: Dye-primer Bodipy: 90% of reads  
 Chemistry: Dye-terminator Big Dye: 10% of reads  
 Assembly program: Phrap; version 0.990329  
 Consensus quality: 96352 bases at least Q40  
 Consensus quality: 119814 bases at least Q30  
 Consensus quality: 130654 bases at least Q20  
 Estimated insert size: 106265; sum-of-contigs estimation  
 Quality coverage: 0x in Q20 bases; agarose-fp estimation  
 Quality coverage: 1.5x in Q20 bases; sum-of-contigs estimation

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 \* NOTE: Estimated insert size may differ from sequence length  
 \* (see [http://www.hgsc.bcm.tmc.edu/docs/genbank\\_draft\\_data.html](http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html)).  
 \* NOTE: This is a 'working draft' sequence. It currently  
 \* consists of 27 contigs. The true order of the pieces  
 \* is not known and their order in this sequence record is  
 \* arbitrary. Gaps between the contigs are represented as  
 \* runs of N, but the exact sizes of the gaps are unknown.  
 \* This record will be updated with the finished sequence,  
 \* as soon as it is available and the accession number will  
 \* be preserved.

1 2726: contig of 2726 bp in length  
 2727 2826: gap of unknown length  
 2827 6807: contig of 3981 bp in length  
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 10328 10427: gap of unknown length  
 10428 14551: contig of 4124 bp in length  
 14552 14651: gap of unknown length  
 14652 17638: contig of 2987 bp in length  
 17639 17738: gap of unknown length  
 17739 23092: contig of 5354 bp in length  
 23093 23192: gap of unknown length  
 23193 25970: contig of 2778 bp in length  
 25971 26070: gap of unknown length  
 26071 28815: contig of 2745 bp in length  
 28816 32008: contig of 3093 bp in length  
 32009 32108: gap of unknown length  
 32109 35879: contig of 3771 bp in length  
 35880 39175: gap of unknown length  
 39176 39275: gap of unknown length  
 39276 41989: contig of 2714 bp in length  
 41990 42089: gap of unknown length  
 42090 44449: contig of 2360 bp in length  
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 44550 47065: contig of 2516 bp in length  
 47066 47165: gap of unknown length  
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 49294 49393: gap of unknown length  
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 52056 54245: contig of 2190 bp in length  
 54246 54345: gap of unknown length  
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 57159 57258: gap of unknown length  
 57259 60206: contig of 2948 bp in length  
 60207 62463: contig of 2157 bp in length  
 62464 62563: gap of unknown length  
 62564 64983: contig of 2420 bp in length  
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 65084 67808: contig of 2725 bp in length  
 67809 70294: gap of unknown length  
 70295 70394: contig of 2386 bp in length  
 70395 72500: contig of 2106 bp in length  
 72501 74613: gap of unknown length  
 74614 74713: gap of unknown length  
 74714 77134: contig of 2421 bp in length  
 77135 77234: gap of unknown length  
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RESULT 12  
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 pieces.  
 AC015497 158264 bp DNA linear HTG 11-APR-2000  
 AC015497.3 GI:75333974  
 VERSION HTG; HTGS\_PHASE1; HTGS\_DRAFT.  
 KEYWORDS Homo sapiens (human)  
 SOURCE  
 ORGANISM  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 158264)  
 AUTHORS Birren,B., Linton,L., Nusbaum,C. and Lander,E.  
 TITLE Homo sapiens, clone RP11-21G10  
 JOURNAL Unpublished  
 REFERENCE 2 (bases 1 to 158264)  
 AUTHORS Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M.,  
 Baldwin,J., Barna,N., Beckerly,R., Boguslavskiy,L., Boukhgalter,B.,  
 Brown,A., Castle,A., Colangelo,M., Collins,S., Collymore,A.,  
 Cooke,P., Dearellano,K., Dewar,K., Domino,M., Donelan,L., Doyle,M.,  
 Ferreira,P., FitzHugh,W., Forrest,C., Funke,R., Gage,D.,  
 Galagan,J., Gardyna,S., Grant,G., Hags,B., Heaford,A., Horton,L.,  
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 Lehotzky,J., Lieu,C., Locke,K., MacDonald,P., Marquis,N.,  
 McEwan,P., McGurk,A., McKernan,K., McLaughlin,J., Meldrum,J.,  
 Morrow,J., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,  
 Peterson,K., Pollara,V., Riley,R., Roy,A., Santos,R., Severy,P.,  
 Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,  
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 Wyman,D., Ye,W.J., Zimmer,A. and Zody,M.  
 DIRECT SUBMISSION  
 TITLE  
 JOURNAL  
 COMMENT  
 Submitted (16-NOV-1999) Whitehead Institute/MIT Center for Genome  
 Research, 320 Charles Street, Cambridge, MA 02141, USA  
 On Apr 11, 2000 this sequence version replaced gi:6587901.  
 All repeats were identified using RepeatMasker:  
 Smit, A.F.A. & Green, P. (1996-1997)  
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>  
 ----- Genome Center  
 Center: Whitehead Institute/ MIT Center for Genome Research  
 Center code: WIBR  
 Web site: <http://www-seq.wi.mit.edu>  
 Contact: [sequence\\_submissions@genome.wi.mit.edu](mailto:sequence_submissions@genome.wi.mit.edu)  
 ----- Project Information  
 Center project name: L4002  
 Center clone name: 21 G 10  
 ----- Summary Statistics  
 Sequencing vector: M13; W7815; 100% of reads  
 Chemistry: Dye-terminator Big Dye; 100% of reads  
 Assembly program: Phrap; version 0.960731  
 Consensus quality: 118404 bases at least Q40  
 Consensus quality: 139706 bases at least Q30  
 Consensus quality: 149210 bases at least Q20  
 Insert size: 111000; agarose-fp  
 Inset size: 155664; sum-of-contigs  
 Quality coverage: 5.1 in Q20 bases; agarose-fp

Quality coverage: 3.6 in Q20 bases; sum-of-contigs

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\* NOTE: This is a 'working draft' sequence. It currently consists of 27 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

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 \* 2209: gap of 100 bp  
 \* 2309: gap of 100 bp  
 \* 2310: contig of 1015 bp in length  
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 \* 3425: contig of 100 bp  
 \* 4909: contig of 1485 bp in length  
 \* 5009: gap of 100 bp  
 \* 5010: contig of 1218 bp in length  
 \* 6227: gap of 100 bp  
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 \* 6328: contig of 1238 bp in length  
 \* 7565: gap of 100 bp  
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 \* 8896: contig of 1991 bp in length  
 \* 10887: contig of 100 bp  
 \* 10987: contig of 2269 bp in length  
 \* 13255: gap of 100 bp  
 \* 13256: contig of 3119 bp in length  
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 \* 19837: gap of 100 bp  
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 \* 39138: gap of 100 bp  
 \* 39238: contig of 5714 bp in length  
 \* 44951: gap of 100 bp  
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 \* 45052: gap of 100 bp  
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 \* 55556: contig of 6068 bp in length  
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 \* 68825: gap of 100 bp  
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 \* 77617: gap of 100 bp  
 \* 77618: contig of 9282 bp in length  
 \* 86999: gap of 100 bp  
 \* 87000: contig of 13223 bp in length  
 \* 87100: gap of 100 bp  
 \* 100322: contig of 13223 bp in length  
 \* 100323: gap of 100 bp  
 \* 100423: contig of 13123 bp in length  
 \* 113546: gap of 100 bp  
 \* 113546: contig of 12825 bp in length  
 \* 126471: gap of 100 bp  
 \* 126471: contig of 31694 bp in length.  
 \* 126571: 158264: contig of 31694 bp in length.

FEATURES  
 source

1. .158264  
 /organism="Homo sapiens"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:9606"  
 /clone="RP11-21G10"  
 /clone\_lib="RP11-11 Human Male BAC"  
 misc\_feature 1. .1059  
 /notes="assembly\_fragment"  
 misc\_feature 1200. .2209

misc\_feature /note="assembly\_fragment"  
 2310. .3324  
 misc\_feature /note="assembly\_fragment"  
 3425. .4909  
 misc\_feature /note="assembly\_fragment"  
 5010. .6227  
 misc\_feature /note="assembly\_fragment"  
 6328. .7565  
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 7666. .8795  
 misc\_feature /note="assembly\_fragment"  
 8896. .10886  
 misc\_feature /note="assembly\_fragment"  
 10987. .13255  
 misc\_feature /note="assembly\_fragment"  
 13356. .16474  
 misc\_feature /note="assembly\_fragment"  
 16575. .19836  
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 19937. .23049  
 misc\_feature /note="assembly\_fragment"  
 23150. .26628  
 misc\_feature /note="assembly\_fragment"  
 26729. .30236  
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 30337. .33987  
 misc\_feature /note="assembly\_fragment"  
 34088. .39137  
 misc\_feature /note="assembly\_fragment"  
 39238. .44951  
 misc\_feature /note="assembly\_fragment"  
 45052. .50383  
 misc\_feature /note="assembly\_fragment"  
 50484. .55555  
 misc\_feature /note="assembly\_fragment"  
 55656. .61723  
 misc\_feature /note="assembly\_fragment"  
 61824. .68824  
 misc\_feature /note="assembly\_fragment"  
 68925. .77617  
 misc\_feature /note="assembly\_fragment"  
 77718. .86999  
 misc\_feature /note="assembly\_fragment"  
 clone\_end:SP6  
 vector\_side:right"  
 87100. .100322  
 misc\_feature /note="assembly\_fragment"  
 100423. .113545  
 misc\_feature /note="assembly\_fragment"  
 113646. .126470  
 misc\_feature /note="assembly\_fragment"  
 clone\_end:T7  
 vector\_side:right"  
 126571. .158264  
 misc\_feature /note="assembly\_fragment"

ORIGIN

Query Match 100.0%; Score 20; DB 2; Length 158264;  
 Best Local Similarity 100.0%; Pred. No. 4.4;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCCCTGCTCTTGG 20  
 |||

Db 66378 CCTTCTCCCTGCTCTTGG 66359

RESULT 13  
 AL359092/c 173463 bp DNA linear PRI 17-MAR-2001  
 LOCUS Human DNA sequence from clone Rp11-57C19 on chromosome 9, complete  
 DEFINITION sequence.  
 ACCESSION AL359092  
 VERSION AL359092.14 GI:13274746



```
repeat_region /notes="AluSx repeat: matches 1. .298 of consensus"
39792. .40097
repeat_region /notes="AluSg repeat: matches 1. .304 of consensus"
40138. .40411
repeat_region /notes="AluY repeat: matches 39. .310 of consensus"
40416. .40636
repeat_region /notes="L1M4 repeat: matches 4539. .4769 of consensus"
40825. .41072
misc_feature /notes="L1 repeat: matches 3771. .4023 of consensus"
complement(40954. .41169)
misc_feature /notes="match: STS: Em:G08714"
complement(40988. .41142)
misc_feature /notes="match: GSS: Em:AZ640566"
40993. .41171
misc_feature /notes="match: GSS: Em:AZ040457"
complement(41024. .41169)
misc_feature /notes="match: STS: Em:G08716"
41025. .41164
misc_feature /notes="match: GSS: Em:AZ838018 Em:AZ838106"
41028. .41169
misc_feature /notes="match: GSS: Em:AZ020257"
complement(41028. .41163)
misc_feature /notes="match: GSS: Em:AZ056687"
complement(41028. .41155)
misc_feature /notes="match: GSS: Em:AZ179869"
complement(41038. .41160)
misc_feature /notes="match: GSS: Em:AZ838018 Em:AZ838106"
41040. .41151
misc_feature /notes="match: STS: Em:L30635"
41041. .41179
misc_feature /notes="match: GSS: Em:AZ921614"
complement(41041. .41171)
misc_feature /notes="match: GSS: Em:AZ035323"
41041. .41169
misc_feature /notes="match: STS: Em:L17666"
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misc_feature /notes="match: GSS: Em:AZ644560"
41052. .41170
misc_feature /notes="match: GSS: Em:AZ975962"
41059. .41222
misc_feature /notes="match: GSS: Em:AZ060388"
complement(41059. .41171)
misc_feature /notes="match: GSS: Em:AZ881617"
complement(41068. .41175)
misc_feature /notes="match: GSS: Em:AZ640589"
complement(41068. .41171)
misc_feature /notes="match: STS: Em:G07990 Em:G07994 Em:G09150"
complement(41069. .41218)
misc_feature /notes="match: GSS: Em:AZ318431"
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Query Match 100.0%; Score 20; DB 9; Length 173463;
Best Local Similarity 100.0%; Pred.No. 4.2;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 CCTCTTCCTGCTCCTTG 20
|||||
Db 109250 CCTCTTCCTGCTCCTTG 109231
```

```
RESULT 14
AL357893
LOCUS AL357893 235338 bp DNA linear HTG 10-JUL-2001
DEFINITION Homo sapiens chromosome 9 clone RP11-253A1, 29 unordered pieces.
ACCESSION AL357893
VERSION AL357893.8 GI:14586541
KEYWORDS HTG; HTGS_PHASE1; HTGS_CANCELLED.
SOURCE Homo sapiens (human)
```

```
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Plumb,B.
TITLE Direct Submission
```

## JOURNAL

## COMMENT

Submitted (09-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk  
On Jul 3, 2001 this sequence version replaced gi:14575206.  
----- Genome Center  
Center: Sanger Centre  
Center code: SC  
Web site: http://www.sanger.ac.uk  
Contact: humquery@sanger.ac.uk  
----- Project Information  
Center project name: BA253A1  
----- Summary Statistics  
Assembly program: XGAP4; version 4.5  
Sequencing vector: plasmid; L08752; 100% of reads  
Chemistry: Dye-terminator Big Dye; 100% of reads  
Consensus quality: 113075 bases at least Q40  
Consensus quality: 120255 bases at least Q30  
Consensus quality: 124314 bases at least Q20  
Insert size: 232538; sum-of-contigs  
Insert size: 166097; 3.1% error; agarose-fp  
Quality coverage: 1.72x in Q20 bases; sum-of-contigs Quality coverage: 2.59x in Q20 bases; agarose-fp  
-----

\* NOTE: This is a 'working draft' sequence. It currently consists of 29 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

1 5789: contig of 5789 bp in length  
\* 5790 5889: gap of 100 bp  
\* 5890 9227: contig of 3338 bp in length  
\* 9228 9327: gap of 100 bp  
\* 9328 15450: contig of 6123 bp in length  
\* 15451 15550: gap of 100 bp  
\* 15551 24512: contig of 8962 bp in length  
\* 24513 24612: gap of 100 bp  
\* 24613 33357: contig of 8745 bp in length  
\* 33358 33457: gap of 100 bp  
\* 33458 45426: contig of 11969 bp in length  
\* 45427 45526: gap of 100 bp  
\* 45527 48337: contig of 2811 bp in length  
\* 48338 48437: gap of 100 bp  
\* 48438 51040: contig of 2603 bp in length  
\* 51041 51141: gap of 100 bp  
\* 51141 53592: contig of 2452 bp in length  
\* 53593 53693: gap of 100 bp  
\* 53693 56387: contig of 2694 bp in length  
\* 56387 56486: gap of 100 bp  
\* 56487 62895: contig of 6509 bp in length  
\* 62896 63095: gap of 100 bp  
\* 63096 66160: contig of 3084 bp in length  
\* 66160 66259: gap of 100 bp  
\* 66260 69523: contig of 3264 bp in length  
\* 69524 74715: contig of 5092 bp in length  
\* 74716 74815: gap of 100 bp  
\* 74816 83735: contig of 8919 bp in length  
\* 83735 83834: gap of 100 bp  
\* 83835 87462: contig of 3627 bp in length  
\* 87462 87562: contig of 31512 bp in length  
\* 87562 119073: gap of 100 bp  
\* 119074 123743: contig of 4570 bp in length  
\* 123744 123843: gap of 100 bp  
\* 123844 129766: contig of 5923 bp in length  
\* 129767 129866: gap of 100 bp  
\* 129867 142567: contig of 12701 bp in length  
\* 142568 151783: contig of 9116 bp in length  
\* 151784 151883: gap of 100 bp

```

* 151884 165129: contig of 13246 bp in length
* 165130 165229: gap of 100 bp
* 165230 169016: contig of 3787 bp in length
* 169017 169116: gap of 100 bp
* 169117 172815: contig of 3699 bp in length
* 172816 172915: gap of 100 bp
* 172916 178100: contig of 5185 bp in length
* 178101 178200: gap of 100 bp
* 178201 186238: contig of 8038 bp in length
* 186239 186338: gap of 100 bp
* 186339 189386: contig of 3048 bp in length
* 189387 189486: gap of 100 bp
* 189487 217139: contig of 27653 bp in length
* 217140 217239: gap of 100 bp
* 217240 235338: contig of 18099 bp in length.
FEATURES
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        1. .235338
            /organism="Homo sapiens"
            /mol_type="genomic DNA"
            /db_xref="taxon:9606"
            /chromosome="9"
            /clone="RP11-253A1"
            /clone_lib="RPC1-11.1"
            1. .5789
            /note="assembly_fragment:01637"
            clone_end:17
            vector_side:left
            5890. .9227
            /note="assembly_fragment:00699"
            fragment_chain:1
            9328. .15450
            /note="assembly_fragment:00899"
            fragment_chain:1
            1551. .24512
            /note="assembly_fragment:01643"
            fragment_chain:2
            24613. .33357
            /note="assembly_fragment:01662"
            fragment_chain:2
            33458. .45426
            /note="assembly_fragment:01699"
            fragment_chain:3
            45527. .48337
            /note="assembly_fragment:01712"
            fragment_chain:3
            48438. .51040
            /note="assembly_fragment:00070"
            51141. .53592
            /note="assembly_fragment:00277"
            53693. .56386
            /note="assembly_fragment:00560"
            56487. .62995
            /note="assembly_fragment:00561.0"
            63096. .66159
            /note="assembly_fragment:00630"
            66260. .69523
            /note="assembly_fragment:00835"
            69624. .74715
            /note="assembly_fragment:00836"
            74816. .83734
            /note="assembly_fragment:01652"
            83835. .87461
            /note="assembly_fragment:01659"
            87562. .119073
            /note="assembly_fragment:01666"
            119174. .123743
            /note="assembly_fragment:01715"
            123844. .129766
            /note="assembly_fragment:01719"
            129867. .142567
            /note="assembly_fragment:01724"
            142688. .151783
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```

```

misc_feature 151884. .165129
              /note="assembly_fragment:01756"
misc_feature 165230. .169016
              /note="assembly_fragment:01773"
misc_feature 169117. .172815
              /note="assembly_fragment:01777"
misc_feature 172916. .178100
              /note="assembly_fragment:01781"
misc_feature 178201. .186238
              /note="assembly_fragment:01788"
misc_feature 186339. .189386
              /note="assembly_fragment:01796"
misc_feature 189487. .217139
              /note="assembly_fragment:01799.0"
misc_feature 217240. .235338
              /note="assembly_fragment:01800"
ORIGIN
Query Match      100.0%; Score 20; DB 2; Length 235338;
Best Local Similarity 100.0%; Pred. No. 3.8;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1 CCTCTCTCCCTGCTCCTTGG 20
        |||||
Db      41866 CCTTCTTCCTGCTCCTTGG 41885

RESULT 15
AC114327/c
LOCUS      AC114327
DEFINITION Canis familiaris clone RP81-158C13, WORKING DRAFT SEQUENCE, 2
            AC114327
            136641 bp DNA linear HTG 07-MAR-2002
            Canis familiaris clone RP81-158C13, WORKING DRAFT SEQUENCE, 2
            unordered pieces.
ACCESSION      AC114327
VERSION      AC114327.1 GI:19224976
KEYWORDS      HTG; HTGS PHASE1; HTGS_DRAFT.
SOURCE      Canis familiaris (dog)
ORGANISM      Canis familiaris
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE      1 (bases 1 to 136641)
AUTHORS      Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
            Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
            Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
            Ho,S.-L., Idol,J.R., Karlins,E., Laric,P., Lee-Lin,S.-Q.,
            Legaspi,R., Maduro,Q.L., Maduro,V.B., Masiello,C., Maskeri,B.,
            Mastrian,S.D., McCloskey,J.C., McDowell,J., Pearson,R., Prasad,A.,
            Stantripop,S., Thomas,J.W., Thomas,P.J., Touchman,J.W.,
            Tsurgon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
            Young,A., Zhang,L.-H. and Green,E.D.
            NISC Comparative Sequencing Initiative
            Unpublished
            2 (bases 1 to 136641)
            Green,E.D.
            Direct Submission
            Submitted (07-MAR-2002) NIH Intramural Sequencing Center, 8717
            Groveomitted Circle, Gaithersburg, MD 20877, USA
            ----- Genome Center
            Center: NIH Intramural Sequencing Center
            Center code: NISC
            Web site: http://www.nisc.nih.gov
            Contact: nisc_mouse@nigrl.nih.gov
            ----- Project Information
            Center project name: cin
            Center clone name: 158C13
            ----- Summary Statistics
            Sequencing vector: plasmid; n/a; 100% of reads
            Chemistry: Dye-terminator Big Dye; 100% of reads
            Assembly program: Phrap; version 0.990319
            Consensus quality: 136372 bases at least Q40
            Consensus quality: 136409 bases at least Q30
            Consensus quality: 136413 bases at least Q20
            Insert size: 109000; agarose-fp
            Insert size: 136541; sum-of-contigs

```

Quality coverage: 12.91x in Q20 bases; agarose-fp  
Quality coverage: 10.31x in Q20 bases; sum-of-contigs

-----  
\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 2 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.

\* 1 49995: contig of 49995 bp in length  
\* 49996 50095: gap of unknown length  
\* 50096 136641: contig of 86546 bp in length.

FEATURES

source

1. .136641  
/organism="Canis familiaris"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9615"  
/clone="RP81-158C13"  
/clone\_lib="RP81"

misc\_feature

1. .49995  
/note="assembly\_fragment"  
clone\_end:SP6  
vector\_side:right"  
50096..136641  
/note="assembly\_fragment"  
clone\_end:T7  
vector\_side:right"

misc\_feature

ORIGIN

Query Match 95.0%; Score 19; DB 2; Length 136641;  
Best Local Similarity 100.0%; Pred.No. 13;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CTTCTTCCCTGCTCCCTTG 20

Db 18215 CTTCTTCCCTGCTCCCTTG 18197

Search completed: May 27, 2004, 02:16:45  
Job time : 426.652 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 26, 2004, 14:55:11 ; Search time 89.1973 Seconds  
(without alignments)  
952.539 Million cell updates/sec

Title: US-09-121-239-14

Perfect score: 20

Sequence: 1 CCTCTTCCCTGCTCCTTTG 20

Scoring table: OLIGO NUC

Gapop 60.0 , Gapext 60.0

Searched: 3373863 seqs, 2124099041 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : N\_Geneseq\_29Jan04.\*  
1: Geneseqn1980s.\*  
2: Geneseqn1990s.\*  
3: Geneseqn2000s.\*  
4: Geneseqn2001as.\*  
5: Geneseqn2001bs.\*  
6: Geneseqn2002s.\*  
7: Geneseqn2003as.\*  
8: Geneseqn2003bs.\*  
9: Geneseqn2003cs.\*  
10: Geneseqn2004s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	20	100.0	20	3 AAZ60852	AAZ60852 Oligonucleotide
C 2	20	100.0	20	3 AAZ60854	AAZ60854 Oligonucleotide
C 3	20	100.0	20	3 AAZ60853	AAZ60853 Oligonucleotide
C 4	20	100.0	299	3 AAZ60864	AAZ60864 Region su
C 5	20	100.0	530	5 AAD08655	AAD08655 Mouse can
C 6	20	100.0	1538	7 ABX05481	ABX05481 Human nov
C 7	20	100.0	5434	6 ABV77964	ABV77964 Hypoxia-r
C 8	20	100.0	35962	7 ABZ09862	ABZ09862 Human 5'
C 9	18	90.0	396	6 ABU69622	ABU69622 Prostate
C 10	18	90.0	474	8 ACH32870	ACH32870 Human end
C 11	18	90.0	543	2 AAT19863	AAT19863 Human gen
C 12	18	90.0	1345	6 ABA94712	ABA94712 Human ami
C 13	18	90.0	1390	4 AAS41347	AAS41347 cDNA enco
C 14	18	90.0	1611	4 AAL06632	AAL06632 Human rep
C 15	18	90.0	1611	5 AAS40715	AAS40715 DNA enco
C 16	18	90.0	1859	4 AAK55488	AAK55488 Human inn
C 17	18	90.0	1869	4 AAI58813	AAI58813 Human pol
C 18	18	90.0	1869	8 ADB48794	ADB48794 Novel hum
C 19	18	90.0	2177	4 AAI60599	AAI60599 Human pol
C 20	18	90.0	3380	7 AB218520	AB218520 Group I II
C 21	17	85.0	416	6 ABN96456	ABN96456 Gene #295
C 22	17	85.0	36305	6 ABK22783	ABK22783 Human hlg
C 23	17	85.0	39729	9 ADC86832	ADC86832 Human gpc

## ALIGNMENTS

## RESULT 1

AAZ60852/c AAZ60852 standard; DNA; 20 BP.

XX AAZ60852;

AC AAZ60852;

XX 16-MAY-2000 (first entry)

XX Oligonucleotide used to detect bcr b3-abl fusion transcripts.

XX Fusion transcript; translocation; bcr b3 region; abl gene;

KW amplification assay; detection assay; medical diagnosis;

KW clinical monitoring; chimeric RNA; fusion RNA; condition marker;

KW disease marker; cancer; leukemia; ss.

XX Synthetic.

OS WO200005418-A1.

XX 03-FEB-2000.

PD 23-JUL-1999; 99WO-US016832.

XX 23-JUL-1998; 98US-00121239.

XX (GENP-) GEN-PROBE INC.

XX Harvey RC, Eastman PS;

XX WPI; 2000-182730/16.

XX Novel methods for preparing RNA from biological samples, used for the

XX detection and measurement of nucleic acids and fusion nucleic acids.

XX Claim 19; Page 42; 49pp; English.

XX Oligonucleotides AAZ60840-62 and AAZ60865-66 are used in the method of the invention to detect fusion transcripts produced from a translocation between the bcr b3 region and the abl gene. The specification describes a method for detecting a fusion nucleic acid (particularly chimeric mRNA species), in a biological sample. The method comprises contacting a sample of fusion nucleic acid with primers, amplifying the hybridized fusion nucleic acid, and detecting the target hybrid. The method is used for the sample and rapid preparation of RNA from a biological sample, particularly from the cytoplasm of eukaryotic cells, which is suitable for use in an amplification and detection assay. The methods are used for

CC the analysis and detection of nucleic acids in biological samples. The  
CC methods are useful in the human medical and veterinary fields, for  
CC medical diagnoses and clinical monitoring of a patient's response to  
CC therapy where a disease or medical condition is associated with a  
CC particular type and/or level of mRNA present in the sample. The methods  
CC are also useful for detecting or quantifying fusion or chimeric RNA  
CC species, and for detecting a translocation as a marker for a given  
CC condition or disease, e.g. translocations associate with cancers,  
CC particularly forms of leukemia

XX Sequence 20 BP; 9 A; 2 C; 9 G; 0 T; 0 U; 0 Other;  
SQ Query Match 100.0%; Score 20; DB 3; Length 20;  
Best Local Similarity 100.0%; Pred. No. 0.73;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCCCTGCTCCTTTG 20  
Db 20 CCTTCTCCCTGCTCCTTTG 1

RESULT 2  
AAZ60854  
ID AAZ60854 standard; RNA; 20 BP.  
XX  
AC AAZ60854;  
XX  
DT 16-MAY-2000 (first entry)  
XX  
DE Oligonucleotide used to detect bcr b3-abl fusion transcripts.  
KW Fusion transcript; translocation; bcr b3 region; abl gene;  
KW amplification assay; detection assay; medical diagnosis;  
KW clinical monitoring; chimeric RNA; fusion RNA; condition marker;  
KW disease marker; cancer; leukemia; ss.  
XX  
OS Synthetic.  
XX  
PN WO200005418-A1.  
XX  
PD 03-FEB-2000.  
XX  
PF 23-JUL-1999; 99WO-US016832.  
XX  
PR 23-JUL-1998; 98US-00121239.  
XX  
PA (GENP-) GEN-PROBE INC.  
XX  
PI Harvey RC, Eastman PS;  
XX  
DR WPI; 2000-182730/16.  
XX  
PT Novel methods for preparing RNA from biological samples, used for the  
PT detection and measurement of nucleic acids and fusion nucleic acids.  
XX  
PS Claim 19; Page 42; 49pp; English.  
XX  
CC Oligonucleotides AAZ60840-62 and AAZ60865-66 are used in the method of  
CC the invention to detect fusion transcripts produced from a translocation  
CC between the bcr b3 region and the abl gene. The specification describes a  
CC method for detecting a fusion nucleic acid (particularly chimeric mRNA  
CC species), in a biological sample. The method comprises contacting a  
CC sample of fusion nucleic acid with primers, amplifying the hybridized  
CC fusion nucleic acid, and detecting the target hybrid. The method is used  
CC for the simple and rapid preparation of RNA from a biological sample,  
CC particularly from the cytoplasm of eukaryotic cells, which is suitable  
CC for use in an amplification and detection assay. The methods are used for  
CC the analysis and detection of nucleic acids in biological samples. The  
CC methods are useful in the human medical and veterinary fields, for  
CC medical diagnoses and clinical monitoring of a patient's response to  
CC therapy where a disease or medical condition is associated with a  
CC particular type and/or level of mRNA present in the sample. The methods  
CC are also useful for detecting or quantifying fusion or chimeric RNA  
CC species, and for detecting a translocation as a marker for a given  
CC condition or disease, e.g. translocations associate with cancers,  
CC particularly forms of leukemia

CC species, and for detecting a translocation as a marker for a given  
CC condition or disease, e.g. translocations associate with cancers,  
CC particularly forms of leukemia

XX Sequence 20 BP; 0 A; 9 C; 2 G; 0 T; 9 U; 0 Other;  
SQ Query Match 100.0%; Score 20; DB 3; Length 20;  
Best Local Similarity 55.0%; Pred. No. 0.73;  
Matches 11; Conservative 9; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCCCTGCTCCTTTG 20  
Db 1 CCUUCUUCUCCUGCUCCUUG 20

RESULT 3  
AAZ60853  
ID AAZ60853 standard; DNA; 20 BP.  
XX  
AC AAZ60853;  
XX  
DT 16-MAY-2000 (first entry)  
XX  
DE Oligonucleotide used to detect bcr b3-abl fusion transcripts.  
KW Fusion transcript; translocation; bcr b3 region; abl gene;  
KW amplification assay; detection assay; medical diagnosis;  
KW clinical monitoring; chimeric RNA; fusion RNA; condition marker;  
KW disease marker; cancer; leukemia; ss.  
XX  
OS Synthetic.  
XX  
PN WO200005418-A1.  
XX  
PD 03-FEB-2000.  
XX  
PF 23-JUL-1999; 99WO-US016832.  
XX  
PR 23-JUL-1998; 98US-00121239.  
XX  
PA (GENP-) GEN-PROBE INC.  
XX  
PI Harvey RC, Eastman PS;  
XX  
DR WPI; 2000-182730/16.  
XX  
PT Novel methods for preparing RNA from biological samples, used for the  
PT detection and measurement of nucleic acids and fusion nucleic acids.  
XX  
PS Claim 19; Page 42; 49pp; English.  
XX  
CC Oligonucleotides AAZ60840-62 and AAZ60865-66 are used in the method of  
CC the invention to detect fusion transcripts produced from a translocation  
CC between the bcr b3 region and the abl gene. The specification describes a  
CC method for detecting a fusion nucleic acid (particularly chimeric mRNA  
CC species), in a biological sample. The method comprises contacting a  
CC sample of fusion nucleic acid with primers, amplifying the hybridized  
CC fusion nucleic acid, and detecting the target hybrid. The method is used  
CC for the simple and rapid preparation of RNA from a biological sample,  
CC particularly from the cytoplasm of eukaryotic cells, which is suitable  
CC for use in an amplification and detection assay. The methods are used for  
CC the analysis and detection of nucleic acids in biological samples. The  
CC methods are useful in the human medical and veterinary fields, for  
CC medical diagnoses and clinical monitoring of a patient's response to  
CC therapy where a disease or medical condition is associated with a  
CC particular type and/or level of mRNA present in the sample. The methods  
CC are also useful for detecting or quantifying fusion or chimeric RNA  
CC species, and for detecting a translocation as a marker for a given  
CC condition or disease, e.g. translocations associate with cancers,  
CC particularly forms of leukemia

XX Sequence 20 BP; 0 A; 9 C; 2 G; 9 T; 0 U; 0 Other;  
SQ



Query Match 100.0%; Score 20; DB 3; Length 20;  
Best Local Similarity 100.0%; Pred. No. 0.73;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCCCTGCTCCTTTG 20  
|||||  
DB 1 CCTTCTCCCTGCTCCTTTG 20

RESULT 4  
ID AAZ60864/c  
XX AAZ60864 standard; DNA; 299 BP.  
AC AAZ60864;  
XX  
DT 16-MAY-2000 (first entry)  
XX  
DE Region surrounding a splice junction in a normal abl transcript.  
XX  
KW Fusion transcript; translocation; bcr b3 region; abl gene;  
KW amplification assay; detection assay; medical diagnosis;  
KW clinical monitoring; chimeric RNA; fusion RNA; condition marker;  
KW disease marker; cancer; leukemia; ss.  
XX  
OS Unidentified.

XX WO200005418-A1.  
XX  
XX  
PD 03-FEB-2000.  
XX  
PF 23-JUL-1999; 99WO-US016832.  
XX  
PR 23-JUL-1998; 98US-00121239.  
XX  
PA (GENP-) GEN-PROBE INC.  
XX  
PI Harvey RC, Eastman PS;  
XX  
XX WPI; 2000-182730/16.  
XX  
PT Novel methods for preparing RNA from biological samples, used for the  
PT detection and measurement of nucleic acids and fusion nucleic acids.  
XX  
PS Disclosure; Fig 3; 49pp; English.

XX The present sequence represents a region surrounding a potential splice  
CC junction in a normal abl transcript. The specification describes  
CC oligonucleotides which are used to detect fusion transcripts produced  
CC from a translocation between the bcr b3 region and the abl gene. The  
CC specification also describes a method for detecting a fusion nucleic acid  
CC (particularly chimeric mRNA species), in a biological sample. The method  
CC comprises contacting a sample of fusion nucleic acid with primers,  
CC amplifying the hybridized fusion nucleic acid, and detecting the target  
CC hybrid. The method is used for the simple and rapid preparation of RNA  
CC from a biological sample, particularly from the cytoplasm of eukaryotic  
CC cells, which is suitable for use in an amplification and detection assay.  
CC The methods are used for the analysis and detection of nucleic acids in  
CC biological samples. The methods are useful in the human medical and  
CC veterinary fields, for medical diagnoses and clinical monitoring of a  
CC patients response to therapy where a disease or medical condition is  
CC associated with a particular type and/or level of mRNA present in the  
CC sample. The methods are also useful for detecting or quantifying fusion  
CC or chimeric RNA species, and for detecting a translocation as a marker  
CC for a given condition or disease, e.g. translocations associate with  
CC cancers, particularly forms of leukemia

XX Sequence 299 BP; 77 A; 70 C; 81 G; 71 T; 0 U; 0 Other;  
SQ  
Query Match 100.0%; Score 20; DB 3; Length 299;  
Best Local Similarity 100.0%; Pred. No. 0.67;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCCCTGCTCCTTTG 20

DB 103 CCTTCTCCCTGCTCCTTTG 84  
|||||

RESULT 5  
AAD08655/c  
ID AAD08655 standard; cDNA; 530 BP.  
XX  
AC AAD08655;  
XX  
DT 04-SEP-2001 (first entry)  
XX  
DE Mouse cancer associated antigen OY-MC-10 cDNA.  
XX  
KW Mouse; OY-MC-10; cytostatic; gene therapy; vaccine; fibrosarcoma cancer;  
KW cancer associated antigen; ss.  
XX  
OS Mus musculus.  
XX  
FH Key Location/Qualifiers  
CDS 2..484  
FT /\*tag= a  
FT /product= "Mouse OY-MC-10 protein"  
FT /note= "CDS does not include start codon"  
FT /partial

XX WO200140271-A2.  
XX  
XX 07-JUN-2001.  
XX  
XX 01-DEC-2000; 2000WO-US032750.  
XX  
XX 01-DEC-1999; 99US-0168353P.  
XX 26-APR-2000; 2000US-0059013.  
XX  
XX (LUDW-) LUDWIG INST CANCER RES.  
XX  
XX Ono T, Nakayama E;  
XX WPI; 2001-397941/42.  
XX P-PSDB; AAE04381.  
XX  
XX Isolated polypeptide, useful in treating disorders such as cancer, is  
XX encoded by a nucleic acid (NA) Group 3 or 4 molecule.

XX Claim 56; Page 117; 127pp; English.  
XX  
XX The invention relates to cancer associated antigens and their nucleic  
XX acids which are expressed in methylcholanthrene-induced fibrosarcoma  
XX cancer cells from mice. Cancer associated antigens and a pharmaceutical  
XX composition containing nucleic acid molecules encoding cancer associated  
XX antigens are used to treat a condition e.g. cancer. Cancer associated  
XX antigens, the nucleotides encoding them, antibodies against them and the  
XX pharmaceutical compositions comprising them are useful for diagnosing,  
XX monitoring and treating the diseases characterised by the expression of  
XX one or more cancer associated antigens, e.g. fibrosarcoma cancer, and for  
XX research purposes. Cancer associated antigens DNA is also useful in gene  
XX therapy. The present sequence is a cDNA encoding mouse cancer associated  
XX antigen OY-MC-10

SQ Sequence 530 BP; 138 A; 125 C; 169 G; 98 T; 0 U; 0 Other;  
Query Match 100.0%; Score 20; DB 5; Length 530;  
Best Local Similarity 100.0%; Pred. No. 0.66;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCCCTGCTCCTTTG 20  
|||||  
DB 389 CCTTCTCCCTGCTCCTTTG 370

RESULT 6  
ABX05481/c



DT 16-JAN-2003 (first entry)  
DE Human 5' and/or regulatory region of ABL1 DNA SEQ ID NO:2.  
XX  
KW Human; haematopoietic cell proliferation disorder; cytostatic;  
KW gene therapy; lymphocytic leukaemia; acute myelogenous leukaemia;  
KW cytosine methylation state; gene; ds.  
XX  
OS Homo sapiens.  
XX  
PN WO200277272-A2.  
XX  
PD 03-OCT-2002.  
XX  
PF 26-MAR-2002; 2002WO-EP003401.  
XX  
PR 26-MAR-2001; 2001US-0278333P.  
XX  
PA (EPIG-) EPIGENOMICS AG.  
XX  
PI Berlin K, Braun A, Diatler J, Guetig D, Howe A, Mueller J;  
PI Olek A, Piepenbrock C, Adorjan P, Grabs G, Lesche R, Leu E;  
PI Lewin A, Lipscher E, Maier S, Model F, Mueller V, Otto T, Pellet C;  
PI Schwobe I, Ziebarth H;  
XX  
DR WPI; 2003-018942/01.  
XX  
DT Detecting and differentiating between hematopoietic cell proliferative  
PT disorders, comprises contacting a target nucleic acid with a reagent that  
PT distinguishes between methylated and non-methylated CpG dinucleotides.  
XX  
PS Claim 38; SEQ ID NO 2; 117pp; English.  
XX  
CC The present invention describes a method for detecting and  
CC differentiating between haematopoietic cell proliferative disorders  
CC associated with at least 1 gene and/or their regulatory regions in a  
CC subject. The method comprises contacting a target nucleic acid in a  
CC biological sample obtained from the subject with at least 1 reagent,  
CC which distinguishes between methylated and non-methylated CpG  
CC dinucleotides within the target nucleic acid. ABZ09861 to ABZ11118  
CC represent specifically claimed nucleotide sequences from the present  
CC invention. Oligonucleotides from the present invention can be used: for  
CC differentiating between healthy haematopoietic cells and proliferative  
CC disorder haematopoietic cells; for differentiating between acute  
CC lymphocytic leukaemia and acute myelogenous leukaemia; as probes for  
CC determining the cytosine methylation state and/or single nucleotide  
CC polymorphisms (SNPs) of haematopoietic cell proliferation disorder  
CC related sequences and their complements; and as primers for the  
CC amplification of haematopoietic cell proliferation disorder related DNA  
CC sequences. The nucleotide sequences from the present invention can also  
CC be used for detecting a predisposition to, differentiation between  
CC subclasses, diagnosis, prognosis, treatment and/or monitoring of  
CC haematopoietic cell proliferative disorders. The present method enables a  
CC highly specific classification of haematopoietic cell proliferative  
CC disorders allowing for improved and informed treatment of patients  
XX  
SQ Sequence 35962 BP; 9078 A; 7926 C; 9130 G; 9828 T; 0 U; 0 Other;  
Query Match 100.0%; Score 20; DB 7; Length 35962;  
Best Local Similarity 100.0%; Pred. No. 0.58;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CCTTCTCCCTGCTCCTTTG 20  
Db 29219 CCTTCTCCCTGCTCCTTTG 29200  
RESULT 9  
ID ABL69622  
XX ABL69622 standard; DNA; 396 BP.  
AC ABL69622;  
XX

DT 15-MAY-2002 (first entry)  
DE Prostate cancer related gene sequence SEQ ID NO:7959.  
XX  
KW Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;  
KW stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;  
KW cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;  
KW gene; ds.  
XX  
OS Homo sapiens.  
XX  
PN WO200194629-A2.  
XX  
PD 13-DEC-2001.  
XX  
PF 30-MAY-2001; 2001WO-US010838.  
XX  
PR 05-JUN-2000; 2000US-0209473P.  
PR 05-JUN-2000; 2000US-0209531P.  
PR 18-SEP-2000; 2000US-0233133P.  
PR 18-SEP-2000; 2000US-0233617P.  
PR 20-SEP-2000; 2000US-0234009P.  
PR 20-SEP-2000; 2000US-0234034P.  
PR 20-SEP-2000; 2000US-0234052P.  
PR 22-SEP-2000; 2000US-0234509P.  
PR 22-SEP-2000; 2000US-0234567P.  
PR 25-SEP-2000; 2000US-0234923P.  
PR 25-SEP-2000; 2000US-0234924P.  
PR 25-SEP-2000; 2000US-0235077P.  
PR 25-SEP-2000; 2000US-0235082P.  
PR 25-SEP-2000; 2000US-0235134P.  
PR 25-SEP-2000; 2000US-0235280P.  
PR 26-SEP-2000; 2000US-0235637P.  
PR 26-SEP-2000; 2000US-0235638P.  
PR 27-SEP-2000; 2000US-0235711P.  
PR 27-SEP-2000; 2000US-0235720P.  
PR 27-SEP-2000; 2000US-0235840P.  
PR 28-SEP-2000; 2000US-0235863P.  
PR 28-SEP-2000; 2000US-0236028P.  
PR 28-SEP-2000; 2000US-0236032P.  
PR 28-SEP-2000; 2000US-0236033P.  
PR 28-SEP-2000; 2000US-0236034P.  
PR 28-SEP-2000; 2000US-0236109P.  
PR 28-SEP-2000; 2000US-0236111P.  
PR 29-SEP-2000; 2000US-0236842P.  
PR 29-SEP-2000; 2000US-0236891P.  
PR 02-OCT-2000; 2000US-0237172P.  
PR 02-OCT-2000; 2000US-0237173P.  
PR 02-OCT-2000; 2000US-0237278P.  
PR 02-OCT-2000; 2000US-0237294P.  
PR 02-OCT-2000; 2000US-0237295P.  
PR 03-OCT-2000; 2000US-0237316P.  
PR 03-OCT-2000; 2000US-0237425P.  
PR 03-OCT-2000; 2000US-0237598P.  
PR 03-OCT-2000; 2000US-0237604P.  
PR 03-OCT-2000; 2000US-0237606P.  
PR 03-OCT-2000; 2000US-0237608P.  
PR 01-NOV-2000; 2000US-0244867P.  
PR 01-NOV-2000; 2000US-0245084P.  
XX  
PA (AVAL-) AVALON PHARM.  
XX  
PI Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;  
PI Soppet DR, Weaver Z;  
XX  
DR WPI; 2002-188264/24.  
XX  
PT Screening for anti-neoplastic agent involves exposing cells to a chemical  
PT agent to be tested for anti-neoplastic activity, and determining a change  
PT in expression of a gene of a signature gene set.  
XX  
PS Claim 1; SEQ ID NO 7959; 44pp; English.  
XX

CC The present invention describes a method (M1) for screening for an anti-neoplastic agent. The method involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, determining a change in expression of at least one gene (I) of a signature gene set, where (I) comprises a sequence (S) selected from 8447 sequences (given in ABL61664 to ABL70110), or is at least 95% identical to (S), where a change in expression is indicative of anti-neoplastic activity. (I) has cytostatic activity and can be used in gene therapy. M1 can be used for screening an anti-neoplastic agent, and can be used for producing a product which is the data collected with respect to the anti-neoplastic agent as a result of M1, and the data is sufficient to convey the chemical structure and/or properties of the agent. M1 can be used in the treatment of cancer such as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney, prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilms' tumour

XX  
SQ Sequence 396 BP; 82 A; 129 C; 85 G; 100 T; 0 U; 0 Other;

Query Match 90.0%; Score 18; DB 6; Length 396;  
Best Local Similarity 100.0%; Pred. No. 6.7;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTCTTCCCTGCTCTTTG 20  
DB 164 TTCTTCCCTGCTCTTTG 181

RESULT 10  
ACH32870/c  
ID ACH32870 standard; cDNA; 474 BP.

AC ACH32870;  
XX  
DT 13-OCT-2003 (first entry)

DE Human endothelial cell cDNA #1003.

KW Human; ss; sequencing by hybridisation; SBH; expressed sequence tag; EST;  
XX genome mapping; biodiversity; genetic disorder.

OS Homo sapiens.

PN US2003073623-A1.

PD 17-APR-2003.

PF 30-JUL-2001; 2001US-00918995.

PR 30-JUL-2001; 2001US-00918995.

XX (DRMA/) DRMANAC R T.

PA (LABA/) LABAT I.

PA (STAC/) STACHE-CRAIN B.

PA (DICK/) DICKSON M C.

PA (JONE/) JONES L W.

XX Drmanac RT, Labat I, Stache-Crain B, Dickson MC, Jones LW;

XX WPI; 2003-615964/58.

XX New polynucleotide sequences obtained from various cDNA libraries, useful as hybridization probes, as oligomers for PCR, for chromosome and gene mapping, in the recombinant production of protein, or in generating antisense DNA or RNA.

XX Claim 1; SEQ ID NO 20082; 44pp; English.

XX The invention relates to an isolated polynucleotide comprising any one of 38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence was determined by the technique of SBH (sequencing by hybridisation). Also included is a purified polypeptide comprising a sequence corresponding to

CC a reading frame of the novel polynucleotide. The nucleic acid sequences are useful in diagnostics as expressed sequence tags (EST) for identifying expressed genes or for physical mapping of the human genome, in forensics, in assessing biodiversity, or in identifying mutations responsible for genetic disorders and other traits. The nucleotide sequences are also useful as hybridisation probes, as oligomers for PCR, for chromosome and gene mapping, in the recombinant production of protein, or in generating antisense DNA or RNA. The purified polypeptide is useful for generating antibodies specific for it. The present sequence is one of the 38043 isolated cDNA/EST sequences. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at seqdata.uspto.gov/sequence.html?DocID=20030073623

XX  
SQ Sequence 474 BP; 118 A; 117 C; 145 G; 92 T; 0 U; 2 Other;

Query Match 90.0%; Score 18; DB 8; Length 474;  
Best Local Similarity 100.0%; Pred. No. 6.7;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTCTTCCCTGCTCTTTG 20  
DB 348 TTCTTCCCTGCTCTTTG 331

RESULT 11  
AAT19863/c  
ID AAT19863 standard; cDNA to mRNA; 543 BP.

AC AAT19863;

DT 26-JUL-1996 (first entry)

DE Human gene signature HUMGS00986.

KW Gene signature; messenger RNA; mRNA; relative abundance; frequency;  
XX human; cloning; mapping; non-biased library; diagnosis; detection;  
XX cell typing; abnormal cell function; ss.

OS Homo sapiens.

PN W09514772-A1.

XX 01-JUN-1995.

PD 11-NOV-1994; 94WO-JP001916.

PF 12-NOV-1993; 93JP-00355504.

PR (MATS/) MATSUBARA K.

XX (OKUB/) OKUBO K.

XX Matsubara K, Okubo K;

XX WPI; 1995-206931/27.

XX Single-stranded DNA for identifying gene signatures - isolated from 3'-directed human cDNA library that reflects relative abundance of corresp. mRNA in specific human tissues.

XX Claim 1; Page 489; 2245pp; Japanese.

XX A single-stranded DNA (or its complementary strand or the corresp. double-stranded DNA) which comprises one of the 7837 "GS" sequences given in AAT19001-T26837 and which is able to hybridise to part of human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature) sequences were obtained from 3'-directed cDNA libraries prepared from various human tissues; synthesis of cDNA was initiated from the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'- untranslated sequence is unique to a particular mRNA species, almost all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library is constructed so as to reflect accurately the relative abundance of different mRNAs in the particular tissue from which it was derived. The appearance frequency of a given GS

CC in a cDNA library can be determined (esp. using primers and probes  
 CC derived from the GS sequences) as a means of diagnosing abnormal cell  
 CC function or for recognising different cell types  
 SQ Sequence 543 BP; 119 A; 115 C; 153 G; 142 T; 0 U; 14 Other;  
 Query Match 90.0%; Score 18; DB 2; Length 543;  
 Best Local Similarity 100.0%; Pred. No. 6.6;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 TTCTTCCCTGCTCCTTTG 20  
 |||||  
 DB 371 TTCTTCCCTGCTCCTTTG 354  
 |||||  
 RESULT 12  
 ID ABA94712/c  
 ID ABA94712 standard; cDNA; 1345 BP.  
 XX ABA94712;  
 AC ABA94712;  
 DT 23-APR-2002 (first entry)  
 DE Human aminoacyl tRNA synthetase (ATRS) encoding cDNA (ID: 1554103CB1).  
 XX Aminoacyl tRNA synthetase; ATRS; antiallergic; antianemic; antiaesthetic;  
 KW osteopathic; antirheumatic; antiarthritic; dermatological; nephrotropic;  
 KW antiinflammatory; vulnerary; antibacterial; virucide; antiparasitic;  
 KW protozoacide; fungicide; antihelminthic; cytostatic; human; enzyme;  
 KW antiarteriosclerotic; hepatotropic; gene therapy; vaccine; ss.  
 XX Homo sapiens.  
 OS Homo sapiens.  
 FH Key Location/Qualifiers  
 FT CDS 1..1269  
 FT /\*tag= a  
 FT /\*product= "ATRS"  
 XX  
 PN WO200204611-A2.  
 XX  
 PD 17-JAN-2002.  
 XX  
 PF 29-JUN-2001; 2001WO-US020723.  
 XX  
 PR 07-JUL-2000; 2000US-0216748P.  
 PR 18-JUL-2000; 2000US-0219019P.  
 PR 04-AUG-2000; 2000US-0223058P.  
 PR 21-SEP-2000; 2000US-0234693P.  
 PR 11-OCT-2000; 2000US-0239797P.  
 XX  
 PA (INCY-) INCYTE GENOMICS INC.  
 PI Lee EA, Tang YT, Lu DAM, Tribouley CM, Gandhi AR, Lu Y;  
 PI Baughn WR, Warren BA, Thornton M, Yue H, Hillman JU, Patterson C;  
 PI Elliott VS, Thangavelu K, Ramkumar J, Wallia NK, Yao MG;  
 DR WPI; 2002-164640/21.  
 DR P-PSDB; ABB07509.  
 XX  
 PT Novel human aminoacyl tRNA synthetases and polynucleotides encoding the  
 PT enzymes, useful for treating, diagnosing or preventing  
 PT autoimmune/inflammatory and cell proliferative disorders.  
 XX  
 PS Claim 5; Page 105; 107pp; English.  
 CC The invention provides human aminoacyl tRNA synthetase (ATRS)  
 CC polypeptides and polynucleotides. The ATRS polypeptides can be expressed  
 CC by standard recombinant methodology. Compositions comprising the  
 CC polypeptide or its modulators are useful for treating a disease or  
 CC condition associated with decreased or increased expression of functional  
 CC ATRS. Compositions comprising antibodies specific for ATRS is useful for  
 CC diagnosing a condition or disease associated with the expression of ATRS  
 CC in a subject. The ATRS polypeptides and polynucleotides are useful for

CC diagnosing, treating and preventing autoimmune/inflammatory (allergies,  
 CC anemia, asthma, osteoporosis, rheumatoid arthritis, atopic dermatitis,  
 CC glomerulonephritis and irritable bowel syndrome, trauma, and bacterial,  
 CC viral, parasitic, protozoal, fungal or helminthic infections), and cell  
 CC proliferative (e.g. cancer, atherosclerosis, and hepatitis). The ATRS  
 CC polypeptides are useful in drug screening techniques, and to analyse the  
 CC proteome of a tissue or cell type. The present sequence represents a  
 CC human ATRS polynucleotide sequence  
 SQ Sequence 1345 BP; 349 A; 300 C; 410 G; 286 T; 0 U; 0 Other;  
 Query Match 90.0%; Score 18; DB 6; Length 1345;  
 Best Local Similarity 100.0%; Pred. No. 6.4;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 TTCTTCCCTGCTCCTTTG 20  
 |||||  
 DB 1172 TTCTTCCCTGCTCCTTTG 1155  
 |||||  
 RESULT 13  
 ID AAS41347/c  
 ID AAS41347 standard; cDNA; 1390 BP.  
 XX AAS41347;  
 AC AAS41347;  
 DT 17-DEC-2001 (first entry)  
 DE cDNA encoding novel human enzyme polypeptide #563.  
 XX Human; oxidoreductase enzyme; transferase; hydrolase; lyase; isomerase;  
 KW ligase; hyperproliferative disorder; immunodeficiency disorder;  
 KW autoimmune disorder; neurological disorder; metabolic disorder;  
 KW inflammatory disorder; cardiovascular disorder; reproductive disorder;  
 KW blood-related disorder; infectious disorder; gene therapy; cytostatic;  
 KW anti arthritic; nephrotropic; anticoagulant; ss.  
 XX Homo sapiens.  
 OS Homo sapiens.  
 PN WO200155301-A2.  
 XX  
 PD 02-AUG-2001.  
 XX  
 PF 17-JAN-2001; 2001WO-US001239.  
 XX  
 PR 31-JAN-2000; 2000US-0179065P.  
 PR 04-FEB-2000; 2000US-0180628P.  
 PR 24-FEB-2000; 2000US-0184664P.  
 PR 02-MAR-2000; 2000US-0186350P.  
 PR 16-MAR-2000; 2000US-0189874P.  
 PR 17-MAR-2000; 2000US-0190076P.  
 PR 18-APR-2000; 2000US-0198123P.  
 PR 19-MAY-2000; 2000US-0205515P.  
 PR 07-JUN-2000; 2000US-0209467P.  
 PR 28-JUN-2000; 2000US-0214886P.  
 PR 30-JUN-2000; 2000US-0215135P.  
 PR 07-JUL-2000; 2000US-0215647P.  
 PR 07-JUL-2000; 2000US-0216880P.  
 PR 11-JUL-2000; 2000US-0217487P.  
 PR 11-JUL-2000; 2000US-0217496P.  
 PR 14-JUL-2000; 2000US-0218290P.  
 PR 26-JUL-2000; 2000US-0220963P.  
 PR 26-JUL-2000; 2000US-0220964P.  
 PR 14-AUG-2000; 2000US-0224518P.  
 PR 14-AUG-2000; 2000US-0224519P.  
 PR 14-AUG-2000; 2000US-0225213P.  
 PR 14-AUG-2000; 2000US-0225214P.  
 PR 14-AUG-2000; 2000US-0225266P.  
 PR 14-AUG-2000; 2000US-0225267P.  
 PR 14-AUG-2000; 2000US-0225268P.  
 PR 14-AUG-2000; 2000US-0225270P.  
 PR 14-AUG-2000; 2000US-0225447P.  
 PR 14-AUG-2000; 2000US-0225757P.

PR 14-AUG-2000; 2000US-0225758P.  
 PR 14-AUG-2000; 2000US-0225759P.  
 PR 18-AUG-2000; 2000US-0226279P.  
 PR 22-AUG-2000; 2000US-0226681P.  
 PR 22-AUG-2000; 2000US-0226868P.  
 PR 22-AUG-2000; 2000US-0227182P.  
 PR 23-AUG-2000; 2000US-0227009P.  
 PR 30-AUG-2000; 2000US-0228924P.  
 PR 01-SEP-2000; 2000US-0229287P.  
 PR 01-SEP-2000; 2000US-0229343P.  
 PR 01-SEP-2000; 2000US-0229344P.  
 PR 01-SEP-2000; 2000US-0229345P.  
 PR 05-SEP-2000; 2000US-0229509P.  
 PR 05-SEP-2000; 2000US-0229513P.  
 PR 06-SEP-2000; 2000US-0230437P.  
 PR 06-SEP-2000; 2000US-0230438P.  
 PR 08-SEP-2000; 2000US-0231124P.  
 PR 08-SEP-2000; 2000US-0231124P.  
 PR 08-SEP-2000; 2000US-0231243P.  
 PR 08-SEP-2000; 2000US-0231244P.  
 PR 08-SEP-2000; 2000US-0231413P.  
 PR 08-SEP-2000; 2000US-0231414P.  
 PR 08-SEP-2000; 2000US-0232080P.  
 PR 08-SEP-2000; 2000US-0232081P.  
 PR 12-SEP-2000; 2000US-0231968P.  
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(HUMA-) HUMAN GENOME SCI INC.

Rosen CA, Barash SC, Ruben SM;

WPI; 2001-465566/50.

P-PSDB; AAU23477.

Novel polypeptides and polynucleotides useful for diagnosing, preventing, treating neural, immune system, muscular, reproductive, pulmonary, cardiovascular, renal, proliferative disorders and cancerous diseases.

Claim 4; SEQ ID NO 573; 1180pp; English.

The present invention relates to the isolation of novel human enzyme polypeptides (AAU22915-AAU23814), and the cDNA and genomic sequences encoding them. The enzyme polypeptides of the invention may comprise the functional classes of oxidoreductases, transferases, hydrolases, lyases, isomerases or ligases. The sequences of the invention are useful in the diagnosis, treatment, prevention and/or prognosis of a wide range of disorders including hyperproliferative disorders (e.g. cancer), immunodeficiency disorders (e.g. AIDS) autoimmune disorders (e.g. arthritis), neurological disorders (e.g. Alzheimer's disease), metabolic disorders (e.g. phenylketonuria), inflammatory disorders (e.g. asthma), cardiovascular disorders (e.g. atherosclerosis), blood-related disorders (e.g. haemophilia), reproductive disorders (e.g. infertility) and infectious disorders (e.g. Influenza). The polynucleotides of the invention can also be used in gene therapy. AAU20785-AAU41684 represent cDNA sequences encoding for the novel human enzyme polypeptides of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

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RESULT 14

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AC AAL06632;

DT 21-NOV-2001 (first entry)

DE Human reproductive system related antigen DNA SEQ ID NO: 9320.

XX Human; reproductive system related antigen; reproductive system disorder;  
 cancer; gene therapy; ds.

OS Homo sapiens.

PN WO200155320-A2.

XX 02-AUG-2001.

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XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX PA
XX PI Rosen CA, Barash SC, Ruben SM;
XX XX
DR WPI; 2001-465570/50.
XX
XX PT Isolated nucleic acid molecule encoding a reproductive system antigen is
XX PT used in preventing, treating or ameliorating a medical condition.
XX
XX PS Disclosure; SEQ ID NO 9320; 1297pp + Sequence Listing; English.
XX
XX CC The present invention provides the protein and coding sequences of a
XX CC number of human reproductive system related antigens. These can be used
XX CC in the prevention and treatment of reproductive system disorders,
XX CC including cancer. The present sequence is a genomic sequence encoding a
XX CC protein of the invention
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Db      166 TTCTTCCCTGCTCCTTTG 183
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XX AC AAS40715;
XX
XX DT 17-DEC-2001 (first entry)
XX
XX DE DNA encoding human prostate cancer antigen, Seq ID No 867.
XX
XX DE Human; prostate cancer antigen; cytostatic; uropathic; diagenosic;
XX KW reproductive system; chromosomal marker; forensic; urinary disorder;
XX KW chronic nephritis; blood-related disorder; thrombosis; ds.
XX
XX OS Homo sapiens.
XX
XX PN WO200155316-A2.
XX
XX PD 02-AUG-2001.
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XX PF 17-JAN-2001; 2001WO-US001328.
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XX PF 31-JAN-2000; 2000US-0179065P.
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C 4	15	75.0	533	US-09-621-976-159	Sequence 159, Appl
C 5	15	75.0	9217	US-09-634-238-402	Sequence 402, Appl
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C 24	14	70.0	41100	US-09-755-665-46	Sequence 46, Appl
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C	35	13	65.0	418	4	US-09-621-976-16177	Sequence 16177, A
C	36	13	65.0	438	4	US-09-621-976-1841	Sequence 1841, Ap
C	37	13	65.0	447	4	US-09-621-976-8713	Sequence 8713, Ap
C	38	13	65.0	462	4	US-09-621-976-15146	Sequence 15146, A
C	39	13	65.0	463	3	US-09-104-308-3	Sequence 3, Appl
C	40	13	65.0	463	3	US-09-321-981-3	Sequence 3, Appl
C	41	13	65.0	463	4	US-09-739-861A-3	Sequence 3, Appl
C	42	13	65.0	463	4	US-09-795-583-3	Sequence 3, Appl
C	43	13	65.0	511	4	US-09-404-879A-70	Sequence 70, Appl
C	44	13	65.0	511	4	US-09-338-933-70	Sequence 70, Appl
C	45	13	65.0	511	4	US-09-215-681-70	Sequence 70, Appl

## ALIGNMENTS

RESULT 1  
US-09-620-312D-704/c  
; Sequence 704, Application US/09620312D  
; Patent No. 6569662  
; GENERAL INFORMATION:  
; APPLICANT: Tang, Y. Tom  
; APPLICANT: Liu, Chenghua  
; APPLICANT: Asundi, Vinod  
; APPLICANT: Zhang, Jie  
; APPLICANT: Ren, Feiyan  
; APPLICANT: Chen, Rui-hong  
; APPLICANT: Zhao, Qing A.  
; APPLICANT: Wehrman, Tom  
; APPLICANT: Xue, Aidong J.  
; APPLICANT: Yang, Yonghong  
; APPLICANT: Wang, Jian-Rui  
; APPLICANT: Zhou, Ping  
; APPLICANT: Ma, Yuning  
; APPLICANT: Wang, Dunrui  
; APPLICANT: Wang, Zhiwei  
; APPLICANT: John Tillinghast  
; APPLICANT: Drmanac, Radoje T.  
; TITLE OF INVENTION: No. 6569662el Nucleic Acids and  
; FILE REFERENCE: 784CIP2B  
; CURRENT APPLICATION NUMBER: US/09/620,312D  
; CURRENT FILING DATE: 2000-07-19  
; PRIOR APPLICATION NUMBER: 09/552,317  
; PRIOR FILING DATE: 2000-04-25  
; PRIOR APPLICATION NUMBER: 09/488,725  
; PRIOR FILING DATE: 2000-01-21  
; NUMBER OF SEQ ID NOS: 1105  
; SOFTWARE: pt\_FL\_genes Version 1.0  
; SEQ ID NO 704  
; LENGTH: 1869  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (161)..(1792)  
US-09-620-312D-704

Query Match 90.0%; Score 18; DB 4; Length 1869;  
Best Local Similarity 100.0%; Pred.No. 0.4;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TTCTTCCCTGCTCCTTTG 20

Db 1695 TTCTTCCCTGCTCCTTTG 1678

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RESULT 2
US-09-676-610B-24
; Sequence 24, Application US/09676610B
; Patent No. 644465
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Jacqueline Wyatt
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: OLIGONUCLEOTIDE INHIBITION OF HER-1 EXPRESSION
; FILE REFERENCE: RTS-0138
; CURRENT APPLICATION NUMBER: US/09/676,610B
; CURRENT FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 182
; SEQ ID NO 24
; LENGTH: 169998
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: exon
; LOCATION: (1208)...(1472)
; NAME/KEY: intron
; LOCATION: (1473)...(124390)
; NAME/KEY: exon
; LOCATION: (124391)...(124544)
; NAME/KEY: intron
; LOCATION: (124545)...(125409)
; NAME/KEY: exon
; LOCATION: (125410)...(125595)
; NAME/KEY: intron
; LOCATION: (125596)...(128711)
; NAME/KEY: exon
; LOCATION: (128712)...(128848)
; NAME/KEY: intron
; LOCATION: (128849)...(133400)
; NAME/KEY: exon
; LOCATION: (133401)...(133469)
; NAME/KEY: intron
; LOCATION: (133470)...(134652)
; NAME/KEY: exon
; LOCATION: (134653)...(134773)
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; LOCATION: (134774)...(136116)
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; LOCATION: (136117)...(136261)
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; LOCATION: (136262)...(137936)
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; NAME/KEY: exon
; LOCATION: (138638)...(138766)
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; LOCATION: (139766)...(139860)
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; LOCATION: (139861)...(142245)
; NAME/KEY: exon
; LOCATION: (142246)...(142445)
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; LOCATION: (142446)...(143605)
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; LOCATION: (143606)...(143738)
; NAME/KEY: intron
; LOCATION: (143739)...(145838)
; NAME/KEY: exon
; LOCATION: (145839)...(145931)
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; NAME/KEY: intron
; LOCATION: (145932)...(147385)
; NAME/KEY: exon
; LOCATION: (147386)...(147544)
; NAME/KEY: intron
; LOCATION: (147545)...(153274)
; NAME/KEY: exon
; LOCATION: (153275)...(153321)
; NAME/KEY: intron
; LOCATION: (153322)...(155088)
; NAME/KEY: exon
; LOCATION: (155089)...(155231)
; NAME/KEY: intron
; LOCATION: (155232)...(156025)
; NAME/KEY: exon
; LOCATION: (156026)...(156151)
; NAME/KEY: intron
; LOCATION: (156152)...(156826)
; NAME/KEY: exon
; LOCATION: (156827)...(156928)
; NAME/KEY: intron
; LOCATION: (156929)...(163399)
; NAME/KEY: exon
; LOCATION: (163400)...(163586)
US-09-676-610B-24

Query Match      80.0%; Score 16; DB 4; Length 169998;
Best Local Similarity 100.0%; Pred. No. 5.1;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 TTCTTCCCTGCTCCTT 18
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Db      89308 TTCTTCCCTGCTCCTT 89323

RESULT 3
US-09-877-177A-10
; Sequence 10, Application US/09877177A
; Patent No. 6582919
; GENERAL INFORMATION:
; APPLICANT: K. Danenberg
; TITLE OF INVENTION: Method of determining Epidermal Growth
; TITLE OF INVENTION: Factor Receptor and HER2-Neu Gene Expression
; TITLE OF INVENTION: and Correlation of Levels Thereof With Survival
; FILE REFERENCE: 11220/120
; CURRENT APPLICATION NUMBER: US/09/877,177A
; CURRENT FILING DATE: 2001-06-11
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 197496
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-877-177A-10

Query Match      80.0%; Score 16; DB 4; Length 197496;
Best Local Similarity 100.0%; Pred. No. 5.1;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 TTCTTCCCTGCTCCTT 18
        |||||
Db      97308 TTCTTCCCTGCTCCTT 97323

RESULT 4
US-09-621-976-159/c
; Sequence 159, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
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FILE REFERENCE: GENSET.054PR2  
CURRENT APPLICATION NUMBER: US/09/621,976  
CURRENT FILING DATE: 2000-07-21  
NUMBER OF SEQ ID NOS: 19335  
SOFTWARE: Patent.pm  
SEQ ID NO 159  
LENGTH: 533  
TYPE: DNA  
ORGANISM: Homo sapiens  
NAME/KEY: CDS  
LOCATION: 55..531  
NAME/KEY: sig\_peptide  
LOCATION: 55..378  
OTHER INFORMATION: Von Heijne matrix  
OTHER INFORMATION: score 5.5  
OTHER INFORMATION: seq RFECLSLSPGVRG/LK  
US-09-621-976-159

Query Match 75.0%; Score 15; DB 4; Length 533;  
Best Local Similarity 100.0%; Pred. No. 15;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CTTCTTCCTGCTCC 16  
Db 217 CTTCTTCCTGCTCC 203

RESULT 5  
US-09-634-238-402/c  
Sequence 402, Application US/09634238  
Patent No. 6544772  
GENERAL INFORMATION:  
APPLICANT: Glenn, Matthew  
APPLICANT: Havukkala, Ilkka J.  
APPLICANT: Bloksberg, Leonard, N.  
APPLICANT: Lubbers, Mark W.  
APPLICANT: Dekker, James  
APPLICANT: Christensen, Anna C.  
APPLICANT: Holland, Ross  
APPLICANT: O'Toole, Paul W.  
APPLICANT: Reid, Julian R.  
APPLICANT: Coolbear, Timothy  
TITLE OF INVENTION: Polynucleotides, materials incorporating  
TITLE OF INVENTION: them and methods for using them.  
FILE REFERENCE: 11000.1043U1  
CURRENT APPLICATION NUMBER: US/09/634,238  
CURRENT FILING DATE: 2000-08-08  
NUMBER OF SEQ ID NOS: 422  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 402  
LENGTH: 9217  
TYPE: DNA  
ORGANISM: Lactobacillus rhamnosus  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1)...(9217)  
OTHER INFORMATION: n = A,T,C or G  
US-09-634-238-402

Query Match 75.0%; Score 15; DB 4; Length 9217;  
Best Local Similarity 100.0%; Pred. No. 16;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CTTCCCTGCTCCTTT 19  
Db 180 CTTCCCTGCTCCTTT 166

RESULT 6  
US-09-313-294A-6758/c  
Sequence 6758, Application US/09313294A  
Patent No. 6476212

GENERAL INFORMATION:  
APPLICANT: Lalgudi, Raghunath V.  
APPLICANT: Ito, Laura Y.  
APPLICANT: Sherman, Bradley K.  
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR  
FILE REFERENCE: PL-0017 US  
CURRENT APPLICATION NUMBER: US/09/313,294A  
CURRENT FILING DATE: 1999-05-14  
NUMBER OF SEQ ID NOS: 7600  
SOFTWARE: PERL Program  
SEQ ID NO 6758  
LENGTH: 303  
TYPE: DNA  
ORGANISM: Zea mays  
FEATURE:  
NAME/KEY: misc\_feature  
OTHER INFORMATION: Incyte ID No. 6476212 700352349H1  
NAME/KEY: unsure  
LOCATION: 164-165, 169, 179, 189-190, 200, 206, 209, 221, 262  
OTHER INFORMATION: a, t, c, g, or other  
US-09-313-294A-6758

Query Match 70.0%; Score 14; DB 4; Length 303;  
Best Local Similarity 100.0%; Pred. No. 50;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTCTTCCTGCT 14  
Db 116 CTTCTTCCTGCT 103

RESULT 7  
US-08-691-814B-105  
Sequence 105, Application US/08691814B  
Patent No. 5981218  
GENERAL INFORMATION:  
APPLICANT: Rio, Marie-Christine  
APPLICANT: Tomasetto, Catherine  
APPLICANT: Bassett, Paul  
APPLICANT: Byrne, Jennifer  
TITLE OF INVENTION: Isolated Nucleic Acid Molecules Useful  
TITLE OF INVENTION: as Leukemia Markers and in Breast Cancer Prognosis  
NUMBER OF SEQUENCES: 124  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.  
STREET: 1100 New York Ave, NW, Suite 600  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005-3934  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/691,814B  
FILING DATE: 31-JUL-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/002,183  
FILING DATE: 09-AUG-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Steffe, Eric K.  
REGISTRATION NUMBER: 36,688  
REFERENCE/DOCKET NUMBER: 1383.0090001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-2600  
TELEFAX: 202-371-2543  
INFORMATION FOR SEQ ID NO: 105:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 418 base pairs  
TYPE: nucleic acid



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; OTHER INFORMATION: Where n is a, c, g or t
; NAME/KEY: modified_base
; LOCATION: (672)
; OTHER INFORMATION: Where n is a, c, g or t
US-09-123-912-33

Query Match          70.0%; Score 14; DB 4; Length 673;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 TTCCCTGCTCCCTTT 19
Db      142 TTCCCTGCTCCCTTT 129

RESULT 11
US-09-643-597-33/c
; Sequence 33, Application US/09643597
; Patent No. 6426072
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy R.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C11
; CURRENT APPLICATION NUMBER: US/09/643,597
; CURRENT FILING DATE: 2000-08-21
; NUMBER OF SEQ ID NOS: 369
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 33
; LENGTH: 673
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(673)
; OTHER INFORMATION: n = A,T,C or G
US-09-643-597-33

Query Match          70.0%; Score 14; DB 4; Length 673;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 TTCCCTGCTCCCTTT 19
Db      142 TTCCCTGCTCCCTTT 129

RESULT 12
US-09-480-884A-33/c
; Sequence 33, Application US/09480884A
; Patent No. 6482597
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Hosken, Nancy A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY
; FILE REFERENCE: 210121.455C6
; CURRENT APPLICATION NUMBER: US/09/480,884A
; CURRENT FILING DATE: 2001-08-27
; NUMBER OF SEQ ID NOS: 330
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; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 33
; LENGTH: 673
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(673)
; OTHER INFORMATION: n = A,T,C or G
US-09-480-884A-33

Query Match          70.0%; Score 14; DB 4; Length 673;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 TTCCCTGCTCCCTTT 19
Db      142 TTCCCTGCTCCCTTT 129

RESULT 13
US-09-542-615A-33/c
; Sequence 33, Application US/09542615A
; Patent No. 6518256
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy A.
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY
; FILE REFERENCE: 210121.455C8
; CURRENT APPLICATION NUMBER: US/09/542,615A
; CURRENT FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 33
; LENGTH: 673
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(673)
; OTHER INFORMATION: n = A,T,C or G
US-09-542-615A-33

Query Match          70.0%; Score 14; DB 4; Length 673;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 TTCCCTGCTCCCTTT 19
Db      142 TTCCCTGCTCCCTTT 129

RESULT 14
US-09-606-421B-33/c
; Sequence 33, Application US/09606421B
; Patent No. 6531315
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C6
; CURRENT APPLICATION NUMBER: US/09/606,421B
; CURRENT FILING DATE: 2001-08-27
; NUMBER OF SEQ ID NOS: 330
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; FILE REFERENCE: 210121.455C9
; CURRENT APPLICATION NUMBER: US/09/606,421B
; CURRENT FILING DATE: 2000-06-28
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 33
; LENGTH: 673
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(673)
; OTHER INFORMATION: n = A,T,C or G
US-09-606-421B-33

Query Match      70.0%; Score 14; DB 4; Length 673;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      6 TTCCCTGCTCCTTT 19
Db      142 TTCCCTGCTCCTTT 129

RESULT 15
US-09-221-107-33/c
; Sequence 33, Application US/09221107
; Patent No. 6660838
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY OF LUNG CANCER
; FILE REFERENCE: 210121.455C2
; CURRENT APPLICATION NUMBER: US/09/221,107
; CURRENT FILING DATE: 1998-12-22
; NUMBER OF SEQ ID NOS: 161
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 33
; LENGTH: 673
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (325)
; OTHER INFORMATION: Where n is a, c, g or t
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (419)
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; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (452)
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; NAME/KEY: modified_base
; LOCATION: (532)
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; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (538)
; OTHER INFORMATION: Where n is a, c, g or t
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (542)
; OTHER INFORMATION: Where n is a, c, g or t
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (571)
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; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (600)
; OTHER INFORMATION: Where n is a, c, g or t
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (616)
; OTHER INFORMATION: Where n is a, c, g or t
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (651)
; OTHER INFORMATION: Where n is a, c, g or t
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (672)
; OTHER INFORMATION: Where n is a, c, g or t
US-09-221-107-33

Query Match      70.0%; Score 14; DB 4; Length 673;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      6 TTCCCTGCTCCTTT 19
Db      142 TTCCCTGCTCCTTT 129

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OM nucleic - nucleic search, using sw model

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- 9: /cgn2\_6/ptodata/2/pubpna/US09A\_PUBCOMB.seq.\*
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- 11: /cgn2\_6/ptodata/2/pubpna/US09C\_PUBCOMB.seq.\*
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- 19: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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C 2	20	100.0	530	17	US-10-148-641A-19
C 3	20	100.0	551	15	US-10-029-386-9533
C 4	20	100.0	3450	16	US-10-457-954-5
C 5	20	100.0	5434	13	US-10-170-385-182
C 6	18	90.0	396	9	US-09-969-708-488
C 7	18	90.0	474	10	US-09-918-995-20082
C 8	18	90.0	620	13	US-10-027-632-278076
C 9	18	90.0	620	16	US-10-027-632-278076
C 10	18	90.0	1345	16	US-10-332-424-9
C 11	18	90.0	1611	10	US-09-764-891-9320
C 12	18	90.0	1611	15	US-10-091-572-867
C 13	18	90.0	1726	16	US-10-108-260A-1
C 14	18	90.0	1869	15	US-10-037-270-704

c 15	18	90.0	1869	16	US-10-117-722-704	Sequence 704, App
c 16	17	85.0	416	9	US-09-880-107-2953	Sequence 2953, Ap
c 17	17	85.0	965	13	US-10-027-632-323768	Sequence 323768,
c 18	17	85.0	965	16	US-10-027-632-323768	Sequence 323768,
c 19	17	85.0	2564	13	US-10-027-632-111606	Sequence 111606,
c 20	17	85.0	2564	16	US-10-027-632-111606	Sequence 111606,
c 21	17	85.0	39725	15	US-10-017-161-1611	Sequence 1611, Ap
c 22	17	85.0	39729	16	US-10-292-798-1285	Sequence 1285, Ap
c 23	17	85.0	55795	9	US-09-880-107-1543	Sequence 1543, Ap
c 24	17	85.0	66933	13	US-10-182-936A-11	Sequence 11, Appl
c 25	17	85.0	66933	16	US-10-374-979-11	Sequence 9, Appl
c 26	17	85.0	72049	13	US-10-182-936A-9	Sequence 9, Appl
c 27	17	85.0	72049	16	US-10-374-979-9	Sequence 1408, Ap
c 28	17	85.0	156843	13	US-10-087-192-1408	Sequence 13435, A
c 29	16	80.0	320	13	US-10-085-783A-13435	Sequence 13435, A
c 30	16	80.0	320	16	US-10-242-535A-13435	Sequence 125717,
c 31	16	80.0	822	13	US-10-027-632-125717	Sequence 125717,
c 32	16	80.0	822	16	US-10-027-632-125717	Sequence 125717,
c 33	16	80.0	1763	9	US-09-891-171-3	Sequence 3, Appl
c 34	16	80.0	1763	15	US-10-266-767-3	Sequence 3, Appl
c 35	16	80.0	2059	13	US-10-027-632-99852	Sequence 99852, A
c 36	16	80.0	2059	16	US-10-027-632-99852	Sequence 99852, A
c 37	16	80.0	6086	16	US-10-062-674-1873	Sequence 1873, Ap
c 38	16	80.0	54929	13	US-10-087-192-823	Sequence 823, App
c 39	16	80.0	169998	16	US-10-380-931-24	Sequence 24, Appl
c 40	16	80.0	197496	9	US-09-877-177-10	Sequence 10, Appl
c 41	16	80.0	197496	13	US-10-426-836-10	Sequence 1461, Ap
c 42	15	75.0	321	11	US-09-864-408A-1461	Sequence 8043, Ap
c 43	15	75.0	410	10	US-09-918-995-8043	Sequence 51, Appl
c 44	15	75.0	486	9	US-09-924-401-61	Sequence 11063, A
c 45	15	75.0	550	10	US-09-918-995-11063	

ALIGNMENTS

RESULT 1

US-10-029-386-23233/c  
; Sequence 23233, Application US/10029386  
; Publication No. US20030194704A1  
; GENERAL INFORMATION:  
; APPLICANT: Penn, Sharon G.  
; APPLICANT: Rank, David R.  
; APPLICANT: Hanzel, David K.  
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G  
; FILE OF INVENTION: EXPRESSION ANALYSIS TWO  
; FILE REFERENCE: AEMICA-X-2  
; CURRENT APPLICATION NUMBER: US/10/029,386  
; NUMBER OF SEQ ID NOS: 34288  
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1  
; SEQ ID NO 23233  
; LENGTH: 186  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: MAP TO CHR9.3  
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.3  
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.4  
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.5  
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.8  
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.3  
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.1  
; OTHER INFORMATION: SWISSPROT HIT: P38571, EVALUE 1.50e+00  
; OTHER INFORMATION: NT HIT: M17310.1, EVALUE 1.00e-100  
; OTHER INFORMATION: EST\_HUMAN HIT: H81820.1, EVALUE 5.00e-95  
US-10-029-386-23233

Query Match 100.0%; Score 20; DB 15; Length 186;  
Best Local Similarity 100.0%; Pred. No. 0.2;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTCTCCCTCCTCTTGG 20

Db 129 CCTTCTCCCTGCTCCTTTG 110  
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RESULT 2  
US-10-148-641A-19/c  
; Sequence 19, Application US/10148641A  
; Publication No. US2004008652A1  
; GENERAL INFORMATION:  
; APPLICANT: Ono, Toshiro and Nakayama, Eiichi  
; TITLE OF INVENTION: CANCER ASSOCIATED ANTIGENS AND USES  
; FILE REFERENCE: L00461.70132.US  
; CURRENT APPLICATION NUMBER: US/10/148,641A  
; CURRENT FILING DATE: 2003-03-18  
; PRIOR APPLICATION NUMBER: US 09/559,013  
; PRIOR FILING DATE: 2000-04-26  
; PRIOR APPLICATION NUMBER: US 60/168,353  
; PRIOR FILING DATE: 1999-12-01  
; NUMBER OF SEQ ID NOS: 39  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 19  
; LENGTH: 530  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-10-148-641A-19  
  
Query Match 100.0%; Score 20; DB 17; Length 530;  
Best Local Similarity 100.0%; Pred. No. 0.17;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 CCTTCTCCCTGCTCCTTTG 20  
|||||

Db 389 CCTTCTCCCTGCTCCTTTG 370  
|||||

RESULT 3  
US-10-029-386-9533/c  
; Sequence 9533, Application US/10029386  
; Publication No. US20030194704A1  
; GENERAL INFORMATION:  
; APPLICANT: Penn, Sharron G.  
; APPLICANT: Hanzel, David K.  
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
; FILE REFERENCE: AEOMICA-X-2  
; CURRENT APPLICATION NUMBER: US/10/029,386  
; CURRENT FILING DATE: 2001-12-20  
; NUMBER OF SEQ ID NOS: 34288  
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1  
; SEQ ID NO 9533  
; LENGTH: 551  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: MAP TO CHR9,3  
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.3  
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.4  
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.5  
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.8  
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.3  
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.1  
; OTHER INFORMATION: NT HIT: M17310.1, EVALUE 0.00e+00  
; OTHER INFORMATION: SWISSPROT HIT: O05974, EVALUE 3.00e+00  
; OTHER INFORMATION: EST\_HUMAN HIT: A1025543.1, EVALUE 0.00e+00  
US-10-029-386-9533  
  
Query Match 100.0%; Score 20; DB 15; Length 551;  
Best Local Similarity 100.0%; Pred. No. 0.17;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 CCTTCTCCCTGCTCCTTTG 20

Db 211 CCTTCTCCCTGCTCCTTTG 192  
|||||

RESULT 4  
US-10-457-954-5/c  
; Sequence 5, Application US/10457954  
; Publication No. US20040005623A1  
; GENERAL INFORMATION:  
; APPLICANT: Longley, B. Jack  
; TITLE OF INVENTION: Method of determining tumor sensitivities to therapeutic drugs  
; FILE REFERENCE: 960296.98890  
; CURRENT APPLICATION NUMBER: US/10/457,954  
; CURRENT FILING DATE: 2003-06-10  
; PRIOR APPLICATION NUMBER: 60/387,370  
; PRIOR FILING DATE: 2002-06-10  
; PRIOR APPLICATION NUMBER: 60/387,406  
; PRIOR FILING DATE: 2002-06-10  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 5  
; LENGTH: 3450  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(3447)  
; FEATURE:  
; NAME/KEY: misc\_structure  
; LOCATION: (730)..(765)  
; OTHER INFORMATION: encode amino acids 244-255 for forming the sides of the enzymatic  
; OTHER INFORMATION: pocket  
; FEATURE:  
; NAME/KEY: misc\_structure  
; LOCATION: (931)..(1077)  
; OTHER INFORMATION: encode amino acids 311-359 for forming the sides of the enzymatic  
; OTHER INFORMATION: pocket  
; FEATURE:  
; NAME/KEY: misc\_structure  
; LOCATION: (114)..(1206)  
; OTHER INFORMATION: encode amino acids 381-402 for forming the enzymatic pocket's  
; OTHER INFORMATION: activation loop  
US-10-457-954-5  
  
Query Match 100.0%; Score 20; DB 16; Length 3450;  
Best Local Similarity 100.0%; Pred. No. 0.13;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 CCTTCTCCCTGCTCCTTTG 20  
|||||

Db 88 CCTTCTCCCTGCTCCTTTG 69  
|||||

RESULT 5  
US-10-170-385-182/c  
; Sequence 182, Application US/10170385  
; Publication No. US20030203372A1  
; GENERAL INFORMATION:  
; APPLICANT: Ward, Neil Raymond  
; APPLICANT: Mundy, Christopher Robert  
; APPLICANT: Kan, On  
; APPLICANT: Harris, Robert Alan  
; APPLICANT: White, Jonathan  
; APPLICANT: Binley, Katie Mary  
; APPLICANT: Rayner, William Nigel  
; APPLICANT: Naylor, Stuart  
; APPLICANT: Kingeman, Susan Mary  
; APPLICANT: Krige, David  
; TITLE OF INVENTION: ANALYSIS METHOD  
; FILE REFERENCE: 532682000100  
; CURRENT APPLICATION NUMBER: US/10/170,385  
; CURRENT FILING DATE: 2002-06-12  
; PRIOR APPLICATION NUMBER: PCT/GB02/01662

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; PRIOR FILING DATE: 2002-04-08
; PRIOR APPLICATION NUMBER: PCT/GB01/05458
; PRIOR FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 549
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 182
; LENGTH: 5434
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-170-385-182

Query Match      100.0%; Score 20; DB 13; Length 5434;
Best Local Similarity 100.0%; Pred. No. 0.12; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTCTTCCCTGCTCCTTTG 20
   |||||
Db 88 CTTCTTCCCTGCTCCTTTG 69

RESULT 6
US-09-969-708-488
; Sequence 488, Application US/09969708
; Patent No. US20020102532A1
; GENERAL INFORMATION:
; APPLICANT: Augustus, Meena
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu
; FILE OF INVENTION: Sets
; FILE REFERENCE: 689290-70
; CURRENT APPLICATION NUMBER: US/09/969,708
; CURRENT FILING DATE: 2001-10-03
; PRIOR APPLICATION NUMBER: US/60/237,606
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: US/60/237,608
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: US/60/237,425
; PRIOR FILING DATE: 2000-10-03
; NUMBER OF SEQ ID NOS: 658
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 488
; LENGTH: 396
; TYPE: DNA
; ORGANISM: Homosapiens
US-09-969-708-488

Query Match      90.0%; Score 18; DB 9; Length 396;
Best Local Similarity 100.0%; Pred. No. 2.1; Indels 0; Gaps 0;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTCTTCCCTGCTCCTTTG 20
   |||||
Db 164 TTCTTCCCTGCTCCTTTG 181

RESULT 7
US-09-918-995-20082/c
; Sequence 20082, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 20082
; LENGTH: 474
; TYPE: DNA
; ORGANISM: Homo sapiens
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; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(474)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-20082

Query Match      90.0%; Score 18; DB 10; Length 474;
Best Local Similarity 100.0%; Pred. No. 2; Indels 0; Gaps 0;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTCTTCCCTGCTCCTTTG 20
   |||||
Db 348 TTCTTCCCTGCTCCTTTG 331

RESULT 8
US-10-027-632-278076/c
; Sequence 278076, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 278076
; LENGTH: 620
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-278076

Query Match      90.0%; Score 18; DB 13; Length 620;
Best Local Similarity 100.0%; Pred. No. 2; Indels 0; Gaps 0;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTCTTCCCTGCTCCTTTG 20
   |||||
Db 60 TTCTTCCCTGCTCCTTTG 43

RESULT 9
US-10-027-632-278076/c
; Sequence 278076, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
```

;; PRIOR FILING DATE: 2000-03-29  
;; PRIOR APPLICATION NUMBER: US 60/185,218  
;; PRIOR FILING DATE: 2000-02-24  
;; PRIOR APPLICATION NUMBER: US 60/167,363  
;; PRIOR FILING DATE: 1999-11-23  
;; PRIOR APPLICATION NUMBER: US 60/156,358  
;; PRIOR FILING DATE: 1999-09-28  
;; PRIOR APPLICATION NUMBER: US 60/146,002  
;; PRIOR FILING DATE: 1999-08-09  
;; NUMBER OF SEQ ID NOS: 325720  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 278076  
;; LENGTH: 620  
;; TYPE: DNA  
;; ORGANISM: Human  
US-10-027-632-278076

Query Match 90.0%; Score 18; DB 16; Length 620;  
Best Local Similarity 100.0%; Pred. No. 2;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTCTTCCCTGCTCCTTTG 20  
|||  
Db 60 TTCTTCCCTGCTCCTTTG 43

RESULT 10  
US-10-332-424-9/c  
;; Sequence 9, Application US/10332424  
;; Publication No. US20040018505A1  
;; GENERAL INFORMATION:  
;; APPLICANT: INCYTE GENOMICS, INC.; LEE, Ernestine A.  
;; APPLICANT: TANG, Y. Tom; LU, Dying Aina M.  
;; APPLICANT: TRIBOULEY, Catherine M.; GANDHI, Ameena R.  
;; APPLICANT: LU, Yan; BAUGHN, Mariah R.  
;; APPLICANT: WARREN, Bridget A.; THORNTON, Michael  
;; APPLICANT: YUE, Henry; JACKSON, Jennifer L.  
;; APPLICANT: ARVIZU, Chandra S.; ELLIOTT, Vicki S.  
;; APPLICANT: THANGAVELU, Kavitha; RAMKUMAR, Jayalaxmi  
;; APPLICANT: CHANLA, Narinder K.; YAO, Monique G.  
;; APPLICANT: GANDHI, Ameena R.  
;; TITLE OF INVENTION: AMINOACYL TRNA SYNTHETASES  
;; FILE REFERENCE: PI-0153 USN  
;; CURRENT APPLICATION NUMBER: US/10/332,424  
;; CURRENT FILING DATE: 2002-01-06  
;; PRIOR APPLICATION NUMBER: US 60/216,748  
;; PRIOR FILING DATE: 2000-07-07  
;; PRIOR APPLICATION NUMBER: US 60/219,019  
;; PRIOR FILING DATE: 2000-07-18  
;; PRIOR APPLICATION NUMBER: US 60/223,058  
;; PRIOR FILING DATE: 2000-08-04  
;; PRIOR APPLICATION NUMBER: US 60/234,693  
;; PRIOR FILING DATE: 2000-09-21  
;; PRIOR APPLICATION NUMBER: US 60/239,797  
;; PRIOR FILING DATE: 2000-10-11  
;; NUMBER OF SEQ ID NOS: 12  
;; SOFTWARE: PERL Program  
;; SEQ ID NO 9  
;; LENGTH: 1345  
;; TYPE: DNA  
;; ORGANISM: Homo sapiens  
;; FEATURE:  
;; NAME/KEY: misc feature  
;; OTHER INFORMATION: Incyte ID No. US20040018505A1 1554103CB1  
US-10-332-424-9

Query Match 90.0%; Score 18; DB 16; Length 1345;  
Best Local Similarity 100.0%; Pred. No. 1.8;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTCTTCCCTGCTCCTTTG 20  
|||  
Db 1172 TTCTTCCCTGCTCCTTTG 1155

RESULT 11  
US-09-764-891-9320  
;; Sequence 9320, Application US/09764891  
;; Publication No. US20030077808A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Rosen et al.  
;; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
;; FILE REFERENCE: PC006  
;; CURRENT APPLICATION NUMBER: US/09/764,891  
;; CURRENT FILING DATE: 2001-01-17  
;; Prior application data removed - consult PALM or file wrapper  
;; NUMBER OF SEQ ID NOS: 10231  
;; SOFTWARE: PatentIn Ver. 2.0  
;; SEQ ID NO 9320  
;; LENGTH: 1611  
;; TYPE: DNA  
;; ORGANISM: Homo sapiens  
US-09-764-891-9320

Query Match 90.0%; Score 18; DB 10; Length 1611;  
Best Local Similarity 100.0%; Pred. No. 1.7;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTCTTCCCTGCTCCTTTG 20  
|||  
Db 166 TTCTTCCCTGCTCCTTTG 183

RESULT 12  
US-10-091-572-867  
;; Sequence 867, Application US/10091572  
;; Publication No. US20030054373A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Rosen et al.  
;; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
;; FILE REFERENCE: P4118C1  
;; CURRENT APPLICATION NUMBER: US/10/091,572  
;; CURRENT FILING DATE: 2002-03-07  
;; PRIOR APPLICATION NUMBER: 09/764,850  
;; PRIOR FILING DATE: 2001-01-17  
;; PRIOR APPLICATION NUMBER: 60/179,065  
;; PRIOR FILING DATE: 2000-01-31  
;; PRIOR APPLICATION NUMBER: 60/180,628  
;; PRIOR FILING DATE: 2000-02-04  
;; PRIOR APPLICATION NUMBER: 60/214,886  
;; PRIOR FILING DATE: 2000-06-28  
;; PRIOR APPLICATION NUMBER: 60/217,487  
;; PRIOR FILING DATE: 2000-07-11  
;; PRIOR APPLICATION NUMBER: 60/225,758  
;; PRIOR FILING DATE: 2000-08-14  
;; PRIOR APPLICATION NUMBER: 60/220,963  
;; PRIOR FILING DATE: 2000-07-26  
;; PRIOR APPLICATION NUMBER: 60/217,496  
;; PRIOR FILING DATE: 2000-07-11  
;; PRIOR APPLICATION NUMBER: 60/225,447  
;; PRIOR FILING DATE: 2000-08-14  
;; PRIOR APPLICATION NUMBER: 60/218,290  
;; PRIOR FILING DATE: 2000-07-14  
;; PRIOR APPLICATION NUMBER: 60/225,757  
;; PRIOR FILING DATE: 2000-08-14  
;; PRIOR APPLICATION NUMBER: 60/226,868  
;; PRIOR FILING DATE: 2000-08-22  
;; PRIOR APPLICATION NUMBER: 60/216,647  
;; PRIOR FILING DATE: 2000-07-07  
;; PRIOR APPLICATION NUMBER: 60/225,267  
;; PRIOR FILING DATE: 2000-08-14  
;; PRIOR APPLICATION NUMBER: 60/216,880  
;; PRIOR FILING DATE: 2000-07-07  
;; PRIOR APPLICATION NUMBER: 60/225,270  
;; PRIOR FILING DATE: 2000-08-14  
;; PRIOR APPLICATION NUMBER: 60/251,869

; PRIOR FILING DATE: 2000-12-08  
 ; PRIOR APPLICATION NUMBER: 60/235,834  
 ; PRIOR FILING DATE: 2000-09-27  
 ; PRIOR APPLICATION NUMBER: 60/234,274  
 ; PRIOR FILING DATE: 2000-09-21  
 ; PRIOR APPLICATION NUMBER: 60/234,223  
 ; PRIOR FILING DATE: 2000-09-21  
 ; PRIOR APPLICATION NUMBER: 60/228,924  
 ; PRIOR FILING DATE: 2000-08-30  
 ; PRIOR APPLICATION NUMBER: 60/224,518  
 ; PRIOR FILING DATE: 2000-08-14  
 ; PRIOR APPLICATION NUMBER: 60/236,369  
 ; PRIOR FILING DATE: 2000-09-29  
 ; PRIOR APPLICATION NUMBER: 60/224,519  
 ; PRIOR FILING DATE: 2000-08-14  
 ; PRIOR APPLICATION NUMBER: 60/220,964  
 ; PRIOR FILING DATE: 2000-07-26  
 ; PRIOR APPLICATION NUMBER: 60/241,809  
 ; PRIOR FILING DATE: 2000-10-20  
 ; PRIOR APPLICATION NUMBER: 60/249,299  
 ; PRIOR FILING DATE: 2000-11-17  
 ; PRIOR APPLICATION NUMBER: 60/236,327  
 ; PRIOR FILING DATE: 2000-09-29  
 ; PRIOR APPLICATION NUMBER: 60/241,785  
 ; PRIOR FILING DATE: 2000-10-20  
 ; PRIOR APPLICATION NUMBER: 60/244,617  
 ; PRIOR FILING DATE: 2000-11-01  
 ; PRIOR APPLICATION NUMBER: 60/225,268  
 ; PRIOR FILING DATE: 2000-08-14  
 ; PRIOR APPLICATION NUMBER: 60/236,368  
 ; PRIOR FILING DATE: 2000-09-29  
 ; PRIOR APPLICATION NUMBER: 60/251,856  
 ; PRIOR FILING DATE: 2000-12-08  
 ; PRIOR APPLICATION NUMBER: 60/251,868  
 ; PRIOR FILING DATE: 2000-12-08  
 ; PRIOR APPLICATION NUMBER: 60/229,344  
 ; PRIOR FILING DATE: 2000-09-01  
 ; PRIOR APPLICATION NUMBER: 60/234,997  
 ; PRIOR FILING DATE: 2000-09-25  
 ; PRIOR APPLICATION NUMBER: 60/229,343  
 ; PRIOR FILING DATE: 2000-09-01  
 ; PRIOR APPLICATION NUMBER: 60/229,345  
 ; PRIOR FILING DATE: 2000-09-01  
 ; PRIOR APPLICATION NUMBER: 60/229,287  
 ; PRIOR FILING DATE: 2000-09-01  
 ; PRIOR APPLICATION NUMBER: 60/229,513  
 ; PRIOR FILING DATE: 2000-09-05  
 ; PRIOR APPLICATION NUMBER: 60/231,413  
 ; PRIOR FILING DATE: 2000-09-08  
 ; PRIOR APPLICATION NUMBER: 60/229,509  
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 ; PRIOR APPLICATION NUMBER: 60/236,367  
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 ; PRIOR FILING DATE: 2000-10-02  
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 ; PRIOR FILING DATE: 2000-09-29  
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 ; PRIOR FILING DATE: 2000-10-02  
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 ; PRIOR FILING DATE: 2000-10-02  
 ; PRIOR APPLICATION NUMBER: 60/237,040  
 ; PRIOR FILING DATE: 2000-10-02  
 ; PRIOR APPLICATION NUMBER: 60/240,960  
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 ; PRIOR APPLICATION NUMBER: 60/239,935  
 ; PRIOR FILING DATE: 2000-10-13  
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 ; PRIOR APPLICATION NUMBER: 60/232,080  
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 ; PRIOR APPLICATION NUMBER: 60/231,244  
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; PRIOR FILING DATE: 2000-09-14  
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; PRIOR APPLICATION NUMBER: 60/231,243  
; PRIOR FILING DATE: 2000-09-08

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Best Local Similarity 100.0%; Pred. No. 1.7;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTCTTCCCTGCTCCTTTG 20  
|||||  
Db 166 TTCTTCCCTGCTCCTTTG 183

RESULT 13  
US-10-108-260A-1/c  
; Sequence 1, Application US/10108260A  
; Publication No. US20040005560A1  
; GENERAL INFORMATION:  
; APPLICANT: HELIX RESEARCH INSTITUTE  
; TITLE OF INVENTION: No. US20040005560A1e1 full length cDNA  
; FILE REFERENCE: H1-A0106  
; CURRENT APPLICATION NUMBER: US/10/108,260A  
; CURRENT FILING DATE: 2002-03-27  
; NUMBER OF SEQ ID NOS: 5458  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 1726  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-108-260A-1

Query Match 90.0%; Score 18; DB 16; Length 1726;  
Best Local Similarity 100.0%; Pred. No. 1.7;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTCTTCCCTGCTCCTTTG 20  
|||||  
Db 1564 TTCTTCCCTGCTCCTTTG 1547

RESULT 14  
US-10-037-270-704/c  
; Sequence 704, Application US/10037270  
; Publication No. US20030104529A1  
; GENERAL INFORMATION:  
; APPLICANT: Tang, Y. Tom  
; APPLICANT: Liu, Chenghua  
; APPLICANT: Asundi, Vinod  
; APPLICANT: Zhang, Jie  
; APPLICANT: Ren, Feiyan  
; APPLICANT: Chen, Rui-hong  
; APPLICANT: Zhao, Qing A.  
; APPLICANT: Wehrman, Tom  
; APPLICANT: Xue, Aidong J.  
; APPLICANT: Yang, Yonghong  
; APPLICANT: Wang, Jian-Rui  
; APPLICANT: Zhou, Ping  
; APPLICANT: Ma, Yungqing  
; APPLICANT: Wang, Dunrui  
; APPLICANT: Wang, Zhiwei  
; APPLICANT: Tillinghast, John  
; APPLICANT: Drmanac, Radoje T.  
; TITLE OF INVENTION: No. US20030104529A1e1 Nucleic Acids and

; TITLE OF INVENTION: Polypeptides  
; FILE REFERENCE: 784CIP2B  
; CURRENT APPLICATION NUMBER: US/10/037,270  
; CURRENT FILING DATE: 2002-01-04  
; PRIOR APPLICATION NUMBER: 09/552,317  
; PRIOR FILING DATE: 2000-04-25  
; PRIOR APPLICATION NUMBER: 09/488,725  
; PRIOR FILING DATE: 2000-01-21  
; NUMBER OF SEQ ID NOS: 1104  
; SOFTWARE: pt\_FL\_genes Version 1.0  
; SEQ ID NO 704  
; LENGTH: 1869  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (161)..(1792)  
US-10-037-270-704

Query Match 90.0%; Score 18; DB 15; Length 1869;  
Best Local Similarity 100.0%; Pred. No. 1.7;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTCTTCCCTGCTCCTTTG 20  
|||||  
Db 1695 TTCTTCCCTGCTCCTTTG 1678

RESULT 15  
US-10-117-722-704/c  
; Sequence 704, Application US/10117722  
; Publication No. US20030219744A1  
; GENERAL INFORMATION:  
; APPLICANT: Tang, Y. Tom  
; APPLICANT: Liu, Chenghua  
; APPLICANT: Asundi, Vinod  
; APPLICANT: Zhang, Jie  
; APPLICANT: Drmanac, Radoje T.  
; TITLE OF INVENTION: Polypeptides  
; FILE REFERENCE: 784CIP2BCIP  
; CURRENT APPLICATION NUMBER: US/10/117,722  
; CURRENT FILING DATE: 2002-04-04  
; PRIOR APPLICATION NUMBER: 09/620,312  
; PRIOR FILING DATE: 2000-07-19  
; PRIOR APPLICATION NUMBER: 09/552,317  
; PRIOR FILING DATE: 2000-04-25  
; PRIOR APPLICATION NUMBER: 09/488,725  
; PRIOR FILING DATE: 2000-01-21  
; NUMBER OF SEQ ID NOS: 1104  
; SOFTWARE: pt\_FL\_genes Version 1.0  
; SEQ ID NO 704  
; LENGTH: 1869  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (161)..(1792)  
US-10-117-722-704

Query Match 90.0%; Score 18; DB 16; Length 1869;  
Best Local Similarity 100.0%; Pred. No. 1.7;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTCTTCCCTGCTCCTTTG 20  
|||||  
Db 1695 TTCTTCCCTGCTCCTTTG 1678

Search completed: May 27, 2004, 14:58:29  
Job time : 106.251 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 26, 2004, 15:22:41 ; Search time 706.154 Seconds  
(without alignments)  
845.770 Million cell updates/sec

Title: US-09-121-239-14

Perfect score: 20

Sequence: 1 CCTTCTTCCCTGCTCCTTTG 20

Scoring table:

OLIGO\_NUC  
Gapop\_60.0 , Gapext 60.0

Searched: 27513289 seqs, 14931090276 residues

Word size : 0

Total number of hits satisfying chosen parameters: 55056578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

EST:\*

1: em\_estba:\*

2: em\_esthum:\*

3: em\_estin:\*

4: em\_estnu:\*

5: em\_estov:\*

6: em\_estpl:\*

7: em\_estro:\*

8: em\_htc:\*

9: gb\_est1:\*

10: gb\_est2:\*

11: gb\_htc:\*

12: gb\_est3:\*

13: gb\_est4:\*

14: gb\_est5:\*

15: em\_estfun:\*

16: em\_estom:\*

17: em\_gss\_hum:\*

18: em\_gss\_inv:\*

19: em\_gss\_pin:\*

20: em\_gss\_vrt:\*

21: em\_gss\_fun:\*

22: em\_gss\_mam:\*

23: em\_gss\_mus:\*

24: em\_gss\_pro:\*

25: em\_gss\_rod:\*

26: em\_gss\_pbg:\*

27: em\_gss\_vrl:\*

28: gb\_ges1:\*

29: gb\_ges2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	115	9	AI025542 ov87a03.s
C 2	20	100.0	195	9	AV303548 AV303548
C 3	20	100.0	196	10	BB047102 BB047102
C 4	20	100.0	198	29	CG636709 CG636709

C 5	20	100.0	209	9	AV173479
C 6	20	100.0	220	10	BB132800
C 7	20	100.0	233	9	AV104236
C 8	20	100.0	237	9	AV323022
C 9	20	100.0	245	10	BB047117
C 10	20	100.0	249	13	BY371403
C 11	20	100.0	250	9	AV136928
C 12	20	100.0	250	9	AV215533
C 13	20	100.0	250	9	AV346046
C 14	20	100.0	253	9	AV296437
C 15	20	100.0	253	10	BB467544
C 16	20	100.0	254	9	AV338176
C 17	20	100.0	256	9	AV218421
C 18	20	100.0	258	9	AV134910
C 19	20	100.0	258	9	AV339053
C 20	20	100.0	262	10	BB916612
C 21	20	100.0	268	9	AA889856
C 22	20	100.0	282	9	AV055312
C 23	20	100.0	295	12	BM122590
C 24	20	100.0	296	9	AV147138
C 25	20	100.0	297	9	AV100468
C 26	20	100.0	298	9	AI025543
C 27	20	100.0	305	9	AA415759
C 28	20	100.0	311	9	AV100354
C 29	20	100.0	319	10	BF456747
C 30	20	100.0	321	10	BB026196
C 31	20	100.0	324	9	AV095169
C 32	20	100.0	326	13	BU842273
C 33	20	100.0	332	12	BG796781
C 34	20	100.0	333	9	AI838832
C 35	20	100.0	340	12	BM115670
C 36	20	100.0	344	9	AI553501
C 37	20	100.0	344	13	EX099890
C 38	20	100.0	344	13	BY709426
C 39	20	100.0	346	10	BB793854
C 40	20	100.0	348	11	AK009808
C 41	20	100.0	352	9	AI154779
C 42	20	100.0	358	13	BY409310
C 43	20	100.0	362	9	AV102009
C 44	20	100.0	364	13	BY395867
C 45	20	100.0	369	13	BY408267

#### ALIGNMENTS

RESULT 1	AI025542	115 bp	mRNA	linear	EST 27-AUG-1998
LOCUS	ov87a03.s	Soares	testis	NHT Homo sapiens	cDNA clone IMAGE:1644268
DEFINITION	3' similar to TR:Q13688	Q13688	ABL	;	mRNA sequence.
ACCESSION	AI025542				
VERSION	AI025542.1	GI:3241155			
KEYWORDS	EST.				
SOURCE	Homo sapiens				
ORGANISM	Homo sapiens (human)				
REFERENCE	1 (bases 1 to 115)				
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
TITLE	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
JOURNAL	NCI-CCGAP http://www.ncbi.nlm.nih.gov/ncicgap.				
COMMENT	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index Unpublished (1997)				
	Contact: Robert Strausberg, Ph.D.				
	Email: cgapbs@mail.nih.gov				
	CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.				
	CDNA Library Arrayed by: Greg Lennon, Ph.D.				
	DNA Sequencing by: Washington University Genome Sequencing Center				
	Clone distribution: NCI-CCGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www.bio.llnl.gov/bbrp/image/image.html				

Trace considered overall poor quality  
 Insert Length: 730 Std Error: 0.00  
 Seq primer: -40ml3 fwd. RT from Amersham  
 High quality sequence stop: 1.

## FEATURES

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1. .115
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1644268"
/sex="male"
/lab_host="DH10B"
/clone_lib="Soares testis NHT"
/notes="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
was prepared from mRNA obtained from Clontech
Laboratories, Inc., and primed with a Not I - oligo(dT)
primer [5'
TGTACCAATCTGAAGTGGGAGCGCGCCCAATTTTTTTTTTTT 3']
Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT73 vector. Library
went through one round of normalization to Cot5, and was
constructed by Bento Soares and M. Fatima Bonaldo."
```

## ORIGIN

```

Query Match      100.0%; Score 20; DB 9; Length 115;
Best Local Similarity 100.0%; Pred. No. 9.7;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```

QY 1 CCTCTTCCTCGTCTCTTTG 20
    |||||
Db 34 CCTCTTCCTCGTCTCTTTG 53
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## RESULT 2

```

AV303548/c
LOCUS BB047102 RIKEN full-length enriched, 8 days embryo Mus musculus
DEFINITION cDNA clone 5730513J17 3', mRNA sequence.
AV303548 195 bp mRNA linear EST 10-NOV-1999
GAGAGAGAGATTCTCGAGTTAATTAATTAATCCCTCCCCCCCC 3']. cDNA
was cloned into the XhoI and BamHI sites. Vector: a
modified pBluescript KS(+) after bulk excision from Lambda
FLC I. Cloning sites, 5' end: SalI; 3' end: BamHI."
```

```

ACCESSION AV303548.1 GI:6336062
VERSION AV303548
KEYWORDS Mus musculus (house mouse)
SOURCE Mus musculus
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## ORGANISM

```

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 195)
Fukuda,S., Fukunishi,Y., Hara,A., Hayatsu,N., Hirozane,T., Hori,F.,
Ishii,Y., Ishikawa,T., Itoh,M., Izawa,M., Kadota,K., Kagawa,I.,
Kai,C., Kawai,J., Kikuchi,N., Kojima,Y., Koya,S., Kusakabe,M.,
Matsuyama,T., Miki,R., Mizuno,Y., Nakamura,M., Oda,H., Okazaki,Y.,
Owa,C., Ozawa,Y., Saifu,H., Sano,M., Sato,K., Shibata,K.,
Shibata,Y., Shigemoto,Y., Shiraki,T., Sogabe,Y., Sugahara,Y.,
Suzuki,H., Suzuki,H., Takahashi,F., Tateno,M., Tominaga,N.,
Tsunoda,Y., Watahiki,A., Watanabe,S., Yamamura,T., Yasunishi,A.,
Yokota,T., Yoshiki,A., Yoshino,M., Muramatsu,M. and Hayashizaki,Y.
RIKEN Mouse ESTs (Konno,H., et al. 1999)
Unpublished (1999)
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Sasaki,N., Izawa,M., Watahiki,M., Ozawa,K., Tanaka,T., Yoneda,Y.,
Matsura,S., Carninci,P., Muramatsu,M., Okazaki,Y. and
Hayashizaki,Y.
```

## TITLE

## JOURNAL

## COMMENT

Transcriptional sequencing: A method for DNA sequencing using RNA

polymerase. Proc. Natl. Acad. Sci. U.S.A. 95 (7), 3455-3460 (1998)  
 Itoh,M., Kitsuai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,  
 Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M.,  
 Okazaki,Y. and Hayashizaki,Y.  
 Automated filtration-based high-throughput plasmid preparation  
 system. Genome Res. 9 (5), 463-470 (1999)  
 Carninci,P. and Hayashizaki,Y.  
 High-efficiency full-length cDNA cloning. Methods Enzymol. 303,  
 19-44 (1999)  
 Please visit our web site (<http://genome.rtc.riken.go.jp>) for  
 further details.

## FEATURES

## source

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Location/Qualifiers
1. .195
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="5730513J17"
/sex="mixed"
/dev_stage="8 days embryo"
/lab_host="DH10B"
/clone_lib="RIKEN full-length enriched, 8 days embryo"
/notes="Site 1: SalI; Site 2: BamHI; cDNA library was
prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. 1st strand cDNA was
primed with a primer [5'
GAGAGAGAGATTCTCGAGTTAATTAATTAATCCCTCCCCCCCC 3']. cDNA was
prepared by using trehalose thermo-activated reverse
transcriptase and subsequently enriched for full-length by
cap-trapper. cDNA went through one round of subtraction to
Ret = 100.0 Second strand cDNA was prepared with the
primer adapter of sequence [5'
GAGAGAGAGATTCTCGAGTTAATTAATTAATCCCTCCCCCCCC 3']. cDNA
was cloned into the XhoI and BamHI sites. Vector: a
modified pBluescript KS(+) after bulk excision from Lambda
FLC I. Cloning sites, 5' end: SalI; 3' end: BamHI."
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## ORIGIN

```

Query Match      100.0%; Score 20; DB 9; Length 195;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 CCTCTTCCTCGTCTCTTTG 20
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Db 53 CCTCTTCCTCGTCTCTTTG 34
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## RESULT 3

## BB047102/c

## LOCUS

## DEFINITION

## BB047102

## ACCESSION

## VERSION

## KEYWORDS

## SOURCE

## ORGANISM

## REFERENCE

## AUTHORS

## 1 (bases 1 to 195)

## Konno,H., Aizawa,K., Akahira,S., Akiyama,J., Arakawa,T.,

## Carninci,P., Endo,T., Fukuda,S., Fukunishi,Y., Hara,A., Hayatsu,N.,

## Hirozane,T., Hori,F., Ishii,Y., Ishikawa,J., Ishikawa,T., Itoh,M.,

## Izawa,M., Kadota,K., Kagawa,I., Kai,C., Kawai,J., Kikuchi,N.,

## Kiyosawa,H., Kojima,Y., Kondo,S., Koya,S., Kurihara,C.,

## Kusakabe,M., Matsuyama,T., Miki,R., Mizuno,Y., Nakamura,M., Oda,H.,

## Okazaki,Y., Ono,T., Owa,C., Saito,H., Sakai,C., Sato,K.,

## Shibata,K., Shibata,Y., Shigemoto,Y., Shinagawa,A., Shiraki,T.,

## Sogabe,Y., Sugahara,Y., Suzuki,H., Tatemoto,H., Tatemoto,H.,

## Takahashi,F., Tominaga,N., Toya,T., Tsunoda,Y., Watahiki,A.,







**TITLE** RIKEN Mouse ESTs  
**UNPUBLISHED** (1999)  
**CONTACT** Chie Owa  
**COMMENT** Genome Science Laboratory  
 RIKEN  
 3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan  
 Tel: 81-298-36-9145  
 Fax: 81-298-36-9098  
 Email: genome-resortc.riken.go.jp  
 Thermostabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA (Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))  
 Transcriptional sequencing: A method for DNA sequencing using RNA polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))  
 Please visit our web site (<http://genome rtc.riken.go.jp>) for further details.

**FEATURES**  
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 /mol\_type="mRNA"  
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**ORIGIN**  
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 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 QY 1 CCTCTTCCTGCTGCTCTTG 20  
 |||||  
 89 CCTCTTCCTGCTGCTCTTG 70

**RESULT 8**  
 AV323022/c  
**LOCUS**  
**DEFINITION** AV323022 RIKEN full-length enriched, 11 days embryo head Mus  
 musculus cDNA clone 6230405E19 3', mRNA sequence.  
**ACCESSION** AV323022  
**VERSION** EST.  
**KEYWORDS** AV323022.1 GI:6292939  
**SOURCE** Mus musculus (house mouse)  
**ORGANISM** Mus musculus  
**REFERENCE** Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 237)  
**AUTHORS** Konno, H., Aizawa, K., Akahira, S., Akiyama, J., Carninci, P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., Hirozane, T., Hori, F., Ishii, Y., Ishikawa, T., Itoh, K., Izawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N., Kojima, Y., Koya, S., Kusakabe, M., Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y., Owa, C., Ozawa, Y., Saito, H., Sano, M., Sato, K., Shibata, K., Shibata, Y., Shigenoto, Y., Shiraki, T., Sogabe, Y., Sugahara, Y., Suzuki, H., Suzuki, H., Takahashi, F., Tateo, M., Tominaga, N., Tsunoda, Y., Wachihi, A., Watanabe, S., Yamamura, T., Yasunishi, A., Yokota, Y., Yoshiki, A., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.  
 RIKEN Mouse ESTs (Konno, H., et al. 1999)  
 Unpublished (1999)  
**TITLE** Contact: Yoshihide Hayashizaki  
**JOURNAL** Laboratory for Genome Exploration Research Group, RIKEN Genomic  
**COMMENT** Sciences Center (GSC), Yokohama Institute  
 The Institute of Physical and Chemical Research (RIKEN)  
 1-7-22 Suehiro-cho, Teurumi-Ku, Yokohama, Kanagawa 230-0045, Japan  
 Tel: 81-45-503-9222  
 Fax: 81-45-503-9216  
 Email: genome-resortc.riken.go.jp  
 URL: <http://genome.gsc.riken.go.jp/>  
 Sasaki, N., Izawa, M., Wachihi, M., Tanaka, T., Yoneda, Y.,



encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)  
 cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.  
 Please visit our web site (<http://genome.gsc.riken.go.jp>) for further details.

## FEATURES

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 Db 108 CTTCTCTCCCTGCTCCTTTG 89

## RESULT 11

AV136928/c

LOCUS AV136928 Mus musculus C57BL/6J 10-11 day embryo Mus musculus cDNA  
 DEFINITION clone 2810029621, mRNA sequence.

ACCESSION AV136928

VERSION AV136928.1 GI:5322658

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 250)

## REFERENCE

AUTHORS

Carninci, P., Shibata, K., Ozawa, Y., Konno, H., Itoh, M., Aizawa, K., Akahira, S., Akiyama, J., Fukuda, S., Fukunishi, Y., Funayama, T., Hara, A., Hayatsu, N., Hori, P., Ishikawa, T., Itoh, M., Izawa, M., Kawai, J., Kikuchi, N., Kojima, Y., Matsuyama, T., Naitsuma, H., Oda, H., Owa, C., Sato, K., Shibata, Y., Shigemoto, Y., Shiraki, T., Sogabe, Y., Sugahara, Y., Suzuki, H., Suzuki, H., Tateno, M., Tomaru, Y., Tominaga, N., Watanabe, S., Yagame, M., Yamamura, T., Yokota, T., Yoshino, M., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y.  
 RIKEN Mouse ESTs  
 Unpublished (1999)  
 Contact: Chie Owa  
 Genome Science Laboratory  
 RIKEN  
 3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan  
 Tel: 81-298-36-9145  
 Fax: 81-298-36-9098  
 Email: genome-res@sc.riken.go.jp

## TITLE

JOURNAL

COMMENT

Thermosensitization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA (Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))  
 Transcriptional sequencing: A method for DNA sequencing using RNA polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))  
 Please visit our web site (<http://genome.rtc.riken.go.jp>) for further details.

## FEATURES

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QY 1 CCTTCTCCCTGCTCCTTTG 20  
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## RESULT 12

AV215533/c

LOCUS

DEFINITION AV215533 RIKEN full-length enriched, ES cells Mus musculus cDNA  
 clone 2410149G15 3', mRNA sequence.

ACCESSION AV215533

VERSION AV215533.1 GI:6156378

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 250)

## REFERENCE

AUTHORS

Konno, H., Aizawa, K., Akahira, S., Akiyama, J., Carninci, P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., Hirozane, T., Hori, F., Ishii, Y., Ishikawa, T., Itoh, M., Izawa, M., Kadota, K., Kagawa, T., Kai, C., Kawai, J., Kikuchi, N., Kojima, Y., Koya, S., Kusakabe, M., Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y., Owa, C., Ozawa, Y., Saito, H., Sano, M., Sato, K., Shibata, K., Shibusata, Y., Shigemoto, Y., Shiraki, T., Sogabe, Y., Sugahara, Y., Suzuki, H., Suzuki, H., Takahashi, F., Tateno, M., Tominaga, N., Tsunoda, Y., Watahiki, A., Watanabe, S., Yamamura, T., Yasunishi, A., Yokota, T., Yoshiki, A., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.  
 RIKEN Mouse ESTs (Konno, H., et al. 1999)  
 Unpublished (1999)  
 Contact: Yoshihide Hayashizaki  
 Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute  
 The Institute of Physical and Chemical Research (RIKEN)  
 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan  
 Tel: 81-45-503-9222  
 Fax: 81-45-503-9216  
 Email: genome-res@sc.riken.go.jp,  
 URL: <http://genome.gsc.riken.go.jp/>

## TITLE

JOURNAL

COMMENT

Transcriptional sequencing: A method for DNA sequencing using RNA polymerase. Proc. Natl. Acad. Sci. U.S.A. 95 (7), 3455-3460 (1998)  
 Itoh, M., Kitsuai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J., Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y.  
 Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)  
 Carninci, P. and Hayashizaki, Y.  
 High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)  
 Please visit our web site (<http://genome.rtc.riken.go.jp>) for further details.

## FEATURES

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Search completed: May 26, 2004, 22:44:29  
Job time : 706.154 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 26, 2004, 16:00:31 ; Search time 425.652 Seconds  
(without alignments)  
2036.547 Million cell updates/sec

Title: US-09-121-239-15

Perfect score: 20  
Sequence: 1 CCUUCUCCUCCUCCUUG 20

Scoring table: OLIGO NUC  
Gapop 60.0 , Gapext 60.0

Searched: 3470272 seqs. 21671516995 residues

Word size : 0 6940544

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

GenEmbl.\*

1: gb\_ba.\*

2: gb\_htg.\*

3: gb\_in.\*

4: gb\_om.\*

5: gb\_ov.\*

6: gb\_pat.\*

7: gb\_ph.\*

8: gb\_pl.\*

9: gb\_pr.\*

10: gb\_ro.\*

11: gb\_sts.\*

12: gb\_sy.\*

13: gb\_un.\*

14: gb\_vl.\*

15: em\_ba.\*

16: em\_fun.\*

17: em\_hum.\*

18: em\_in.\*

19: em\_mu.\*

20: em\_om.\*

21: em\_or.\*

22: em\_ov.\*

23: em\_pat.\*

24: em\_ph.\*

25: em\_pl.\*

26: em\_ro.\*

27: em\_sts.\*

28: em\_un.\*

29: em\_vl.\*

30: em\_htg\_hum.\*

31: em\_htg\_inv.\*

32: em\_htg\_other.\*

33: em\_htg\_mus.\*

34: em\_htg\_pln.\*

35: em\_htg\_rod.\*

36: em\_htg\_mam.\*

37: em\_htg\_vrt.\*

38: em\_sy.\*

39: em\_htgo\_hum.\*

40: em\_htgo\_mus.\*

41: em\_htgo\_other.\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
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C 2	20	100.0	20	6	BD222536	BD222536 Methods f
C 3	20	100.0	20	6	BD222537	BD222537 Methods f
C 4	20	100.0	299	6	BD222547	BD222547 Methods f
C 5	20	100.0	532	9	HUMABLBA	M14753 Human abl m
C 6	20	100.0	1346	10	BC005711	BC005711 Mus muscu
C 7	20	100.0	2795	9	HUMABL1B	M17310 Human c-abl
C 8	20	100.0	35737	10	AL732315	AL732315 Mouse DNA
C 9	20	100.0	35962	6	AX598662	AX598662 Sequence
C 10	20	100.0	35962	9	HSABLCR1	U07561 Human ABL g
C 11	20	100.0	79302	2	AC023898	AC023898 Mus muscu
C 12	20	100.0	158264	2	AC015497	AC015497 Homo sapi
C 13	20	100.0	173463	9	AL359092	AL359092 Human DNA
C 14	20	100.0	235338	2	AL357893	AL357893 Homo sapi
C 15	19	95.0	136641	2	AC114327	AC114327 Canis fam
C 16	19	95.0	171026	9	AL590416	AL590416 Human DNA
C 17	19	95.0	184509	2	AC113237	AC113237 Canis fam
C 18	18	90.0	396	6	AX337450	AX337450 Sequence
C 19	18	90.0	543	11	G28197	G28197 human STS S
C 20	18	90.0	1345	6	AX380370	AX380370 Sequence
C 21	18	90.0	1726	6	AX832877	AX832877 Sequence
C 22	18	90.0	1726	9	AK094084	AK094084 Homo sapi
C 23	18	90.0	1835	9	BC004172	BC004172 Homo sapi
C 24	18	90.0	1835	9	BC019324	BC019324 Homo sapi
C 25	18	90.0	1869	6	AR339213	AR339213 Sequence
C 26	18	90.0	3868	9	AL627389	AL627389 Human DNA
C 27	18	90.0	3994	10	AL714015	AL714015 Mouse DNA
C 28	18	90.0	87430	9	AL139400	AL139400 Human DNA
C 29	18	90.0	142422	9	AC113935	AC113935 Homo sapi
C 30	18	90.0	158911	2	AC113803	AC113803 Rattus no
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C 32	18	90.0	172613	9	AC093433	AC093433 Homo sapi
C 33	18	90.0	173995	2	AC073027	AC073027 Homo sapi
C 34	18	90.0	184660	2	AC123734	AC123734 Mus muscu
C 35	18	90.0	189149	2	AC046171	AC046171 Homo sapi
C 36	18	90.0	189616	2	AC128538	AC128538 Rattus no
C 37	18	90.0	203295	10	AL663049	AL663049 Mouse DNA
C 38	18	90.0	203812	2	AC026874	AC026874 Homo sapi
C 39	18	90.0	204746	9	AC055866	AC055866 Homo sapi
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C 41	18	90.0	217415	2	AC123346	AC123346 Rattus no
C 42	18	90.0	218127	2	AC132713	AC132713 Rattus no
C 43	18	90.0	218800	2	AC094410	AC094410 Rattus no
C 44	18	90.0	237998	2	BX544886	BX544886 Mus muscu
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ALIGNMENTS

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LOCUS BD222535 20 bp DNA linear PAT 17-JUL-2003  
DEFINITION Methods for detecting and measuring spliced nucleic acids.  
ACCESSION BD222535  
VERSION BD222535.1 GI:33032305  
KEYWORDS JP 2002521037-A/13.  
SOURCE synthetic construct  
ORGANISM artificial sequences.  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Harvey,R.C. and Eastman,P.S.  
TITLES Methods for detecting and measuring spliced nucleic acids  
JOURNAL Patent: JP 2002521037-A 13 16-JUL-2002;  
GEN PROBE INC

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COMMENT      OS      Artificial Sequence
              PN      JP 2002521037-A/13
              PD      16-JUL-2002
              PF      23-JUL-1999 JP 2000561364
              PR      23-JUL-1998 US 09/121239
              PI      RICHARD C HARVEY, PAUL S EASTMAN
              PC      C12Q1/68, C12N15/09, C12N15/00
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ACCESSION      BD222536
VERSION      BD222536.1 GI:33032306
KEYWORDS      JP 2002521037-A/14.
SOURCE      synthetic construct
ORGANISM      artificial sequences.
REFERENCE      1 (bases 1 to 20)
AUTHORS      Harvey, R.C. and Eastman, P.S.
TITLE      Methods for detecting and measuring spliced nucleic acids
JOURNAL      Patent: JP 2002521037-A 14 16-JUL-2002;
GEN PROBE INC

COMMENT      OS      Artificial Sequence
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              PI      RICHARD C HARVEY, PAUL S EASTMAN
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DEFINITION      Methods for detecting and measuring spliced nucleic acids.
ACCESSION      BD222537
VERSION      BD222537.1 GI:33032307
KEYWORDS      JP 2002521037-A/15.
SOURCE      synthetic construct
ORGANISM      artificial sequences.
REFERENCE      1 (bases 1 to 20)
AUTHORS      Harvey, R.C. and Eastman, P.S.
TITLE      Methods for detecting and measuring spliced nucleic acids
JOURNAL      Patent: JP 2002521037-A 15 16-JUL-2002;
GEN PROBE INC

COMMENT      OS      Artificial Sequence
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              PD      16-JUL-2002
              PF      23-JUL-1999 JP 2000561364
              PR      23-JUL-1998 US 09/121239
              PI      RICHARD C HARVEY, PAUL S EASTMAN
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Best Local Similarity 55.0%; Pred. No. 1.2e+02;
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ACCESSION      BD222547
VERSION      BD222547.1 GI:33032317
KEYWORDS      JP 2002521037-A/25.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
              Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 299)
AUTHORS      Harvey, R.C. and Eastman, P.S.
TITLE      Methods for detecting and measuring spliced nucleic acids
JOURNAL      Patent: JP 2002521037-A 25 16-JUL-2002;
GEN PROBE INC

COMMENT      OS      Homo sapiens (human)
              PN      JP 2002521037-A/25
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              PI      RICHARD C HARVEY, PAUL S EASTMAN
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ACCESSION      BD222547
VERSION      BD222547.1 GI:33032317
KEYWORDS      JP 2002521037-A/25.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
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              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 299)
AUTHORS      Harvey, R.C. and Eastman, P.S.
TITLE      Methods for detecting and measuring spliced nucleic acids
JOURNAL      Patent: JP 2002521037-A 25 16-JUL-2002;
GEN PROBE INC

COMMENT      OS      Homo sapiens (human)
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              PR      23-JUL-1998 US 09/121239
              PI      RICHARD C HARVEY, PAUL S EASTMAN
              PC      C12Q1/68, C12N15/09, C12N15/00
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ORIGIN

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DEFINITION      Methods for detecting and measuring spliced nucleic acids.
ACCESSION      BD222537
VERSION      BD222537.1 GI:33032307
KEYWORDS      JP 2002521037-A/15.
SOURCE      synthetic construct
ORGANISM      artificial sequences.
REFERENCE      1 (bases 1 to 20)
AUTHORS      Harvey, R.C. and Eastman, P.S.
TITLE      Methods for detecting and measuring spliced nucleic acids
JOURNAL      Patent: JP 2002521037-A 15 16-JUL-2002;
GEN PROBE INC

COMMENT      OS      Artificial Sequence
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              PD      16-JUL-2002
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Best Local Similarity 55.0%; Pred. No. 1.2e+02;
Matches 11; Conservative 9; Mismatches 0; Indels 0; Gaps 0;

QY      1 CCUCUUCUCCUGCUCUCCUUG 20
      ||:||||:||||:||||:|
Db      1 CCTCTCTCCCTGCTCCTTG 20

RESULT 4
BD222547/c
LOCUS
DEFINITION      Methods for detecting and measuring spliced nucleic acids.
ACCESSION      BD222547
VERSION      BD222547.1 GI:33032317
KEYWORDS      JP 2002521037-A/25.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
              Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 299)
AUTHORS      Harvey, R.C. and Eastman, P.S.
TITLE      Methods for detecting and measuring spliced nucleic acids
JOURNAL      Patent: JP 2002521037-A 25 16-JUL-2002;
GEN PROBE INC

COMMENT      OS      Homo sapiens (human)
              PN      JP 2002521037-A/25
              PD      16-JUL-2002
              PF      23-JUL-1999 JP 2000561364
              PR      23-JUL-1998 US 09/121239
              PI      RICHARD C HARVEY, PAUL S EASTMAN
              PC      C12Q1/68, C12N15/09, C12N15/00
              CC      Methods for detecting and measuring spliced nucleic acids FH
              PH      Key      Location/Qualifiers
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FEATURES
source
1. .299
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

ORIGIN

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Query Match      100.0%; Score 20; DB 6; Length 299;
Best Local Similarity 55.0%; Pred. No. 43;
Matches 11; Conservative 9; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCUUCUCCUCCUCCUCCUUG 20
    ||:||||:||||:||||:||||:
Db 103 CCTTCTTCCCTGCTCCTTGG 84

RESULT 5
HUMABLA/C
LOCUS HUMABLA 532 bp mRNA linear PRI 30-OCT-1994
DEFINITION Human abl mRNA containing alternative first exons.
ACCESSION M14753
VERSION M14753.1 GI:177945
KEYWORDS c-myc proto-oncogene; protein kinase.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
1 (bases 1 to 532)
AUTHORS Shivelman,E., Lifshitz,B., Gale,R.P., Roe,B.A. and Canaani,E.
TITLE Alternative splicing of RNAs transcribed from the human abl gene
and from the bcr-abl fused gene
JOURNAL Cell 47 (2), 277-284 (1986)
MEDLINE 87028219
PUBMED 3021337
COMMENT Original source text: Human cDNA to mRNA, clone K8.
FEATURES
    source
        Location/Qualifiers
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                /mol_type="mRNA"
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            /db_xref="GI:177946"
            /db_xref="GDB:600-119-640"
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ORIGIN

Query Match      100.0%; Score 20; DB 9; Length 532;
Best Local Similarity 55.0%; Pred. No. 35;
Matches 11; Conservative 9; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCUUCUCCUCCUCCUCCUUG 20
    ||:||||:||||:||||:||||:
Db 428 CCTTCTTCCCTGCTCCTTGG 409

RESULT 6
BC005711/c
LOCUS BC005711 1346 bp mRNA linear ROD 03-OCT-2003
DEFINITION Mus musculus RIKEN cDNA 231004P18 gene, mRNA (CDNA clone MGC:11770
IMAGE:3497962), complete cds.
ACCESSION BC005711
VERSION BC005711.1 GI:13543068
KEYWORDS MGC.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 1346)
AUTHORS Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
Altshul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,

```

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Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,P.,
Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
Scheetz,T.E., Brownstein,M.J., Ustin,T.B., Toshiyuki,S.,
Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
Worley,K.C., Hale,S., Garcia,A.M., Gay,D.J., Hulyk,S.W.,
Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
Fahey,J., Helton,E., Kettman,M., Madan,A., Rodriguez,S.,
Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smalls,D.E.,
Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
22388257
12477932
2 (bases 1 to 1346)
Direct Submission
Submitted (02-APR-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H.,
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
A.N., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAK Plate: 16 Row: n Column: 3
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 21450212.

FEATURES
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            /mol_type="mRNA"
            /strain="FVB/N"
            /db_xref="taxon:10090"
            /clone="MGC:11770 IMAGE:3497962"
            /tissue_type="Mammary tumor. C3 (1)-Tag model. Infiltrating
            ductal carcinoma. 5 month old virgin mouse."
            /clone_lib="NCI CGAP Mam6"
            /lab_host="DH10B"
            /note="Vector: pCMV-SPORT6"
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DLQVILKTEKGNKNSLFIAGNRVLKMERHSGSEKALTSLLKCCVEDHRAVK  
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SEETLLFTVGEKAGLFLAGPAENVETLGRVAEVLGKAGKGRFQKATKMS  
RRAEQAALLQDVTVSQSAEE"

## misc\_feature

67..789

/note="COG2872; Region: Predicted metal-dependent  
hydrolases related to alanyl-tRNA synthetase HxxxH domain  
[general function prediction only]"  
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## ORIGIN

Query Match 100.0%; Score 20; DB 10; Length 1346;  
Best Local Similarity 55.0%; Pred. No. 25;  
Matches 11; Conservative 9; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCUUCUCCUGCUCUCCUUG 20

Db 1189 CCTTCTCCCTGCTCCTTG 1170

## RESULT 7

HUMABLAB/c  
LOCUS HUMABLAB 2795 bp DNA linear PRI 30-OCT-1994  
DEFINITION Human c-abl gene, exon 1b.

ACCESSION M17310

VERSION M17310.1 GI:177941

KEYWORDS abl proto-oncogene; c-myc proto-oncogene; cellular oncogene;  
proto-oncogene; translocation.

SOURCE Homo sapiens (human)

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 2278 to 2795)

REFERENCE Paskind,M.

JOURNAL Unpublished (1987)

REFERENCE 2 (bases 1 to 2277)

AUTHORS Bernards,A., Rubin,C.M., Westbrook,C.A., Paskind,M. and  
Baltimore,D.

TITLE The first intron in the human c-abl gene is at least 200 kilobases  
long and is a target for translocations in chronic myelogenous  
leukemia

JOURNAL Mol. Cell. Biol. 7 (9), 3231-3236 (1987)

MEDLINE 88038877

PubMed 3113010

COMMENT Original source text: Human DNA, clone pHR7.5.  
Draft entry and computer-readable sequence [2], [1] kindly submitted  
by A. Bernards (23-OCT-1987).

## FEATURES

## source

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Location/Qualifiers  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"  
/map="9q34.1"

## repeat\_region

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/note="Alu repeat"

751..2795

/gene="ABL1"

751..2162

/gene="ABL1"

/note="G00-119-640"

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2163..&gt;2795

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/note="intron A; G00-119-640"

/note="About 0.1 kb downstream from XhoI site; chromosome 9q34.

## ORIGIN

Query Match 100.0%; Score 20; DB 9; Length 2795;  
Best Local Similarity 55.0%; Pred. No. 19;  
Matches 11; Conservative 9; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCUUCUCCUGCUCUCCUUG 20

Db 2114 CCTTCTCCCTGCTCCTTG 2095

||||:||||:||||:||||:|

## RESULT 8

AL732315

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

AL732315  
Mouse DNA sequence from clone RP23-124N11 on chromosome 11,  
complete sequence.  
AL732315  
HTG.  
AL732315.7 GI:23337296  
Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 35737)  
Direct Submision  
Submitted (26-SEP-2002) Wellcome Trust Sanger Institute, Hinxton,  
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:  
humquerry@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk  
On Sep 27, 2002 this sequence version replaced gi:22798063.  
----- Genome Center  
Center: Wellcome Trust Sanger Institute  
Center code: SC  
Web site: http://www.sanger.ac.uk  
Contact: humquerry@sanger.ac.uk  
-----  
During sequence assembly data is compared from overlapping clones.  
Where differences are found these are annotated as variations  
together with a note of the overlapping clone name. Note that the  
variation annotation may not be found in the sequence submission  
corresponding to the overlapping clone, as we submit sequences with  
only a small overlap as described above.  
This sequence was finished as follows unless otherwise noted: all  
regions were either double-stranded or sequenced with an alternate  
chemistry or covered by high quality data (i.e., phred quality >=  
30); an attempt was made to resolve all sequencing problems, such  
as compressions and repeats; all regions were covered by at least  
one plasmid subclone or more than one M13 subclone; and the  
assembly was confirmed by restriction digest. The following  
abbreviations are used to associate primary accession numbers given  
in the feature table with their source databases: Em, EMBL; Sw,  
SWISSPROT; Tr, TrEMBL; Wp, WORMPEP; Information on the WORMPEP  
database can be found at  
http://www.sanger.ac.uk/Projects/C\_elegans/wormpep RP23-124N11 is  
from the RPCI-23 Mouse PAC Library  
constructed by the group of Pieter de Jong.  
For further details see http://www.chori.org/bacpac/home.htm  
VECTOR: pBACE3.6  
Location/Qualifiers  
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/clone\_lib="RPCI-23"

AL732315  
100.0%; Score 20; DB 10; Length 35737;  
Best Local Similarity 55.0%; Pred. No. 7.6;  
Matches 11; Conservative 9; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCUUCUCCUGCUCUCCUUG 20

Db 19459 CCTTCTCCCTGCTCCTTG 19478

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AX598662/c

RESULT 9

AX598662/c

LOCUS

AX598662

35962 bp

DNA

linear

PAT 14-FEB-2003

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DEFINITION Sequence 2 from Patent WO02077272.
ACCESSION AX598662
VERSION AX598662.1 GI:28398798
KEYWORDS Homo sapiens (human)
SOURCE ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Euthera; Primates; Catarrhini; Hominiidae; Homo.
1 Berlin,K., Braun,A., Distler,J., Guetig,D., Howe,A., Mueller,J.,
Olek,A., Piepenbrock,C., Adorian,P., Grabs,G., Lesche,R., Leu,E.,
Lewin,A., Lipscher,E., Maier,S., Model,F., Mueller,V., Otto,T.,
Pellet,C. and Ziebarth,H.
TITLE Methods and nucleic acids for the analysis of hematopoietic cell
proliferative disorders
JOURNAL Patent: WO 02077272-A 2 03-OCT-2002;
FEATURES Epigenomics AG (DE)
source Location/Qualifiers
1..35962
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Query Match 100.0%; Score 20; DB 6; Length 35962;
Best Local Similarity 55.0%; Pred. No. 7.5;
Matches 11; Conservative 9; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCUUCUCCUCCUCCUCCUUG 20
Db 29219 CCTTCTCCCTGCTCTCTTG 29200

RESULT 10
LOCUS HSABLGR1/c
DEFINITION Human ABL gene, exon 1b and intron 1b, and putative M8604 Met
protein (M8604 Met) gene, complete cds.
ACCESSION U07561
VERSION U07561.1 GI:514262
KEYWORDS 1 of 3
SEGMENT 1
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Euthera; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 35962)
Chissoe,S.L., Bodenteich,A., Wang,Y., Jian,L., Burian,D.,
Carttree,J.S., Freeman,A., Hamed,O.S., McLaury,H., Pan,H., Toth,S.,
Wang,Z., Zhang,G., Clifton,S., Groffen,J., Heisterkamp,N. and
Roe,B.A.
TITLE Sequence and analysis of the human ABL gene, the BCR gene, and
regions involved in the Philadelphia chromosomal translocation
JOURNAL Genomics 27 (1), 67-82 (1995)
MEDLINE 95394474
PUBMED 7665185
REFERENCE 2 (bases 1 to 35962)
AUTHORS Groffen,J., Heisterkamp,N., Grosveld,F., Van de Ven,W. and
Stephenson,J.R.
TITLE Isolation of human oncogene sequences (v-fes homolog) from a cosmid
library
JOURNAL Science 216 (4550), 1136-1138 (1982)
MEDLINE 82199444
PUBMED 6281890
REFERENCE 3 (bases 1 to 35962)
AUTHORS Morris,C.M., Heisterkamp,N., Groffen,J. and Fitzgerald,P.H.
TITLE Entire ABL gene is joined with 5'-BCR in some patients with
Philadelphia-positive leukemia
JOURNAL Blood 78 (4), 1078-1084 (1991)
MEDLINE 91329820
PUBMED 1868241
REFERENCE 4 (bases 27793 to 28338; 28792 to 29265)
AUTHORS ShriveIman,E., Lifshitz,B., Gale,R.P., Roe,B.A. and Canaani,B.

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TITLE Alternative splicing of RNAs transcribed from the human abl gene
and from the bcr-abl fused gene
JOURNAL Cell 47 (2), 277-284 (1986)
MEDLINE 87028219
PUBMED 3021337
REFERENCE 5 (bases 27108 to 29899)
AUTHORS Bernards,A., Rubin,C.M., Westbrook,C.A., Paskind,M. and
Baltimore,D.
TITLE The first intron in the human c-abl gene is at least 200 kilobases
long and is a target for translocations in chronic myelogenous
leukemia
JOURNAL Mol. Cell. Biol. 7 (9), 3231-3236 (1987)
MEDLINE 88038877
PUBMED 3133010
REFERENCE 6 (bases 1 to 35962)
AUTHORS Mount,S.M.
TITLE A catalogue of splice junction sequences
JOURNAL Nucleic Acids Res. 10 (2), 459-472 (1982)
MEDLINE 82150208
PUBMED 7063411
REFERENCE 7 (bases 1 to 35962)
AUTHORS Adams,M.D., Dubnick,M., Kerlavage,A.R., Moreno,R., Kelley,J.M.,
Utterback,T.R., Nagle,J.W., Fields,C. and Venter,J.C.
TITLE Sequence identification of 2,375 human brain genes
JOURNAL Nature 355 (6361), 632-634 (1992)
MEDLINE 92168112
PUBMED 1538749
REFERENCE 8 (bases 1 to 35962)
AUTHORS Zhu,Q.S., Heisterkamp,N. and Groffen,J.
TITLE Characterization of the human ABL promoter regions
JOURNAL Oncogene 5 (6), 885-891 (1990)
MEDLINE 90295283
PUBMED 2163052
REFERENCE 9 (bases 1 to 35962)
AUTHORS Paskind,M.
TITLE Personal communication
JOURNAL Unpublished
REFERENCE 10 (bases 1 to 35962)
AUTHORS Tatusov,R. and Lipman,D.J.
TITLE Using local similarities for pattern detection in
nucleotide/protein sequences
JOURNAL Unpublished
REFERENCE 11 (bases 1 to 35962)
AUTHORS Groffen,J., Stephenson,J.R., Heisterkamp,N., de Klein,A.,
Bartram,C.R. and Grosveld,G.
TITLE Philadelphia chromosomal breakpoints are clustered within a limited
region, bcr, on chromosome 22
JOURNAL Cell 36 (1), 93-99 (1984)
MEDLINE 84106827
PUBMED 6319012
REFERENCE 12 (bases 1 to 35962)
AUTHORS Chissoe,S.L.
TITLE Sequence of the human abl and bcr genes
JOURNAL Thesis (1994) University of Oklahoma
REFERENCE 13 (bases 1 to 35962)
AUTHORS Roe,B.A.
TITLE Direct Submission
JOURNAL Submitted (08-MAR-1994) Bruce A. Roe, Dept. of Chem. and Biochem.,
University of Oklahoma, 620 Parrington Oval, Rm 208, Norman, OK
73019, USA
FEATURES source Location/Qualifiers
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/mol_type="genomic DNA"
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complement(448..783)
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/citation=[7]
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/evidence=experimental
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ASVILGNNGFIWIYTPPEKKEEAGGFIANLPVSLADREVISRLENCIISLVQRM
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Query Match 100.0%; Score 20; DB 9; Length 35962;
Best Local Similarity 55.0%; Pred. No. 7.5;
Matches 11; Conservative 9; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCUCUCCUCGUCUUG 20
||:||||:||||:|
Db 29219 CCTCTCCCTGCTCCTTG 29200

RESULT 11
AC023898 79302 bp DNA linear HTG 16-OCT-2001
LOCUS Mus musculus clone RP23-281H12, *** SEQUENCING IN PROGRESS ***, 27
DEFINITION unordered pieces.
ACCESSION AC023898
VERSION AC023898.7 GI:16118065
KEYWORDS HTG; HTGS_PHASE1.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
1 (bases 1 to 79302)
AUTHORS Metzker,M.L., Lewis,L.R., Hume,J., Edwards,C., Harris,C.,
Dederich,D., Thomas,S., Okwuonu,G., Carlock,C., Garner,T.,
Addison,S., Pace,A., Williams,G., Bonnin,D., Brooks,A., Brown,J.,
Buhay,C., Bunac,C., Burkett,C., Chacko,J., Chen,G., Chen,Z.,
Cox,C., Davis,C., Delgado,O., Ding,Y., Dugan-Rocha,S.,
Gorraldez,C., Ferraguto,D., Forcum-Tansey,J., Gill,R.,
Hosak,H., Hou,X., Huber,J., Jackson,L., Jia,Y., Kelly,J., Kelly,S.,
Kovar,C., Liu,J., Liu,W., Louissegh,H., Lozado,R.J., Martin,R.,
Massey,S., McLeod,M.P., Mei,G., Moore,S., Morgan,M., Morris,S.,
Neal,D., Nelson,A., Nguyen,R., Nguyen,N., Oguh,M., Parish,B.,
Perez,L., Reiter,D., Say,J., Shen,H., Vasquez,L., Watlington,S.,
Williamson,A., Wrensford,G., Zhou,X., Bouck,J., Hodgson,A.,
Muzny,D.M., Rives,M., Scherer,S., Sodergren,E., Weinstock,G.,
Worley,K. and Gibbs,R.
Direct Submission
Unpublished
2 (bases 1 to 79302)
Worley,K.C.
Direct Submission
Submitted (20-FEB-2000) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Oct 14, 2001 this sequence version replaced gi:11079363.
----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: MABD
Center clone name: RP23-281H12
----- Summary Statistics
Sequencing vector: M13; L08821
```

Chemistry: Dye-primer Bodipy: 90% of reads  
 Chemistry: Dye-terminator Big Dye: 10% of reads  
 Assembly program: Phrap; version 0.990329  
 Consensus quality: 96352 bases at least Q40  
 Consensus quality: 119814 bases at least Q30  
 Consensus quality: 130654 bases at least Q20  
 Estimated insert size: 106365; sum-of-contigs estimation  
 Quality coverage: 0.5x in Q20 bases; agarose-gel estimation  
 Quality coverage: 1x in Q20 bases; sum-of-contigs estimation

\* NOTE: Estimated insert size may differ from sequence length  
 \* (see [http://www.hgsc.bcm.tmc.edu/docs/genbank\\_draft\\_data.html](http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html)).  
 \* NOTE: This is a 'working draft' sequence. It currently  
 \* consists of 27 contigs. The true order of the pieces  
 \* is not known and their order in this sequence record is  
 \* arbitrary. Gaps between the contigs are represented as  
 \* runs of N, but the exact sizes of the gaps are unknown.  
 \* This record will be updated with the finished sequence  
 \* as soon as it is available and the accession number will  
 \* be preserved.

1	2726:	contig	of 2726 bp in length
2727	2826:	gap	of unknown length
2827	6807:	contig	of 3981 bp in length
6808	6907:	gap	of unknown length
6908	10327:	contig	of 3420 bp in length
10328	10427:	gap	of unknown length
10428	14551:	contig	of 4124 bp in length
14552	14651:	gap	of unknown length
14652	17638:	contig	of 2987 bp in length
17639	17738:	gap	of unknown length
17739	23092:	contig	of 5354 bp in length
23093	23192:	gap	of unknown length
23193	25970:	contig	of 2778 bp in length
25971	26070:	gap	of unknown length
26071	28815:	contig	of 2745 bp in length
28816	28915:	gap	of unknown length
28916	32008:	contig	of 3093 bp in length
32009	32108:	gap	of unknown length
32109	35879:	contig	of 3771 bp in length
35880	35979:	gap	of unknown length
35980	39175:	contig	of 3196 bp in length
39176	39275:	gap	of unknown length
39276	41989:	contig	of 2714 bp in length
41990	42089:	gap	of unknown length
42090	44449:	contig	of 2360 bp in length
44450	44549:	gap	of unknown length
44550	47065:	contig	of 2516 bp in length
47066	47166:	gap	of unknown length
47166	49293:	contig	of 2128 bp in length
49294	49393:	gap	of unknown length
49394	51955:	contig	of 2562 bp in length
51956	52055:	gap	of unknown length
52056	52425:	contig	of 2190 bp in length
52426	54345:	gap	of unknown length
54346	54346:	contig	of 2813 bp in length
57159	57258:	gap	of unknown length
57259	60206:	contig	of 2948 bp in length
60207	60306:	gap	of unknown length
60307	62463:	contig	of 2157 bp in length
62464	62563:	gap	of unknown length
62564	64983:	contig	of 2420 bp in length
64984	65083:	gap	of unknown length
65084	67808:	contig	of 2725 bp in length
67809	67908:	gap	of unknown length
67909	70294:	contig	of 2396 bp in length
70295	70394:	gap	of unknown length
70395	72500:	contig	of 2106 bp in length
72501	72600:	gap	of unknown length
72601	74613:	contig	of 2013 bp in length
74614	74713:	gap	of unknown length
74714	77134:	contig	of 2421 bp in length
77135	77234:	gap	of unknown length
77235	79302:	contig	of 2068 bp in length

FEATURES	SOURCE
1. The first two columns of the table are labeled 'FEATURES' and 'SOURCE' respectively.	

```
Location/Qualifiers
1. .79302
/organism="Mus musculus"
/mol_type="genomic DNA"
./db_xref="taxon:10090"
/clone="RP23-281H12"
```

## ORIGIN

Query Match 100.0%; Score 20; DB 2; Length 79302;  
Best Local Similarity 55.0%; Pred. No. 5.7;  
Matches 11; Conservative 9; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCUCUCCCGUCUCUUUG 20  
||:|:|:|:|:|:|:|:|:  
Db 58976 CCTCTCCGCTCCTTG 58995

RESULT 12  
AC015497/c

AC015497	158264 bp	DNA linear	HTG 11-APR-2000
LOCUS	Homo sapiens clone RP11-21G10,	WORKING DRAFT SEQUENCE, 27 unordered pieces.	
DEFINITION			

AC015497  
AC015497.3 GI:7533974  
HTG; HTGS\_PHASE1; HTGS\_DRAFT.  
Homo sapiens (human)

**SOURCE ORGANISM**

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 158264)  
 REFERENCE  
 AUTHORS Birren, B., Linton, L., Nusbaum, C. and Lander, E.  
 TITLE Homo sapiens, clone RP11-21G10

JOURNAL REFERENCE	Unpublished 2 (bases 1 to 158264)

## EXPERIENCE AUTHORS

AUTHORS

Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Baldwin, J., Barna, N., Beckerly, R., Boguslavsky, L., Boukhgalter, B., Brown, A., Castile, A., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M., Ferrie, P., Fitzhugh, W., Forrest, C., Funke, R., Gage, D., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heard, A., Horton, L., Howland, J. C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Lehoczy, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., McLaughlin, J., Meldrim, J., Morrow, J., Naylor, J., Norman, C. H., O'Connor, T., O'Donnell, P., Peterson, K., Pollara, V., Riley, R., Roy, A., Santos, R., Severy, P., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Tirrell, A., Vassiliev, H., Vo, A., Wheeler, J., Wu, X., Wyman, D., Ye, W. J., Zimmer, A. and Zody, M.

**TITLE**  
**JOURNAL**

DATE	DESCRIPTION
JOURNAL	Submitted (16-NOV-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
COMMENT	On Apr 11, 2000 this sequence version replaced gi:6587901. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)

<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

----- Genome Center  
<http://zcp.genome.washington.edu/jn/dependencies.html>

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIBR

Web site: <http://www-seq.wi.mit.edu>

Contact: [sequence\\_submissions@genome.wi.mit.edu](mailto:sequence_submissions@genome.wi.mit.edu)

----- Project Informa

Center project name: L4002

Center clone name: 21\_G\_10

----- Summary Statistics

Sequencing vector: M13; M77815; 100% of reads

Chemistry: Dye-terminator Big Dye; 100% of reads

Assembly program: Phrap; version 0.960731

Consensus quality: 118404 bases at least Q40

Consensus quality: 139706 bases at least Q30  
Consensus quality: 140210 bases at least Q30

Consensus quality: 149210 bases at least Q20  
Insert size: 111000: 333333-fn

Insert size: 11100; agarose-  
Insert size: 15564; sum of contents

Insert size: 155664; sum-of-configs  
Quality coverage: 5.1 in 020 bases: average-fn

Quality coverage: 3.1 in Q20 bases; agarose-gel

Quality coverage: 3.6 in Q20 bases; sum-of-contigs  
-----  
\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 27 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.

1  
1099: contig of 1099 bp in length  
1100: gap of 100 bp  
1200: contig of 1010 bp in length  
2209: contig of 1010 bp in length  
2309: gap of 100 bp  
2310: contig of 1015 bp in length  
3324: contig of 1015 bp in length  
3424: gap of 100 bp  
4909: contig of 1485 bp in length  
5009: gap of 100 bp  
6227: contig of 1218 bp in length  
6328: gap of 100 bp  
7565: contig of 1238 bp in length  
7656: gap of 100 bp  
8795: contig of 1130 bp in length  
8895: gap of 100 bp  
10887: contig of 1991 bp in length  
10986: gap of 100 bp  
13255: contig of 2269 bp in length  
13355: gap of 100 bp  
16474: contig of 3119 bp in length  
16475: gap of 100 bp  
19837: contig of 3262 bp in length  
19936: gap of 100 bp  
23049: contig of 3113 bp in length  
23149: gap of 100 bp  
26628: contig of 3479 bp in length  
26728: gap of 100 bp  
30236: contig of 3508 bp in length  
30336: gap of 100 bp  
33987: contig of 3651 bp in length  
34087: gap of 100 bp  
39137: contig of 5050 bp in length  
39237: gap of 100 bp  
44951: contig of 5714 bp in length  
45051: gap of 100 bp  
50383: contig of 5332 bp in length  
50483: gap of 100 bp  
55555: contig of 5072 bp in length  
55655: gap of 100 bp  
61723: contig of 6068 bp in length  
61823: gap of 100 bp  
68824: contig of 7001 bp in length  
68924: gap of 100 bp  
77617: contig of 8693 bp in length  
77717: gap of 100 bp  
86999: contig of 9282 bp in length  
87099: gap of 100 bp  
100322: contig of 13223 bp in length  
100323: gap of 100 bp  
113545: contig of 13123 bp in length  
113646: gap of 100 bp  
126470: contig of 12825 bp in length  
126471: gap of 100 bp  
126570: gap of 100 bp  
126571: 158264: contig of 31694 bp in length.

FEATURES

source

1. .158264  
/organism="Homo sapiens"  
/mol\_type="Genomic DNA"  
/db\_xref="taxon:9606"  
/clone="RP11-21G10"  
/clone\_lib="RP11-11 Human Male BAC"

1. .1059

misc\_feature

/note="assembly\_fragment"

misc\_feature

1200. .2209

misc\_feature  
/note="assembly\_fragment"  
2310. .3324  
/note="assembly\_fragment"  
3425. .4909  
/note="assembly\_fragment"  
5010. .6227  
/note="assembly\_fragment"  
6328. .7565  
/note="assembly\_fragment"  
7666. .8795  
/note="assembly\_fragment"  
8896. .10886  
/note="assembly\_fragment"  
10987. .13255  
/note="assembly\_fragment"  
13356. .16474  
/note="assembly\_fragment"  
16575. .19836  
/note="assembly\_fragment"  
19937. .23049  
/note="assembly\_fragment"  
23150. .26628  
/note="assembly\_fragment"  
26729. .30236  
/note="assembly\_fragment"  
30337. .33987  
/note="assembly\_fragment"  
34088. .39137  
/note="assembly\_fragment"  
39238. .44951  
/note="assembly\_fragment"  
45052. .50383  
/note="assembly\_fragment"  
50484. .55555  
/note="assembly\_fragment"  
55656. .61723  
/note="assembly\_fragment"  
61824. .68824  
/note="assembly\_fragment"  
68925. .77617  
/note="assembly\_fragment"  
77718. .86999  
/note="assembly\_fragment"  
clone\_end:SP6  
vector\_side:right"  
87100. .100322  
/note="assembly\_fragment"  
100423. .113545  
/note="assembly\_fragment"  
113646. .126470  
/note="assembly\_fragment"  
clone\_end:T7  
vector\_side:right"  
126571. .158264  
/note="assembly\_fragment"

ORIGIN

Query Match 100.0%; Score 20; DB 2; Length 158264;  
Best Local Similarity 55.0%; Pred.No.4.4;  
Matches 11; Conservative 9; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCUUCUUCUCCUGCUUUG 20

-Db 66378 CTTCTTCCTGCTCTTG 66359

RESULT 13

AL359092/c

LOCUS

DEFINITION

Human DNA sequence from clone Rp11-57C19 on chromosome 9, complete

sequence.

AL359092

ACCESSION

AL359092.14

VERSION

GI:13274746



## KEYWORDS

HTG. Homo sapiens (human)

## SOURCE

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

## REFERENCE

1 (bases 1 to 173463)

## AUTHORS

Lloyd, D.

## JOURNAL

Direct Submission

## COMMENT

Submitted (15-MAR-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquerry@sanger.ac.uk  
 requests: clonerequest@sanger.ac.uk  
 On Mar 12, 2001 this sequence version replaced gi:13273753.  
 During sequence assembly data is compared from overlapping clones.  
 where differences are found these are annotated as variations  
 together with a note of the overlapping clone name. Note that the  
 variation annotation may not be found in the sequence submission  
 corresponding to the overlapping clone, as we submit sequences with  
 only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all  
 regions were either double-stranded or sequenced with an alternate  
 chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such  
 as compressions and repeats; all regions were covered by at least  
 one plasmid subclone or more than one M13 subclone; and the  
 assembly was confirmed by restriction digest. The following  
 abbreviations are used to associate primary accession numbers given  
 in the feature table with their source databases: Em, EMBL; Swi,  
 SWISSPROT; Tr, TREMBL; Wp, WORMPEP; Information on the WORMPEP  
 database can be found at

[http://www.sanger.ac.uk/Projects/C\\_elegans/wormpep](http://www.sanger.ac.uk/Projects/C_elegans/wormpep) This sequence  
 was generated from part of bacterial clone contigs of human  
 chromosome 9, constructed by the Sanger Centre Chromosome 9 Mapping  
 Group. Further information can be found at

<http://www.sanger.ac.uk/HGP/Chr9>

RP11-57C19 is from the library RPC1-11.1 constructed by the group  
 of Pieter de Jong. For further details see

<http://www.chori.org/bacpac/home.htm>

VECTOR: pBACe3.6

This sequence is the entire insert of clone RP11-57C19 The true  
 left end of clone RP11-83J21 is at 160857 in this sequence. The  
 true right end of clone RP11-17L7 is at 26509 in this sequence.

## FEATURES

## source

1..173463  
 /organism="Homo sapiens"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:9606"  
 /chromosome="9"  
 /clone="RP11-57C19"  
 /clone\_lib="RPC1-11.1"

## misc\_feature

1..183  
 /note="match: GSS: Em:AQ035345"

## misc\_feature

6..403  
 /note="match: GSS: Em:AQ115418"

## repeat\_region

90..213  
 /note="12 repeat: matches 2575..2708 of consensus"

## repeat\_region

545..848  
 /note="AluX repeat: matches 1..304 of consensus"

## repeat\_region

1382..1677  
 /note="AluSp repeat: matches 1..297 of consensus"

## repeat\_region

1845..2114  
 /note="AluX repeat: matches 1..269 of consensus"

## repeat\_region

5671..5722  
 /note="26 copies 2 mer tt 71% conserved"

## misc\_feature

6481..6706  
 /note="match: GSS: Em:AQ088691"

## misc\_feature

complement(9530..10310)  
 /note="match: GSS: Em:AQ040221"

## misc\_feature

10440..10705  
 /note="match: GSS: Em:AQ097316"

## repeat\_region

10785..10968  
 /note="12 repeat: matches 2524..2707 of consensus"

## repeat\_region

11894..11943  
 /note="MER46C repeat: matches 284..333 of consensus"

## misc\_feature

complement(12898..13402)  
 /note="match: GSS: Em:B71356"

## repeat\_region

12899..13060  
 /note="MER3 repeat: matches 33..208 of consensus"

## repeat\_region

13559..13598  
 /note="2 copies 20 mer 100% conserved"

## repeat\_region

14220..14327  
 /note="L1MC4 repeat: matches 7751..7885 of consensus"

## misc\_feature

15419..15887  
 /note="match: GSS: Em:AQ545312"

## repeat\_region

15665..16010  
 /note="L1MB4 repeat: matches 5817..6185 of consensus"

## repeat\_region

16051..16318  
 /note="AluJo repeat: matches 7..265 of consensus"

## repeat\_region

16468..16770  
 /note="AluSg repeat: matches 1..303 of consensus"

## repeat\_region

16894..17185  
 /note="AluX repeat: matches 1..305 of consensus"

## repeat\_region

17193..17488  
 /note="AluX repeat: matches 1..297 of consensus"

## repeat\_region

19180..19344  
 /note="MER5A repeat: matches 1..173 of consensus"

## repeat\_region

19356..19597  
 /note="MER30 repeat: matches 1..230 of consensus"

## repeat\_region

19649..19778  
 /note="AluSg/x repeat: matches 1..132 of consensus"

## repeat\_region

19781..20059  
 /note="AluSg repeat: matches 1..290 of consensus"

## repeat\_region

22904..22983  
 /note="4 copies 20 mer 76% conserved"

## repeat\_region

23603..23911  
 /note="AluSp repeat: matches 1..310 of consensus"

## misc\_feature

complement(23996..24443)  
 /note="match: GSS: Em:AQ239485"

## misc\_feature

26524..26927  
 /note="match: GSS: Em:AQ893594"

## misc\_feature

26667..26930  
 /note="match: GSS: Em:AQ083068"

## misc\_feature

32584..32978  
 /note="match: GSS: Em:AQ112811"

## misc\_feature

34131..34553  
 /note="match: GSS: Em:AQ763967"

## misc\_feature

34143..34353  
 /note="match: GSS: Em:AQ001150"

## repeat\_region

35569..35654  
 /note="WIR repeat: matches 81..172 of consensus"

## repeat\_region

35847..36321  
 /note="MER82 repeat: matches 160..653 of consensus"

## repeat\_region

36322..36629  
 /note="AluX repeat: matches 1..309 of consensus"

## repeat\_region

36630..36672  
 /note="MER82 repeat: matches 117..160 of consensus"

## repeat\_region

36673..36841  
 /note="FAM repeat: matches 5..173 of consensus"

## repeat\_region

36844..37154  
 /note="AluX repeat: matches 1..312 of consensus"

## repeat\_region

37155..37312  
 /note="MER82 repeat: matches 1..117 of consensus"

## repeat\_region

37324..37374  
 /note="WIR repeat: matches 122..170 of consensus"

## repeat\_region

37375..37679  
 /note="AluSg repeat: matches 1..305 of consensus"

## repeat\_region

37680..37718  
 /note="WIR repeat: matches 83..122 of consensus"

## repeat\_region

37738..37817  
 /note="WIR repeat: matches 81..170 of consensus"

## repeat\_region

38230..38536  
 /note="AluJo repeat: matches 1..300 of consensus"

## repeat\_region

38537..38840  
 /note="AluX repeat: matches 1..302 of consensus"

## repeat\_region

38841..39144  
 /note="Alu repeat: matches 1..311 of consensus"

## repeat\_region

39417..39697



[illegible][illegible]

Quality coverage: 12.91x in Q20 bases; agarose-fp  
Quality coverage: 10.31x in Q20 bases; sum-of-contigs

-----  
\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 2 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.

\* 1 49995: contig of 49995 bp in length  
\* 49996 50095: gap of unknown length  
\* 50096 136641: contig of 86546 bp in length.

#### FEATURES

source

1..136641  
/organism="Canis familiaris"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9615"  
/clone="RP81-158C13"  
/clone\_lib="RP81"

misc\_feature

1..49995  
/note="assembly\_fragment"  
clone\_end:SP6  
vector\_side:right"

misc\_feature

50096..136641  
/note="assembly\_fragment"  
clone\_end:r7  
vector\_side:right"

#### ORIGIN

Query Match 95.0%; Score 19; DB 2; Length 136641;  
Best Local Similarity 52.6%; Pred. No. 13;  
Matches 10; Conservative 9; Mismatches 0; Indels 0; Gaps 0;

QY 2 CUUCUUCUCCUGCCUUCUUG 20

Db 18215 CTTCTTCCTGCTCCTTG 18197  
|:::|:::|:::|:::|:::|

Search completed: May 27, 2004, 02:16:45  
Job time : 425.652 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 26, 2004, 14:55:11 ; Search time 89.1973 Seconds  
(without alignments)  
952.539 Million cell updates/sec

Title: US-09-121-239-15

Perfect score: 20

Sequence: 1 CCUUCUCCUGCUCCUUG 20

Scoring table: OLIGO\_NUC

Gapop 60.0 , Gapext 60.0

Searched: 337863 seqs, 2124099041 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : N\_Geneseq\_29Jan04.\*  
1: Geneseqn1980s.\*  
2: Geneseqn1990s.\*  
3: Geneseqn2000s.\*  
4: Geneseqn2001as.\*  
5: Geneseqn2001bs.\*  
6: Geneseqn2002s.\*  
7: Geneseqn2003as.\*  
8: Geneseqn2003bs.\*  
9: Geneseqn2003cs.\*  
10: Geneseqn2004s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
C 1	20	100.0	20	3	AAZ60852	Oligonucleotide used to detect bcr b3-abl fusion transcripts.
C 2	20	100.0	20	3	AAZ60854	Fusion transcript; translocation; bcr b3 region; abl gene; amplification assay; detection assay; medical diagnosis;
C 3	20	100.0	20	3	AAZ60853	clinical monitoring; chimeric RNA; fusion RNA; condition marker; disease marker; cancer; leukemia; ss.
C 4	20	100.0	299	3	AAZ60864	Synthetic.
C 5	20	100.0	530	5	AAZ60855	WO2000054118-A1.
C 6	20	100.0	1538	7	ABX05481	03-FEB-2000.
C 7	20	100.0	5434	6	ABV77964	23-JUL-1999; 99WO-US016832.
C 8	20	100.0	35962	7	ABZ09862	23-JUL-1998; 98US-00121239.
C 9	18	90.0	396	6	ABL69622	(GENP-) GEN-PROBE INC.
C 10	18	90.0	474	8	ACH32870	Harvey RC, Eastman PS;
C 11	18	90.0	543	2	AAT19863	WPI; 2000-182730/16.
C 12	18	90.0	1345	6	ABA94712	Novel methods for preparing RNA from biological samples, used for the detection and measurement of nucleic acids and fusion nucleic acids.
C 13	18	90.0	1390	4	ADA57705	Claim 19; Page 42; 49pp; English.
C 14	18	90.0	1611	4	AAZ60852	Oligonucleotides AAZ60840-62 and AAZ60865-66 are used in the method of the invention to detect fusion transcripts produced from a translocation between the bcr b3 region and the abl gene. The specification describes a method for detecting a fusion nucleic acid (particularly chimeric mRNA species), in a biological sample. The method comprises contacting a sample of fusion nucleic acid with primers, amplifying the hybridized fusion nucleic acid, and detecting the target hybrid. The method is used for the sample and rapid preparation of RNA from a biological sample, particularly from the cytoplasm of eukaryotic cells, which is suitable for use in an amplification and detection assay. The methods are used for
C 15	18	90.0	1611	5	AAZ60853	
C 16	18	90.0	1859	4	AAZ60854	
C 17	18	90.0	1869	4	AAZ60855	
C 18	18	90.0	1869	8	ADA57705	
C 19	18	90.0	2177	4	AAZ60864	
C 20	18	90.0	3380	7	ABX05481	
C 21	17	85.0	416	6	ABV77964	
C 22	17	85.0	36305	6	ABZ09862	
C 23	17	85.0	39729	9	ACH32870	

24	17	85.0	55795	6	ABL68242	Ab168242 Kidney ca
25	17	85.0	55795	6	ABL68863	Ab168863 Kidney ca
26	17	85.0	55795	6	ABL68484	Ab168484 Kidney ca
27	17	85.0	55795	6	ABN95045	Abn95045 Gene #154
28	17	85.0	57273	6	ABK22784	Abk22784 Human hlg
29	17	85.0	66933	5	ABA82625	ABA82625 Human HBM
30	17	85.0	66933	7	ACC45366	ACC45366 Human HBM
31	17	85.0	66933	9	ADB98066	ADB98066 HBM-relat
32	17	85.0	66933	9	ADE82435	ADE82435 Human DNA
33	17	85.0	72049	5	ABA82623	ABA82623 Human HBM
34	17	85.0	72049	9	ACC45364	ACC45364 Human HBM
35	17	85.0	72049	9	ADB98064	ADB98064 HBM-relat
36	17	85.0	72049	9	ADE82433	ADE82433 Human DNA
37	16	80.0	444	4	AAZ60852	AAZ60852 Human sec
38	16	80.0	621	5	AAZ60852	AAZ60852 Human sec
39	16	80.0	1763	5	AAZ60852	AAZ60852 Human sec
40	16	80.0	1876	4	AAZ60852	AAZ60852 Human sec
41	16	80.0	2162	9	ADC32407	ADC32407 Human nov
42	16	80.0	2307	4	AAZ60852	AAZ60852 Human sec
43	16	80.0	2491	4	AAH15154	AAH15154 Human CON
44	16	80.0	3598	7	ADA57705	ADA57705 BAC fragm
45	16	80.0	3598	7	ADA41572	ADA41572 Human sec

## ALIGNMENTS

### RESULT 1

AAZ60852/c  
ID AAZ60852 standard; DNA; 20 BP.

XX AC AAZ60852;

XX DT 16-MAY-2000 (first entry)

XX DE Oligonucleotide used to detect bcr b3-abl fusion transcripts.

XX KW Fusion transcript; translocation; bcr b3 region; abl gene;

XX KW amplification assay; detection assay; medical diagnosis;

XX KW clinical monitoring; chimeric RNA; fusion RNA; condition marker;

XX KW disease marker; cancer; leukemia; ss.

XX OS Synthetic.

XX PN WO2000054118-A1.

XX PD 03-FEB-2000.

XX PF 23-JUL-1999; 99WO-US016832.

XX PR 23-JUL-1998; 98US-00121239.

XX PA (GENP-) GEN-PROBE INC.

XX PI Harvey RC, Eastman PS;

XX DR WPI; 2000-182730/16.

XX PT Novel methods for preparing RNA from biological samples, used for the detection and measurement of nucleic acids and fusion nucleic acids.

XX PT Claim 19; Page 42; 49pp; English.

XX PS Oligonucleotides AAZ60840-62 and AAZ60865-66 are used in the method of the invention to detect fusion transcripts produced from a translocation between the bcr b3 region and the abl gene. The specification describes a method for detecting a fusion nucleic acid (particularly chimeric mRNA species), in a biological sample. The method comprises contacting a sample of fusion nucleic acid with primers, amplifying the hybridized fusion nucleic acid, and detecting the target hybrid. The method is used for the sample and rapid preparation of RNA from a biological sample, particularly from the cytoplasm of eukaryotic cells, which is suitable for use in an amplification and detection assay. The methods are used for

CC the analysis and detection of nucleic acids in biological samples. The  
 CC methods are useful in the human medical and veterinary fields, for  
 CC medical diagnoses and clinical monitoring of a patient's response to  
 CC therapy where a disease or medical condition is associated with a  
 CC particular type and/or level of mRNA present in the sample. The methods  
 CC are also useful for detecting or quantifying fusion or chimeric RNA  
 CC species, and for detecting a translocation as a marker for a given  
 CC condition or disease, e.g. translocations associate with cancers,  
 CC particularly forms of leukemia  
 XX  
 SQ Sequence 20 BP; 9 A; 2 C; 9 G; 0 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 20; DB 3; Length 20;  
 Best Local Similarity 55.0%; Pred. No. 0.73;  
 Matches 11; Conservative 9; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 CCUCUUCUCCUGCUCUUCUUG 20  
 Db 20 CCTTCTTCCGTGCTCCTTGG 1  
 RESULT 2  
 AAZ60854  
 ID AAZ60854 standard; RNA; 20 BP.  
 XX  
 AC AAZ60854;  
 XX  
 DT 16-MAY-2000 (first entry)  
 XX  
 DE Oligonucleotide used to detect bcr b3-abl fusion transcripts.  
 XX  
 KW Fusion transcript; translocation; bcr b3 region; abl gene;  
 KW amplification assay; detection assay; medical diagnosis;  
 KW clinical monitoring; chimeric RNA; fusion RNA; condition marker;  
 KW disease marker; cancer; leukemia; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200005418-A1.  
 XX  
 PD 03-FEB-2000.  
 XX  
 PF 23-JUL-1999; 99WO-US016832.  
 XX  
 PR 23-JUL-1998; 98US-00121239.  
 XX  
 PA (GENP-) GEN-PROBE INC.  
 XX  
 PI Harvey RC, Eastman PS;  
 XX  
 DR WPI; 2000-182730/16.  
 XX  
 PT Novel methods for preparing RNA from biological samples, used for the  
 PT detection and measurement of nucleic acids and fusion nucleic acids.  
 XX  
 PS Claim 19; Page 42; 49pp; English.  
 XX  
 CC Oligonucleotides AAZ60840-62 and AAZ60865-66 are used in the method of  
 CC the invention to detect fusion transcripts produced from a translocation  
 CC between the bcr b3 region and the abl gene. The specification describes a  
 CC method for detecting a fusion nucleic acid (particularly chimeric mRNA  
 CC species), in a biological sample. The method comprises contacting a  
 CC sample of fusion nucleic acid with primers, amplifying the hybridized  
 CC fusion nucleic acid, and detecting the target hybrid. The method is used  
 CC for the simple and rapid preparation of RNA from a biological sample,  
 CC particularly from the cytoplasm of eukaryotic cells, which is suitable  
 CC for use in an amplification and detection assay. The methods are used for  
 CC the analysis and detection of nucleic acids in biological samples. The  
 CC methods are useful in the human medical and veterinary fields, for  
 CC medical diagnoses and clinical monitoring of a patient's response to  
 CC therapy where a disease or medical condition is associated with a  
 CC particular type and/or level of mRNA present in the sample. The methods  
 CC are also useful for detecting or quantifying fusion or chimeric RNA  
 CC species, and for detecting a translocation as a marker for a given  
 CC condition or disease, e.g. translocations associate with cancers,  
 CC particularly forms of leukemia  
 CC are also useful for detecting or quantifying fusion or chimeric RNA

CC species, and for detecting a translocation as a marker for a given  
 CC condition or disease, e.g. translocations associate with cancers,  
 CC particularly forms of leukemia  
 XX  
 SQ Sequence 20 BP; 0 A; 9 C; 2 G; 0 T; 9 U; 0 Other;  
 Query Match 100.0%; Score 20; DB 3; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 0.73;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 CCUCUUCUCCUGCUCUUCUUG 20  
 Db 1 CCUCUUCUCCUGCUCUUCUUG 20  
 RESULT 3  
 AAZ60853  
 ID AAZ60853 standard; DNA; 20 BP.  
 XX  
 AC AAZ60853;  
 XX  
 DT 16-MAY-2000 (first entry)  
 XX  
 DE Oligonucleotide used to detect bcr b3-abl fusion transcripts.  
 XX  
 KW Fusion transcript; translocation; bcr b3 region; abl gene;  
 KW amplification assay; detection assay; medical diagnosis;  
 KW clinical monitoring; chimeric RNA; fusion RNA; condition marker;  
 KW disease marker; cancer; leukemia; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200005418-A1.  
 XX  
 PD 03-FEB-2000.  
 XX  
 PF 23-JUL-1999; 99WO-US016832.  
 XX  
 PR 23-JUL-1998; 98US-00121239.  
 XX  
 PA (GENP-) GEN-PROBE INC.  
 XX  
 PI Harvey RC, Eastman PS;  
 XX  
 DR WPI; 2000-182730/16.  
 XX  
 PT Novel methods for preparing RNA from biological samples, used for the  
 PT detection and measurement of nucleic acids and fusion nucleic acids.  
 XX  
 PS Claim 19; Page 42; 49pp; English.  
 XX  
 CC Oligonucleotides AAZ60840-62 and AAZ60865-66 are used in the method of  
 CC the invention to detect fusion transcripts produced from a translocation  
 CC between the bcr b3 region and the abl gene. The specification describes a  
 CC method for detecting a fusion nucleic acid (particularly chimeric mRNA  
 CC species), in a biological sample. The method comprises contacting a  
 CC sample of fusion nucleic acid with primers, amplifying the hybridized  
 CC fusion nucleic acid, and detecting the target hybrid. The method is used  
 CC for the simple and rapid preparation of RNA from a biological sample,  
 CC particularly from the cytoplasm of eukaryotic cells, which is suitable  
 CC for use in an amplification and detection assay. The methods are used for  
 CC the analysis and detection of nucleic acids in biological samples. The  
 CC methods are useful in the human medical and veterinary fields, for  
 CC medical diagnoses and clinical monitoring of a patient's response to  
 CC therapy where a disease or medical condition is associated with a  
 CC particular type and/or level of mRNA present in the sample. The methods  
 CC are also useful for detecting or quantifying fusion or chimeric RNA  
 CC species, and for detecting a translocation as a marker for a given  
 CC condition or disease, e.g. translocations associate with cancers,  
 CC particularly forms of leukemia  
 XX  
 SQ Sequence 20 BP; 0 A; 9 C; 2 G; 9 T; 0 U; 0 Other;

Query Match	100.0%; Score 20; DB 3; Length 20;
Best Local Similarity	55.0%; Pred. No. 0.73;
Matches 11; Conservative	9; Mismatches 0; Indels 0; Gaps 0;
QY	1 CCUCUCCCGGCUCCUUUG 20   :::  :::  :::  ::   ::
DB	1 CCTTCCTCCCGCCTCCCTTG 20
RESULT 4	
AAZ60864/c	ID AAZ60864 standard; DNA; 299 BP.
XX AC	AAZ60864;
XX AC	
DT DT	16-MAY-2000 (first entry)
XX DE	Region surrounding a splice junction in a normal abl transcript.
XX KW	Fusion transcript; translocation; bcr b3 region; abl gene;
KW KW	amplification assay; detection assay; medical diagnosis;
KW KW	clinical monitoring; chimeric RNA; fusion RNA; condition marker;
KW XX	disease marker; cancer; leukemia; ss.
OS OS	Unidentified.
XX PN	WO200005418-A1.
XX PD	03-FEB-2000.
XX PF	23-JUL-1999; 99WO-US016832.
XX PR	23-JUL-1998; 98US-00121239.
XX PA	(GENP-) GEN-PROBE INC.
XX PI	Harvey RC, Eastman PS;
XX DR	WPI; 2000-182730/16.
XX PT	Novel methods for preparing RNA from biological samples, used for the
PT PT	detection and measurement of nucleic acids and fusion nucleic acids.
XX PS	Disclosure; Fig 3; 49pp; English.
XX CC	The present sequence represents a region surrounding a potential splice
CC CC	junction in a normal abl transcript. The specification describes
CC CC	oligonucleotides which are used to detect fusion transcripts produced
CC CC	from a translocation between the bcr b3 region and the abl gene. The
CC CC	specification also describes a method for detecting a fusion nucleic acid
CC CC	(particularly chimeric mRNA species), in a biological sample. The method
CC CC	comprises contacting a sample of fusion nucleic acid with primers,
CC CC	amplifying the hybridized fusion nucleic acid, and detecting the target
CC CC	hybrid. The method is used for the simple and rapid preparation of RNA
CC CC	from a biological sample, particularly from the cytoplasm of eukaryotic
CC CC	cells, which is suitable for use in an amplification and detection assay.
CC CC	The methods are used for the analysis and detection of nucleic acids in
CC CC	biological samples. The methods are useful in the human medical and
CC CC	veterinary fields, for medical diagnoses and clinical monitoring of a
CC CC	patients response to therapy where a disease or medical condition is
CC CC	associated with a particular type and/or level of mRNA present in the
CC CC	sample. The methods are also useful for detecting or quantifying fusion
CC CC	or chimeric RNA species, and for detecting a translocation as a marker
CC CC	for a given condition or disease, e.g. translocations associate with
CC CC	cancers, particularly forms of leukemia
XX SQ	Sequence 299 BP; 77 A; 70 C; 81 G; 71 T; 0 U; 0 Other;
Query Match	100.0%; Score 20; DB 3; Length 299;
Best Local Similarity	55.0%; Pred. No. 0.67;
Matches 11; Conservative	9; Mismatches 0; Indels 0; Gaps 0;
Qy	1 CCUCUCCCGGCUCCUUUG 20

ID ABX05481 standard; cDNA; 1538 BP.  
 AC ABX05481;  
 XX  
 DT 17-JAN-2003 (first entry)  
 DE XX  
 DE Human novel polynucleotide #496.  
 XX  
 KW Human; gene; ss; genetic disorder; gene mapping; medical imaging; cancer;  
 KW neurodegenerative disorder; lymphoid cell disorder; osteoporosis;  
 KW Parkinson's disease; Alzheimer's disease; bone degenerative disorder;  
 KW osteoarthritis; periodontal disease; liver fibrosis; viral infection;  
 KW fungal infection; bacterial infection; autoimmune disease; diabetes;  
 KW atopic dermatitis.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200274961-A1.  
 XX  
 PD 26-SEP-2002.  
 XX  
 PF 14-MAR-2002; 2002WO-US005109.  
 XX  
 PR 15-MAR-2001; 2001US-00810173.  
 XX  
 PA (HYSE-) HYSEQ INC.  
 XX  
 PI Tang YT, Zhou P, Goodrich R, Asundi V, Zhang J, Zhao QA, Ren F;  
 PI Xue AJ, Yang Y, Ma Y, Yamazaki V, Chen R, Wang Z, Ghosh M;  
 PI Wehrman T, Wang J, Wang D, Drmanac RT;  
 XX  
 DR WPI: 2003-040556/03.  
 DR P-PSDB; ABU00403.  
 XX  
 PT New isolated polypeptides and polynucleotides, useful for preventing,  
 PT treating or ameliorating medical conditions, such as cancer,  
 PT neurodegenerative disorders, lymphoid cell disorders, bone degenerative  
 PT disorders, and infections.  
 XX  
 PS Claim 1; SEQ ID NO 496; 235pp; English.  
 XX  
 CC The invention relates to human polynucleotides and the polypeptides they  
 CC encode. The polynucleotides and polypeptides are useful in diagnostics,  
 CC forensics, gene mapping, medical imaging, identification of mutations,  
 CC responsible for genetic disorders or other traits, assessing biodiversity  
 CC and producing many other types of data and products dependent on DNA and  
 CC amino acid sequences. They are also useful for preventing, treating or  
 CC ameliorating medical conditions, such as cancer, neurodegenerative  
 CC disorders (e.g. Parkinson's disease, Alzheimer's disease), lymphoid cell  
 CC disorders, osteoporosis, osteoarthritis, bone degenerative disorders,  
 CC periodontal disease, liver fibrosis, infections (e.g. viral, fungal or  
 CC bacterial) or autoimmune diseases (e.g. diabetes, atopic dermatitis).  
 CC Sequences ABX04986-ABX05511 represent human polynucleotides of the  
 CC invention. Note: The sequence data for this patent is not represented in  
 CC the printed specification but is based on sequence information supplied  
 CC by the European Patent Office  
 XX  
 SQ Sequence 1538 BP; 344 A; 399 C; 410 G; 385 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 20; DB 7; Length 1538;  
 Best Local Similarity 55.0%; Pred. No. 0.64;  
 Matches 11; Conservative 9; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CCUUCUCCUGCUCUUG 20  
 ||:||||:||||:||||:  
 DB 1346 CCTTCTCCCTGCTCTTTG 1327  
 RESULT 7  
 ABV77964/C  
 ID ABV77964 standard; DNA; 5434 BP.  
 XX  
 AC ABV77964;

XX  
 DT 12-NOV-2002 (first entry)  
 XX  
 DE Hypoxia-repressed protein coding sequence #32.  
 XX  
 KW Cytostatic; vasotropic; tranquiliser; antiatherosclerotic; gene therapy;  
 KW antiinflammatory; vulnary; gynecological; ophthalmological; vaccine;  
 KW hypoxia; tumorigenesis; angiogenesis; apoptosis; cancer;  
 KW ischaemic condition; reperfusion injury; retinopathy; neonatal stress;  
 KW presclamsia; atherosclerosis; inflammatory condition; wound healing;  
 KW inflammation; erythropoiesis; hair loss; human; gene; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200246465-A2.  
 XX  
 PD 13-JUN-2002.  
 XX  
 PF 10-DEC-2001; 2001WO-GB005458.  
 XX  
 PR 08-DEC-2000; 2000GB-00030076.  
 PR 08-FEB-2001; 2001GB-0003156.  
 PR 25-OCT-2001; 2001GB-00025666.  
 XX  
 PA (OXFO-) OXFORD BIOMEDICA UK LTD.  
 XX  
 PI White J, Mundy CR, Ward NR, Krige D, Kingsman SM, Harris RA;  
 PI Rayner WN;  
 XX  
 DR WPI: 2002-627238/67.  
 XX  
 PT Identifying a gene involved in disease for treating hypoxia-regulated  
 PT conditions, comprises comparing the transcriptome/proteome of two cell  
 PT types under different conditions and identifying a differentially  
 PT regulated gene.  
 XX  
 PS Claim 23; Page 326-327; 538pp; English.  
 XX  
 CC The present invention relates to methods for identifying genes and  
 CC proteins that are implicated in a specific disease or physiological  
 CC condition. The method comprises comparing the transcriptome/proteome of a  
 CC specialised cell type implicated in a disease or condition with that of a  
 CC second specialised cell type, under two experimental conditions, and  
 CC identifying a gene that is differentially regulated in the two  
 CC specialised cell types under experimental conditions. ABV77873-ABV78116  
 CC and ABP65061-ABP65257 were identified using the methods of the invention.  
 CC The coding sequences and proteins are useful for treating a disease in a  
 CC patient, for manufacture of a medicament for treating hypoxia-regulated  
 CC conditions, and for regulating tumorigenesis, angiogenesis, apoptosis,  
 CC biological response to hypoxia conditions, or hypoxic-associated  
 CC pathology in a patient. The coding sequences and proteins are also useful  
 CC for monitoring the therapeutic treatment of a disease or physiological  
 CC condition, such as cancer, ischaemic conditions, reperfusion injury,  
 CC retinopathy, neonatal stress, presclamsia, atherosclerosis, inflammatory  
 CC conditions, wound healing, inflammation, erythropoiesis or hair loss  
 XX  
 SQ Sequence 5434 BP; 1208 A; 1632 C; 1529 G; 1065 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 20; DB 6; Length 5434;  
 Best Local Similarity 55.0%; Pred. No. 0.61;  
 Matches 11; Conservative 9; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CCUUCUCCUGCUCUUG 20  
 ||:||||:||||:||||:  
 DB 88 CCTTCTCCCTGCTCTTTG 69  
 RESULT 8  
 ABZ09862/C  
 ID ABZ09862 standard; DNA; 35962 BP.  
 XX  
 AC ABZ09862;











QY 3 UCUUCCUGGCUUUG 20  
 Db 1182 TTCTCCGCGCTGTG 1165

RESULT 14

AA06632

ID AAL06632 standard; DNA; 1611 BP.

XX AC AAL06632;

XX DT 21-NOV-2001 (first entry)

XX DE Human reproductive system related antigen DNA SEQ ID NO: 9320.

XX KW Human; reproductive system related antigen; reproductive system disorder;

XX KW cancer; gene therapy; ds.

XX OS Homo sapiens.

XX PN WO200155320-A2.

XX PD 02-AUG-2001.

XX PF 17-JAN-2001; 2001WO-US001339.

XX 31-JAN-2000; 2000US-0179065P.

PR 04-FEB-2000; 2000US-0180628P.

PR 24-FEB-2000; 2000US-0184664P.

PR 16-MAR-2000; 2000US-0186350P.

PR 16-MAR-2000; 2000US-0189874P.

PR 17-MAR-2000; 2000US-0190076P.

PR 18-APR-2000; 2000US-0198123P.

PR 19-MAY-2000; 2000US-0205515P.

PR 07-JUN-2000; 2000US-0209467P.

PR 28-JUN-2000; 2000US-0214886P.

PR 30-JUN-2000; 2000US-0215135P.

PR 07-JUL-2000; 2000US-0216647P.

PR 07-JUL-2000; 2000US-0216880P.

PR 11-JUL-2000; 2000US-0217487P.

PR 11-JUL-2000; 2000US-0217496P.

PR 14-JUL-2000; 2000US-0218290P.

PR 26-JUL-2000; 2000US-0220963P.

PR 26-JUL-2000; 2000US-0220964P.

PR 14-AUG-2000; 2000US-0224518P.

PR 14-AUG-2000; 2000US-0224519P.

PR 14-AUG-2000; 2000US-0225213P.

PR 14-AUG-2000; 2000US-0225214P.

PR 14-AUG-2000; 2000US-0225266P.

PR 14-AUG-2000; 2000US-0225267P.

PR 14-AUG-2000; 2000US-0225268P.

PR 14-AUG-2000; 2000US-0225270P.

PR 14-AUG-2000; 2000US-0225447P.

PR 14-AUG-2000; 2000US-0225757P.

PR 14-AUG-2000; 2000US-0225758P.

PR 14-AUG-2000; 2000US-0225759P.

PR 18-AUG-2000; 2000US-0226279P.

PR 22-AUG-2000; 2000US-0226681P.

PR 22-AUG-2000; 2000US-0226688P.

PR 22-AUG-2000; 2000US-0227182P.

PR 23-AUG-2000; 2000US-0227009P.

PR 30-AUG-2000; 2000US-0228924P.

PR 01-SEP-2000; 2000US-0229287P.

PR 01-SEP-2000; 2000US-0229343P.

PR 01-SEP-2000; 2000US-0229344P.

PR 01-SEP-2000; 2000US-0229345P.

PR 05-SEP-2000; 2000US-0229509P.

PR 05-SEP-2000; 2000US-0229513P.

PR 06-SEP-2000; 2000US-0230437P.

PR 06-SEP-2000; 2000US-0230438P.

PR 08-SEP-2000; 2000US-0231242P.

PR 08-SEP-2000; 2000US-0231243P.

PR 08-SEP-2000; 2000US-0231244P.  
 PR 08-SEP-2000; 2000US-0231413P.  
 PR 08-SEP-2000; 2000US-0231414P.  
 PR 08-SEP-2000; 2000US-0232080P.  
 PR 08-SEP-2000; 2000US-0232081P.  
 PR 12-SEP-2000; 2000US-0231968P.  
 PR 14-SEP-2000; 2000US-0232397P.  
 PR 14-SEP-2000; 2000US-0232398P.  
 PR 14-SEP-2000; 2000US-0232399P.  
 PR 14-SEP-2000; 2000US-0232400P.  
 PR 14-SEP-2000; 2000US-0232401P.  
 PR 14-SEP-2000; 2000US-0233063P.  
 PR 14-SEP-2000; 2000US-0233064P.  
 PR 14-SEP-2000; 2000US-0233065P.  
 PR 21-SEP-2000; 2000US-0234223P.  
 PR 21-SEP-2000; 2000US-0234274P.  
 PR 25-SEP-2000; 2000US-0234997P.  
 PR 25-SEP-2000; 2000US-0234998P.  
 PR 26-SEP-2000; 2000US-0235484P.  
 PR 27-SEP-2000; 2000US-0235834P.  
 PR 27-SEP-2000; 2000US-0235836P.  
 PR 29-SEP-2000; 2000US-0236327P.  
 PR 29-SEP-2000; 2000US-0236367P.  
 PR 29-SEP-2000; 2000US-0236368P.  
 PR 29-SEP-2000; 2000US-0236369P.  
 PR 29-SEP-2000; 2000US-0236370P.  
 PR 02-OCT-2000; 2000US-0236802P.  
 PR 02-OCT-2000; 2000US-0237037P.  
 PR 02-OCT-2000; 2000US-0237038P.  
 PR 02-OCT-2000; 2000US-0237039P.  
 PR 02-OCT-2000; 2000US-0237040P.  
 PR 13-OCT-2000; 2000US-0239935P.  
 PR 20-OCT-2000; 2000US-0239937P.  
 PR 20-OCT-2000; 2000US-0240960P.  
 PR 20-OCT-2000; 2000US-0241221P.  
 PR 20-OCT-2000; 2000US-0241785P.  
 PR 20-OCT-2000; 2000US-0241786P.  
 PR 20-OCT-2000; 2000US-0241787P.  
 PR 20-OCT-2000; 2000US-0241808P.  
 PR 20-OCT-2000; 2000US-0241809P.  
 PR 01-NOV-2000; 2000US-0244617P.  
 PR 08-NOV-2000; 2000US-0246474P.  
 PR 08-NOV-2000; 2000US-0246475P.  
 PR 08-NOV-2000; 2000US-0246476P.  
 PR 08-NOV-2000; 2000US-0246477P.  
 PR 08-NOV-2000; 2000US-0246478P.  
 PR 08-NOV-2000; 2000US-0246523P.  
 PR 08-NOV-2000; 2000US-0246524P.  
 PR 08-NOV-2000; 2000US-0246525P.  
 PR 08-NOV-2000; 2000US-0246526P.  
 PR 08-NOV-2000; 2000US-0246527P.  
 PR 08-NOV-2000; 2000US-0246528P.  
 PR 08-NOV-2000; 2000US-0246532P.  
 PR 08-NOV-2000; 2000US-0246609P.  
 PR 08-NOV-2000; 2000US-0246610P.  
 PR 08-NOV-2000; 2000US-0246611P.  
 PR 08-NOV-2000; 2000US-0246613P.  
 PR 17-NOV-2000; 2000US-0249207P.  
 PR 17-NOV-2000; 2000US-0249208P.  
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 PR 17-NOV-2000; 2000US-0249211P.  
 PR 17-NOV-2000; 2000US-0249212P.  
 PR 17-NOV-2000; 2000US-0249213P.  
 PR 17-NOV-2000; 2000US-0249214P.  
 PR 17-NOV-2000; 2000US-0249215P.  
 PR 17-NOV-2000; 2000US-0249216P.  
 PR 17-NOV-2000; 2000US-0249217P.  
 PR 17-NOV-2000; 2000US-0249218P.  
 PR 17-NOV-2000; 2000US-0249244P.  
 PR 17-NOV-2000; 2000US-0249245P.  
 PR 17-NOV-2000; 2000US-0249264P.



PR 13-OCT-2000; 2000US-0239937P.  
 PR 20-OCT-2000; 2000US-0240960P.  
 PR 20-OCT-2000; 2000US-0241221P.  
 PR 20-OCT-2000; 2000US-0241785P.  
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 PR 20-OCT-2000; 2000US-0241808P.  
 PR 20-OCT-2000; 2000US-0241809P.  
 PR 20-OCT-2000; 2000US-0241826P.  
 PR 01-NOV-2000; 2000US-0244617P.  
 PR 08-NOV-2000; 2000US-0246474P.  
 PR 08-NOV-2000; 2000US-0246475P.  
 PR 08-NOV-2000; 2000US-0246476P.  
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 PR 08-NOV-2000; 2000US-0246478P.  
 PR 08-NOV-2000; 2000US-0246523P.  
 PR 08-NOV-2000; 2000US-0246525P.  
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 PR 17-NOV-2000; 2000US-0249216P.  
 PR 17-NOV-2000; 2000US-0249217P.  
 PR 17-NOV-2000; 2000US-0249218P.  
 PR 17-NOV-2000; 2000US-0249244P.  
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 PR 17-NOV-2000; 2000US-0249264P.  
 PR 17-NOV-2000; 2000US-0249265P.  
 PR 17-NOV-2000; 2000US-0249297P.  
 PR 17-NOV-2000; 2000US-0249299P.  
 PR 01-DEC-2000; 2000US-0249300P.  
 PR 01-DEC-2000; 2000US-0250160P.  
 PR 05-DEC-2000; 2000US-0250391P.  
 PR 05-DEC-2000; 2000US-0251030P.  
 PR 05-DEC-2000; 2000US-0251988P.  
 PR 05-DEC-2000; 2000US-0256719P.  
 PR 06-DEC-2000; 2000US-0251479P.  
 PR 08-DEC-2000; 2000US-0251856P.  
 PR 08-DEC-2000; 2000US-0251868P.  
 PR 08-DEC-2000; 2000US-0251869P.  
 PR 08-DEC-2000; 2000US-0251989P.  
 PR 08-DEC-2000; 2000US-0251990P.  
 PR 11-DEC-2000; 2000US-0254097P.  
 PR 05-JAN-2001; 2001US-0259678P.  
 (HUMA-) HUMAN GENOME SCI INC.

PA  
 XX  
 PI Rosen CA, Barash SC, Ruben SM;  
 XX WPI; 2001-451929/48.

XX Isolated polypeptide for treating, preventing and/ or prognosing  
 PT disorders related to the reproductive system including prostate cancer  
 PT and also for testing and detection e.g. diagnosis.

XX Disclosure; SEQ ID NO 867; 546pp; English.

XX The invention relates to novel isolated human prostate cancer antigen  
 CC polynucleotides (I) and polypeptides (II). (I) and (II) are useful for

CC preventing, treating or ameliorating a medical condition when  
 CC administered. (I), (II) and the antibody to (II) are useful for treating,  
 CC preventing and/ or prognosing disorders related to the reproductive  
 CC system including prostate cancers; urinary disorders e.g. chronic  
 CC nephritis; and blood-related disorders e.g. thrombosis. (II) can be used  
 CC for testing and detection e.g. as a chromosomal marker and in forensics.  
 CC (I) and the anti-(II) antibody can be used in testing and detection in  
 CC immunoassays. AAS40061-AAS40775 represent the human prostate cancer  
 CC antigen coding sequences, and related PCR primers and sequences of the  
 CC invention. Note: The sequence data for this patent did not form part of  
 CC the printed specification, but was obtained in electronic format directly  
 CC from WIPO at: ftp.wipo.int/pub/published\_pct\_sequences  
 XX

SQ Sequence 1611 BP; 491 A; 377 C; 391 G; 352 T; 0 U; 0 Other;

Query Match 90.0%; Score 18; DB 5; Length 1611;  
 Best Local Similarity 50.0%; Pred. No. 6.4;  
 Matches 9; Conservative 9; Mismatches 0; Indels 0; Gaps 0;

QY 3 UUCUUCUCCUGCUCUUUG 20  
 ::::||||:|::|::|  
 Db 166 TTCTTCCCTGCTCTTTG 183

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GenCore version 5.1.1.6  
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OM nucleic - nucleic search, using sw model

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Title: US-09-121-239-15

Perfect score: 20

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Gapop 60.0 , Gapext 60.0

Searched: 682709 seqs, 277475446 residues

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5: /cgn2\_6/ptodata/2/ina/PTUS\_COMB.seq:\*  
6: /cgn2\_6/ptodata/2/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 2	16	80.0	16938	4	US-09-676-610B-24
C 3	16	80.0	197496	4	US-09-877-177A-10
C 4	15	75.0	533	4	US-09-621-976-159
C 5	15	75.0	9217	4	US-09-634-238-402
C 6	14	70.0	303	4	US-09-313-294A-6758
C 7	14	70.0	418	2	US-08-691-814B-105
C 8	14	70.0	440	4	US-09-621-976-14605
C 9	14	70.0	673	3	US-09-040-984-33
C 10	14	70.0	673	4	US-09-123-912-33
C 11	14	70.0	673	4	US-09-643-597-33
C 12	14	70.0	673	4	US-09-480-884A-33
C 13	14	70.0	673	4	US-09-542-615A-33
C 14	14	70.0	673	4	US-09-606-421B-33
C 15	14	70.0	673	4	US-09-221-107-33
C 16	14	70.0	1350	4	US-09-149-476-248
C 17	14	70.0	1503	4	US-09-254-465A-5
C 18	14	70.0	1521	2	US-09-004-502-2
C 19	14	70.0	1521	3	US-09-360-125-2
C 20	14	70.0	1590	4	US-09-369-247-14
C 21	14	70.0	1744	4	US-09-484-970B-83
C 22	14	70.0	2181	4	US-09-254-465A-7
C 23	14	70.0	2181	4	US-09-254-465A-11
C 24	14	70.0	41100	4	US-09-755-665-46
C 25	14	70.0	62804	4	US-09-800-960-3
C 26	14	70.0	62804	4	US-10-096-960-3
C 27	13	65.0	249	4	US-09-107-532A-2549

C	28	13	65.0	287	4	US-09-313-294A-1166	Sequence 1166, Ap
	29	13	65.0	302	4	US-09-313-294A-1121	Sequence 1121, Ap
	30	13	65.0	333	4	US-09-621-976-16174	Sequence 16174, A
	31	13	65.0	352	4	US-09-621-976-1644	Sequence 1644, Ap
C	32	13	65.0	387	4	US-09-489-039A-6598	Sequence 6598, Ap
	33	13	65.0	400	4	US-09-621-976-16175	Sequence 16175, A
	34	13	65.0	404	4	US-09-539-333D-202	Sequence 202, App
	35	13	65.0	418	4	US-09-621-976-16177	Sequence 16177, A
	36	13	65.0	438	4	US-09-621-976-1841	Sequence 1841, Ap
C	37	13	65.0	447	4	US-09-621-976-1813	Sequence 8713, Ap
	38	13	65.0	462	4	US-09-621-976-15146	Sequence 15146, A
C	39	13	65.0	463	3	US-09-104-308-3	Sequence 3, Appli
	40	13	65.0	463	3	US-09-321-981-3	Sequence 3, Appli
	41	13	65.0	463	4	US-09-739-861A-3	Sequence 3, Appli
C	42	13	65.0	463	4	US-09-795-583-3	Sequence 3, Appli
	43	13	65.0	511	4	US-09-404-879A-70	Sequence 70, Appl
	44	13	65.0	511	4	US-09-338-933-70	Sequence 70, Appl
	45	13	65.0	511	4	US-09-215-681-70	Sequence 70, Appl

ALIGNMENTS

RESULT 1  
US-09-620-312D-704/c  
; Sequence 704, Application US/09620312D  
; Patent No. 6569662  
; GENERAL INFORMATION:  
; APPLICANT: Tang, Y. Tom  
; APPLICANT: Liu, Chenghua  
; APPLICANT: Asundi, Vinod  
; APPLICANT: Zhang, Jie  
; APPLICANT: Ren, Feiyan  
; APPLICANT: Chen, Rui-hong  
; APPLICANT: Zhao, Qing A.  
; APPLICANT: Wehrman, Tom  
; APPLICANT: Xue, Aidong J.  
; APPLICANT: Yang, Yonghong  
; APPLICANT: Wang, Jian-Rui  
; APPLICANT: Zhou, Ping  
; APPLICANT: Ma, Yunqing  
; APPLICANT: Wang, Dunrui  
; APPLICANT: Wang, Zhiwei  
; APPLICANT: John Tillinghast  
; APPLICANT: Drmanac, Radoje T.  
; TITLE OF INVENTION: No. 6569662el Nucleic Acids and  
; FILE REFERENCE: 784CIP2B  
; CURRENT APPLICATION NUMBER: US/09/620,312D  
; CURRENT FILING DATE: 2000-07-19  
; PRIOR APPLICATION NUMBER: 09/552,317  
; PRIOR FILING DATE: 2000-04-25  
; PRIOR APPLICATION NUMBER: 09/488,725  
; PRIOR FILING DATE: 2000-01-21  
; NUMBER OF SEQ ID NOS: 1105  
; SOFTWARE: pt FL\_genes Version 1.0  
; SEQ ID NO 704  
; LENGTH: 1869  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (161)..(1792)  
US-09-620-312D-704

Query Match 90.0%; Score 18; DB 4; Length 1869;  
Best Local Similarity 50.0%; Pred. No. 0.4;  
Matches 9; Conservative 9; Mismatches 0; Indels 0; Gaps 0;  
Qy 3 UUCUUCUCCGUCUUG 20  
DB 1695 TCCTCCCTGCTCCCTTG 1678

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US-09-676-610B-24
; Sequence 24, Application US/09676610B
; Patent No. 644465
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Jacqueline Wyatt
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: OLIGONUCLEOTIDE INHIBITION OF HER-1 EXPRESSION
; FILE REFERENCE: R1S-0138
; CURRENT APPLICATION NUMBER: US/09/676,610B
; CURRENT FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 182
; SEQ ID NO 24
; LENGTH: 169998
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: exon
; LOCATION: (1208)...(1472)
; NAME/KEY: intron
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; LOCATION: (124391)...(124544)
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Matches 8; Conservative 8; Mismatches 0; Indels 0; Gaps 0;
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RESULT 3
US-09-877-177A-10
; Sequence 10, Application US/09877177A
; Patent No. 6582919
; GENERAL INFORMATION:
; APPLICANT: K. Danenberg
; TITLE OF INVENTION: Method of determining Epidermal Growth
; TITLE OF INVENTION: Factor Receptor and HER2-Neu Gene Expression
; TITLE OF INVENTION: and Correlation of Levels Thereof with Survival
; FILE REFERENCE: 11220/120
; CURRENT APPLICATION NUMBER: US/09/877,177A
; CURRENT FILING DATE: 2001-06-11
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 197496
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-877-177A-10
Query Match 80.0%; Score 16; DB 4; Length 197496;
Best Local Similarity 50.0%; Pred. No. 5.1;
Matches 8; Conservative 8; Mismatches 0; Indels 0; Gaps 0;
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Db 97308 TTCTTCCCTGCTCCTT 97323
RESULT 4
US-09-621-976-159/c
; Sequence 159, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
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; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
US-08-691-814B-105

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Best Local Similarity 57.1%; Pred. No. 51;
Matches 8; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCUUCUCCUCCU 14
Db 348 CCTTCTCCCTGCT 361

RESULT 8
US-09-621-976-14605
; Sequence 14605, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 14605
; LENGTH: 440
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-621-976-14605

Query Match          70.0%; Score 14; DB 4; Length 440;
Best Local Similarity 57.1%; Pred. No. 51;
Matches 8; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

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Db 301 CTTCCCTGCTCCTT 314

RESULT 9
US-09-040-984-33/c
; Sequence 33, Application US/09040984
; Patent No. 6210883
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Wang, Tongtong
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS
; TITLE OF INVENTION: OF LUNG CANCER
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSES: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/040,984
; FILING DATE: 18-MAR-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.456

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-622-4900
; TELEFAX: 206-282-6031
; TELEX:
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 673 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-040-984-33

Query Match          70.0%; Score 14; DB 3; Length 673;
Best Local Similarity 50.0%; Pred. No. 51;
Matches 7; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 6 UUCCUCCUCCU 19
Db 142 TTCCTGCTCCTTT 129

RESULT 10
US-09-123-912-33/c
; Sequence 33, Application US/09123912A
; Patent No. 6312695
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Wang, Tongtong
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY OF LUNG CANCER
; FILE REFERENCE: 210121.455C1
; CURRENT APPLICATION NUMBER: US/09/123,912A
; CURRENT FILING DATE: 1998-07-27
; PRIOR APPLICATION NUMBER: 09/040,802
; PRIOR FILING DATE: 1998-03-18
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 33
; LENGTH: 673
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
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; LOCATION: (538)
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; LOCATION: (542)
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; LOCATION: (616)
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; NAME/KEY: modified_base
; LOCATION: (651)
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; NAME/KEY: modified_base
; LOCATION: (653)
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; OTHER INFORMATION: Where n is a, c, g or t
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; LOCATION: (672)
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US-09-123-912-33

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Db      142 TTCCCTGCTCCTTT 129

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; Patent No. 6426072
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C11
; CURRENT APPLICATION NUMBER: US/09/643,597
; CURRENT FILING DATE: 2000-08-21
; NUMBER OF SEQ ID NOS: 369
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 33
; LENGTH: 673
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(673)
; OTHER INFORMATION: n = A,T,C or G
US-09-643-597-33

Query Match          70.0%; Score 14; DB 4; Length 673;
Best Local Similarity 50.0%; Pred. No. 51;
Matches 7; Conservative 0; Indels 0; Gaps 0;

Qy      6 UUUCCUGGCUCCUUU 19
Db      142 TTCCCTGCTCCTTT 129

RESULT 12
US-09-480-884A-33/c
; Sequence 33, Application US/09480884A
; Patent No. 6482597
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Hosken, Nancy A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C6
; CURRENT APPLICATION NUMBER: US/09/480,884A
; CURRENT FILING DATE: 2001-08-27
; NUMBER OF SEQ ID NOS: 330

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; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 33
; LENGTH: 673
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(673)
; OTHER INFORMATION: n = A,T,C or G
US-09-480-884A-33

Query Match          70.0%; Score 14; DB 4; Length 673;
Best Local Similarity 50.0%; Pred. No. 51;
Matches 7; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

Qy      6 UUUCCUGGCUCCUUU 19
Db      142 TTCCCTGCTCCTTT 129

RESULT 13
US-09-542-615A-33/c
; Sequence 33, Application US/09542615A
; Patent No. 6518256
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy A.
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C8
; CURRENT APPLICATION NUMBER: US/09/542,615A
; CURRENT FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 33
; LENGTH: 673
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(673)
; OTHER INFORMATION: n = A,T,C or G
US-09-542-615A-33

Query Match          70.0%; Score 14; DB 4; Length 673;
Best Local Similarity 50.0%; Pred. No. 51;
Matches 7; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

Qy      6 UUUCCUGGCUCCUUU 19
Db      142 TTCCCTGCTCCTTT 129

RESULT 14
US-09-606-421B-33/c
; Sequence 33, Application US/09606421B
; Patent No. 6531315
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER

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; FILE REFERENCE: 210121.455C9
; CURRENT APPLICATION NUMBER: US/09/606,421B
; CURRENT FILING DATE: 2000-06-28
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 33
; LENGTH: 673
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(673)
; OTHER INFORMATION: n = A,T,C or G
US-09-606-421B-33

Query Match      70.0%; Score 14; DB 4; Length 673;
Best Local Similarity 50.0%; Pred. No. 51;
Matches 7; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

Qy      6 UUUCCUGGCUCCUUU 19
      ::|||::|||::|||::
Db      142 TTCCTGTCTCCTTT 129

RESULT 15
US-09-221-107-33/c
; Sequence 33, Application US/09221107
; Patent No. 6660838
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY OF LUNG CANCER
; FILE REFERENCE: 210121.455C2
; CURRENT APPLICATION NUMBER: US/09/221,107
; CURRENT FILING DATE: 1998-12-22
; NUMBER OF SEQ ID NOS: 161
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 33
; LENGTH: 673
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (325)
; OTHER INFORMATION: Where n is a, c, g or t
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (419)
; OTHER INFORMATION: Where n is a, c, g or t
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (452)
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; NAME/KEY: modified_base
; LOCATION: (532)
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; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (538)
; OTHER INFORMATION: Where n is a, c, g or t
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (542)
; OTHER INFORMATION: Where n is a, c, g or t
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (571)
; OTHER INFORMATION: Where n is a, c, g or t
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (600)
; OTHER INFORMATION: Where n is a, c, g or t
; FEATURE:

; NAME/KEY: modified_base
; LOCATION: (616)
; OTHER INFORMATION: Where n is a, c, g or t
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (651)
; OTHER INFORMATION: Where n is a, c, g or t
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (653)
; OTHER INFORMATION: Where n is a, c, g or t
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (672)
; OTHER INFORMATION: Where n is a, c, g or t
US-09-221-107-33

Query Match      70.0%; Score 14; DB 4; Length 673;
Best Local Similarity 50.0%; Pred. No. 51;
Matches 7; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

Qy      6 UUUCCUGGCUCCUUU 19
      ::|||::|||::|||::
Db      142 TTCCTGTCTCCTTT 129

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Job time : 16.8562 secs
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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: May 27, 2004, 11:30:47 ; Search time 105.251 Seconds  
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Title: US-09-121-239-15  
Perfect score: 20  
Sequence: 1 CCUUCUCCUGCUCCUUG 20

Scoring table: OLIGO.NUC  
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Searched: 2960401 seqs, 2274450654 residues

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- 9: /cgn2\_6/ptodata/2/pubpna/US09A\_PUBCOMB.seq.\*
- 10: /cgn2\_6/ptodata/2/pubpna/US09B\_PUBCOMB.seq.\*
- 11: /cgn2\_6/ptodata/2/pubpna/US09C\_PUBCOMB.seq.\*
- 12: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq.\*
- 13: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq.\*
- 14: /cgn2\_6/ptodata/2/pubpna/US10A\_PUBCOMB.seq.\*
- 15: /cgn2\_6/ptodata/2/pubpna/US10B\_PUBCOMB.seq.\*
- 16: /cgn2\_6/ptodata/2/pubpna/US10C\_PUBCOMB.seq.\*
- 17: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq.\*
- 18: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq.\*
- 19: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	20	100.0	186	15	US-10-029-386-23233
C 2	20	100.0	530	17	US-10-148-641A-19
C 3	20	100.0	551	15	US-10-029-386-9533
C 4	20	100.0	3450	16	US-10-457-954-5
C 5	20	100.0	5434	13	US-10-170-385-182
C 6	18	90.0	396	9	US-09-969-708-488
C 7	18	90.0	474	10	US-09-918-995-20082
C 8	18	90.0	620	13	US-10-027-632-278076
C 9	18	90.0	620	16	US-10-027-632-278076
C 10	18	90.0	1345	16	US-10-332-424-9
C 11	18	90.0	1611	10	US-09-764-891-9320
C 12	18	90.0	1611	15	US-10-091-572-867
C 13	18	90.0	1726	16	US-10-108-260A-1
C 14	18	90.0	1869	15	US-10-037-270-704

C 15	18	90.0	1869	16	US-10-117-722-704	Sequence 704, Ap
C 16	17	85.0	416	9	US-09-880-107-2953	Sequence 2953, Ap
C 17	17	85.0	965	13	US-10-027-632-323768	Sequence 323768, Ap
C 18	17	85.0	965	16	US-10-027-632-323768	Sequence 323768, Ap
C 19	17	85.0	2564	13	US-10-027-632-111606	Sequence 111606, Ap
C 20	17	85.0	2564	16	US-10-027-632-111606	Sequence 111606, Ap
C 21	17	85.0	39725	15	US-10-017-161-1611	Sequence 1611, Ap
C 22	17	85.0	39725	16	US-10-292-798-1285	Sequence 1285, Ap
C 23	17	85.0	55795	9	US-09-880-107-1543	Sequence 1543, Ap
C 24	17	85.0	66933	13	US-10-182-936A-11	Sequence 11, Appl
C 25	17	85.0	66933	16	US-10-374-979-11	Sequence 11, Appl
C 26	17	85.0	72049	13	US-10-182-936A-9	Sequence 9, Appl
C 27	17	85.0	72049	16	US-10-374-979-9	Sequence 9, Appl
C 28	17	85.0	156843	13	US-10-087-192-1408	Sequence 1408, Ap
C 29	16	80.0	320	13	US-10-085-783A-13435	Sequence 13435, A
C 30	16	80.0	320	16	US-10-242-535A-13435	Sequence 13435, A
C 31	16	80.0	822	13	US-10-027-632-125717	Sequence 125717, Ap
C 32	16	80.0	822	16	US-10-027-632-125717	Sequence 125717, Ap
C 33	16	80.0	1763	9	US-09-891-171-3	Sequence 3, Appl
C 34	16	80.0	1763	15	US-10-286-767-3	Sequence 3, Appl
C 35	16	80.0	2059	13	US-10-027-632-99852	Sequence 99852, A
C 36	16	80.0	2059	16	US-10-027-632-99852	Sequence 99852, A
C 37	16	80.0	6086	16	US-10-062-674-1873	Sequence 1873, Ap
C 38	16	80.0	54929	13	US-10-087-192-823	Sequence 823, Ap
C 39	16	80.0	169998	16	US-10-380-931-24	Sequence 24, Appl
C 40	16	80.0	197496	9	US-09-877-177-10	Sequence 10, Appl
C 41	16	80.0	197496	13	US-10-426-836-10	Sequence 10, Appl
C 42	15	75.0	321	11	US-09-864-408A-1461	Sequence 1461, Ap
C 43	15	75.0	410	10	US-09-918-995-8043	Sequence 8043, Ap
C 44	15	75.0	486	9	US-09-924-401-61	Sequence 61, Appl
C 45	15	75.0	550	10	US-09-918-995-11063	Sequence 11063, A

## ALIGNMENTS

### RESULT 1

US-10-029-386-23233/c  
; Sequence 23233, Application US/10029386  
; Publication No. US20030194704A1  
; GENERAL INFORMATION:  
; APPLICANT: Penn, Sharon G.  
; APPLICANT: Rank, David R.  
; APPLICANT: Hanzel, David K.  
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G  
; TITLE OF INVENTION: EXPRESSION ANALYSIS TWO  
; FILE REFERENCE: AEMICA-X-2  
; CURRENT APPLICATION NUMBER: US/10/029,386  
; CURRENT FILING DATE: 2001-12-20  
; NUMBER OF SEQ ID NOS: 34288  
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1  
; SEQ ID NO 23233  
; LENGTH: 186  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: MAP TO CHR9.3  
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.3  
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.4  
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.5  
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.8  
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.3  
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.1  
; OTHER INFORMATION: SWISSPROT HIT: P38571, EVALUE 1.50e+00  
; OTHER INFORMATION: NT HIT: M17310.1, EVALUE 1.00e+00  
; OTHER INFORMATION: EST\_HUMAN HIT: H81820.1, EVALUE 5.00e-95  
US-10-029-386-23233

Query Match 100.0%; Score 20; DB 15; Length 186;  
Best Local Similarity 55.0%; Pred. No. 0.2;  
Matches 11; Conservative 9; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCUUCUCCUGCUCCUUG 20





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; PRIOR FILING DATE: 2002-04-08
; PRIOR APPLICATION NUMBER: PCT/GS01/05458
; PRIOR FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 549
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 182
; LENGTH: 5434
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-170-385-182

Query Match      100.0%; Score 20; DB 13; Length 5434;
Best Local Similarity 55.0%; Pred. No. 0.12;
Matches 11; Conservative 9; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CCUUCUCCCGCUCUUCUUG 20
Db      88 CTTCTCCCTGCTCCTTTG 69

RESULT 6
US-09-969-708-488
; Sequence 488, Application US/09969708
; Patent No. US20020102532A1
; GENERAL INFORMATION:
; APPLICANT: Augustus, Meena
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu
; TITLE OF INVENTION: Sets
; FILE REFERENCE: 689290-70
; CURRENT APPLICATION NUMBER: US/09/969,708
; CURRENT FILING DATE: 2001-10-03
; PRIOR APPLICATION NUMBER: US/60/237,606
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: US/60/237,608
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: US/60/237,425
; PRIOR FILING DATE: 2000-10-03
; NUMBER OF SEQ ID NOS: 658
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 488
; LENGTH: 396
; TYPE: DNA
; ORGANISM: Homosapiens
US-09-969-708-488

Query Match      90.0%; Score 18; DB 9; Length 396;
Best Local Similarity 50.0%; Pred. No. 2.1;
Matches 9; Conservative 9; Mismatches 0; Indels 0; Gaps 0;

Qy      3 UUCUUCUCCGUCUUCUUG 20
Db      164 TTCCTCCCTGCTCCTTTG 181

RESULT 7
US-09-918-995-20082/c
; Sequence 20082, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 20082
; LENGTH: 474
; TYPE: DNA
; ORGANISM: Homo sapiens
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; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)...(474)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-20082

Query Match      90.0%; Score 18; DB 10; Length 474;
Best Local Similarity 50.0%; Pred. No. 2;
Matches 9; Conservative 9; Mismatches 0; Indels 0; Gaps 0;

Qy      3 UUCUUCUCCGUCUUCUUG 20
Db      348 TTCCTCCCTGCTCCTTTG 331

RESULT 8
US-10-027-632-278076/c
; Sequence 278076, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 278076
; LENGTH: 620
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-278076

Query Match      90.0%; Score 18; DB 13; Length 620;
Best Local Similarity 50.0%; Pred. No. 2;
Matches 9; Conservative 9; Mismatches 0; Indels 0; Gaps 0;

Qy      3 UUCUUCUCCGUCUUCUUG 20
Db      60 TTCCTCCCTGCTCCTTTG 43

RESULT 9
US-10-027-632-278076/c
; Sequence 278076, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
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; PRIOR FILING DATE: 2000-03-29  
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 ; PRIOR FILING DATE: 1999-11-23  
 ; PRIOR APPLICATION NUMBER: US 60/156,358  
 ; PRIOR FILING DATE: 1999-09-28  
 ; PRIOR APPLICATION NUMBER: US 60/146,002  
 ; PRIOR FILING DATE: 1999-08-09  
 ; NUMBER OF SEQ ID NOS: 325720  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 278076  
 ; LENGTH: 620  
 ; TYPE: DNA  
 ; ORGANISM: Human  
 US-10-027-632-278076

Query Match 90.0%; Score 18; DB 16; Length 620;  
 Best Local Similarity 50.0%; Pred. No. 2;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 UUCUCCCGUCUCCUUG 20  
 DB 60 TTCTTCCCTGCTCCTTG 43

RESULT 10  
 US-10-332-424-9/c  
 ; Sequence 9, Application US/10332424  
 ; Publication No. US20040018505A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: INCYTE GENOMICS, INC.; LEE, Ernestine A.  
 ; APPLICANT: TANG, Y. Tom; LU, Dyung Aina M.  
 ; APPLICANT: TRIBOULEY, Catherine M.; GANDHI, Ameena R.  
 ; APPLICANT: LU, Yan; BAUGHN, Mariah R.  
 ; APPLICANT: WARREN, Bridget A.; THORNTON, Michael  
 ; APPLICANT: YUE, Henry; JACKSON, Jennifer L.  
 ; APPLICANT: ARVIZU, Chandra S.; ELLIOTT, Vicki S.  
 ; APPLICANT: THANGAVELU, Kavitha; RAMKUMAR, Javalaxmi  
 ; APPLICANT: CHAWLA, Narinder K.; YAO, Monique G.  
 ; APPLICANT: GANDHI, Ameena R.  
 ; TITLE OF INVENTION: AMINOACYL TRNA SYNTHETASES  
 ; FILE REFERENCE: PI-0153 USN  
 ; CURRENT APPLICATION NUMBER: US/10/332,424  
 ; CURRENT FILING DATE: 2002-01-06  
 ; PRIOR APPLICATION NUMBER: US 60/216,748  
 ; PRIOR FILING DATE: 2000-07-07  
 ; PRIOR APPLICATION NUMBER: US 60/219,019  
 ; PRIOR FILING DATE: 2000-07-18  
 ; PRIOR APPLICATION NUMBER: US 60/223,058  
 ; PRIOR FILING DATE: 2000-08-04  
 ; PRIOR APPLICATION NUMBER: US 60/234,693  
 ; PRIOR FILING DATE: 2000-09-21  
 ; PRIOR APPLICATION NUMBER: US 60/239,797  
 ; PRIOR FILING DATE: 2000-10-11  
 ; NUMBER OF SEQ ID NOS: 12  
 ; SOFTWARE: PERL Program  
 ; SEQ ID NO 9  
 ; LENGTH: 1345  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: misc feature  
 ; OTHER INFORMATION: Incyte ID No. US20040018505A1 1554103CB1  
 US-10-332-424-9

Query Match 90.0%; Score 18; DB 16; Length 1345;  
 Best Local Similarity 50.0%; Pred. No. 1.8;  
 Matches 9; Conservative 9; Mismatches 0; Indels 0; Gaps 0;

QY 3 UUCUCCCGUCUCCUUG 20  
 DB 1172 TTCTTCCCTGCTCCTTG 1155

RESULT 11  
 US-09-764-891-9320  
 ; Sequence 9320, Application US/09764891  
 ; Publication No. US20030077808A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Rosen et al.  
 ; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
 ; FILE REFERENCE: PC006  
 ; CURRENT APPLICATION NUMBER: US/09/764,891  
 ; CURRENT FILING DATE: 2001-01-17  
 ; Prior application data removed - consult PALM or file wrapper  
 ; NUMBER OF SEQ ID NOS: 10231  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 9320  
 ; LENGTH: 1611  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-09-764-891-9320

Query Match 90.0%; Score 18; DB 10; Length 1611;  
 Best Local Similarity 50.0%; Pred. No. 1.7;  
 Matches 9; Conservative 9; Mismatches 0; Indels 0; Gaps 0;

QY 3 UUCUCCCGUCUCCUUG 20  
 DB 166 TTCTTCCCTGCTCCTTG 183

RESULT 12  
 US-10-091-572-867  
 ; Sequence 867, Application US/10091572  
 ; Publication No. US20030054373A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Rosen et al.  
 ; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
 ; FILE REFERENCE: PA118C1  
 ; CURRENT APPLICATION NUMBER: US/10/091,572  
 ; CURRENT FILING DATE: 2002-03-07  
 ; PRIOR APPLICATION NUMBER: 09/764,850  
 ; PRIOR FILING DATE: 2001-01-17  
 ; PRIOR APPLICATION NUMBER: 60/179,065  
 ; PRIOR FILING DATE: 2000-01-31  
 ; PRIOR APPLICATION NUMBER: 60/180,628  
 ; PRIOR FILING DATE: 2000-02-04  
 ; PRIOR APPLICATION NUMBER: 60/214,886  
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 ; PRIOR FILING DATE: 2000-08-14  
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 ; PRIOR APPLICATION NUMBER: 60/225,757  
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 ; PRIOR FILING DATE: 2000-08-22  
 ; PRIOR APPLICATION NUMBER: 60/216,647  
 ; PRIOR FILING DATE: 2000-07-07  
 ; PRIOR APPLICATION NUMBER: 60/225,267  
 ; PRIOR FILING DATE: 2000-08-14  
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 ; PRIOR FILING DATE: 2000-07-07  
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; PRIOR FILING DATE: 2000-09-29  
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; PRIOR APPLICATION NUMBER: 60/237,038  
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; PRIOR APPLICATION NUMBER: 60/236,370  
; PRIOR FILING DATE: 2000-09-29  
; PRIOR APPLICATION NUMBER: 60/236,802  
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; PRIOR FILING DATE: 2000-10-02  
; PRIOR APPLICATION NUMBER: 60/237,040  
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; PRIOR APPLICATION NUMBER: 60/240,960  
; PRIOR FILING DATE: 2000-10-20  
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; PRIOR FILING DATE: 2000-10-13  
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; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/246,474  
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; PRIOR APPLICATION NUMBER: 60/230,438  
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; PRIOR APPLICATION NUMBER: 60/215,135  
; PRIOR FILING DATE: 2000-06-30  
; PRIOR APPLICATION NUMBER: 60/225,266  
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 ; PRIOR FILING DATE: 2000-09-08

Query Match 90.0%; Score 18; DB 15; Length 1611;  
 Best Local Similarity 50.0%; Pred. No. 1.7;  
 Matches 9; Conservative 9; Mismatches 0; Indels 0; Gaps 0;

QY 3 UUCUUCUCCUGCUCCUUUG 20  
 Db 166 TTCTTCCCTGCTCCTTTG 183

RESULT 13  
 US-10-108-260A-1/c  
 ; Sequence 1, Application US/10108260A  
 ; Publication No. US20040005560A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: HELIX RESEARCH INSTITUTE  
 ; TITLE OF INVENTION: NO. US20040005560A1 full length cDNA  
 ; FILE REFERENCE: H1-A0106  
 ; CURRENT APPLICATION NUMBER: US/10/108,260A  
 ; CURRENT FILING DATE: 2002-03-27  
 ; NUMBER OF SEQ ID NOS: 5458  
 ; SOFTWARE: Patentin Ver. 2.1  
 ; SEQ ID NO 1  
 ; LENGTH: 1726  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-10-108-260A-1

Query Match 90.0%; Score 18; DB 16; Length 1726;  
 Best Local Similarity 50.0%; Pred. No. 1.7;  
 Matches 9; Conservative 9; Mismatches 0; Indels 0; Gaps 0;

QY 3 UUCUUCUCCUGCUCCUUUG 20  
 Db 1564 TTCTTCCCTGCTCCTTTG 1547

RESULT 14  
 US-10-037-270-704/c  
 ; Sequence 704, Application US/10037270  
 ; Publication No. US20030104529A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Tang, Y. Tom  
 ; APPLICANT: Liu, Chenghua  
 ; APPLICANT: Asundi, Vinod  
 ; APPLICANT: Zhang, Jie  
 ; APPLICANT: Ren, Feiyan  
 ; APPLICANT: Chen, Rui-hong  
 ; APPLICANT: Zhao, Qing A.  
 ; APPLICANT: Wehrman, Tom  
 ; APPLICANT: Xue, Aidong J.  
 ; APPLICANT: Yang, Yonghong  
 ; APPLICANT: Wang, Jian-Rui  
 ; APPLICANT: Zhou, Ping  
 ; APPLICANT: Ma, Yungqing  
 ; APPLICANT: Wang, Dunrui  
 ; APPLICANT: Wang, Zhiwei  
 ; APPLICANT: Tillinghast, John  
 ; APPLICANT: Drmanac, Radoje T.  
 ; TITLE OF INVENTION: NO. US20030104529A1 Nucleic Acids and

; TITLE OF INVENTION: Polypeptides  
 ; FILE REFERENCE: 784CIP2B  
 ; CURRENT APPLICATION NUMBER: US/10/037,270  
 ; CURRENT FILING DATE: 2002-01-04  
 ; PRIOR APPLICATION NUMBER: 09/552,317  
 ; PRIOR FILING DATE: 2000-04-25  
 ; PRIOR APPLICATION NUMBER: 09/488,725  
 ; PRIOR FILING DATE: 2000-01-21  
 ; NUMBER OF SEQ ID NOS: 1104  
 ; SOFTWARE: pt\_FL\_genes Version 1.0  
 ; SEQ ID NO 704  
 ; LENGTH: 1869  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: (161)..(1792)  
 US-10-037-270-704

Query Match 90.0%; Score 18; DB 15; Length 1869;  
 Best Local Similarity 50.0%; Pred. No. 1.7;  
 Matches 9; Conservative 9; Mismatches 0; Indels 0; Gaps 0;

QY 3 UUCUUCUCCUGCUCCUUUG 20  
 Db 1695 TTCTTCCCTGCTCCTTTG 1678

RESULT 15  
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 ; Sequence 704, Application US/10117722  
 ; Publication No. US20030219744A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Tang, Y. Tom  
 ; APPLICANT: Liu, Chenghua  
 ; APPLICANT: Asundi, Vinod  
 ; APPLICANT: Zhang, Jie  
 ; APPLICANT: Drmanac, Radoje T.  
 ; TITLE OF INVENTION: NO. US20030219744A1 Nucleic Acids and  
 ; TITLE OF INVENTION: Polypeptides  
 ; FILE REFERENCE: 784CIP2B/CIP  
 ; CURRENT APPLICATION NUMBER: US/10/117,722  
 ; CURRENT FILING DATE: 2002-04-04  
 ; PRIOR APPLICATION NUMBER: 09/620,312  
 ; PRIOR FILING DATE: 2000-07-19  
 ; PRIOR APPLICATION NUMBER: 09/552,317  
 ; PRIOR FILING DATE: 2000-04-25  
 ; PRIOR APPLICATION NUMBER: 09/488,725  
 ; PRIOR FILING DATE: 2000-01-21  
 ; NUMBER OF SEQ ID NOS: 1104  
 ; SOFTWARE: pt\_FL\_genes Version 1.0  
 ; SEQ ID NO 704  
 ; LENGTH: 1869  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: (161)..(1792)  
 US-10-117-722-704

Query Match 90.0%; Score 18; DB 16; Length 1869;  
 Best Local Similarity 50.0%; Pred. No. 1.7;  
 Matches 9; Conservative 9; Mismatches 0; Indels 0; Gaps 0;

QY 3 UUCUUCUCCUGCUCCUUUG 20  
 Db 1695 TTCTTCCCTGCTCCTTTG 1678

Search completed: May 27, 2004, 14:58:29  
 Job time : 105.251 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 26, 2004, 15:22:41 ; Search time 706.154 Seconds  
(without alignments)  
845.770 Million cell updates/sec

Title: US-09-121-239-15

Perfect score: 20

Sequence: 1 CCUUCUCCUCGUUUUG 20

Scoring table: OLIGO\_NUC

Gapop 60.0 , Gapext 60.0

Searched: 27513289 seqs, 14931090276 residues

Word size : 0

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

EST:\*

1: em\_estba:\*

2: em\_estba:\*

3: em\_estin:\*

4: em\_estmu:\*

5: em\_estov:\*

6: em\_estpl:\*

7: em\_estro:\*

8: em\_htc:\*

9: gb\_est1:\*

10: gb\_est2:\*

11: gb\_htc:\*

12: gb\_est3:\*

13: gb\_est4:\*

14: gb\_est5:\*

15: em\_estfun:\*

16: em\_estom:\*

17: em\_gsa\_hum:\*

18: em\_gsa\_inv:\*

19: em\_gsa\_pln:\*

20: em\_gsa\_vrt:\*

21: em\_gsa\_fun:\*

22: em\_gsa\_mam:\*

23: em\_gsa\_mus:\*

24: em\_gsa\_pro:\*

25: em\_gsa\_rod:\*

26: em\_gsa\_pbg:\*

27: em\_gsa\_vrl:\*

28: gb\_gsa1:\*

29: gb\_gsa2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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C 3	20	100.0	196	10	BB047102	BB047102 BB047102
C 4	20	100.0	198	29	CG636709	CG636709 OST361614

C 5	20	100.0	209	9	AV173479	AV173479 AV173479
C 6	20	100.0	220	10	BB132800	BB132800 BB132800
C 7	20	100.0	233	9	AV104236	AV104236 AV104236
C 8	20	100.0	237	9	AV323022	AV323022 AV323022
C 9	20	100.0	245	10	BB047117	BB047117 BB047117
C 10	20	100.0	249	13	BY371403	BY371403 BY371403
C 11	20	100.0	250	9	AV136928	AV136928 AV136928
C 12	20	100.0	250	9	AV215533	AV215533 AV215533
C 13	20	100.0	250	9	AV346046	AV346046 AV346046
C 14	20	100.0	253	9	AV296437	AV296437 AV296437
C 15	20	100.0	253	10	BB467544	BB467544 BB467544
C 16	20	100.0	254	9	AV338176	AV338176 AV338176
C 17	20	100.0	256	9	AV218421	AV218421 AV218421
C 18	20	100.0	258	9	AV134910	AV134910 AV134910
C 19	20	100.0	258	9	AV339053	AV339053 AV339053
C 20	20	100.0	262	10	BE916612	BE916612 601667217
C 21	20	100.0	268	9	AA898956	AA898956 al52a12.s
C 22	20	100.0	282	9	AV055312	AV055312 AV055312
C 23	20	100.0	295	12	BM122590	BM122590 L0512C06-
C 24	20	100.0	296	9	AV147138	AV147138 AV147138
C 25	20	100.0	297	9	AV100468	AV100468 AV100468
C 26	20	100.0	298	9	AI025543	AI025543 ov87a04.s
C 27	20	100.0	305	9	AA415759	AA415759 va32609.r
C 28	20	100.0	311	9	AV100354	AV100354 AV100354
C 29	20	100.0	319	10	BF456747	BF456747 UI-M-BZ1-
C 30	20	100.0	321	10	BB026196	BB026196 BB026196
C 31	20	100.0	324	9	AV095169	AV095169 AV095169
C 32	20	100.0	326	13	BU842273	BU842273 AGENCOURT
C 33	20	100.0	332	12	BG796781	BG796781 UTSW SM5C
C 34	20	100.0	333	9	AI838832	AI838832 UI-M-A10-
C 35	20	100.0	340	12	BM115670	BM115670 L0824A07-
C 36	20	100.0	344	9	AI553501	AI553501 vw37602.x
C 37	20	100.0	344	13	EX099890	EX099890 BX099890
C 38	20	100.0	344	13	BY709426	BY709426 BY709426
C 39	20	100.0	346	10	BB793854	BB793854 BB793854
C 40	20	100.0	348	11	AK009808	AK009808 Mus muscu
C 41	20	100.0	352	9	AI154779	AI154779 ud59g05.r
C 42	20	100.0	358	13	BY409310	BY409310 BY409310
C 43	20	100.0	362	9	AV102009	AV102009 AV102009
C 44	20	100.0	364	13	BY395867	BY395867 BY395867
C 45	20	100.0	369	13	BY408267	BY408267 BY408267

#### ALIGNMENTS

RESULT 1  
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LOCUS ov87a03.s1 Soares testis NHT Homo sapiens cDNA clone IMAGE:1644268  
DEFINITION 3', similar to TR:Q13688 Q13688 ABL ; mRNA sequence.  
ACCESSION AI025542  
VERSION AI025542.1 GI:3241155  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 115)  
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
Tumor Gene Index  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Unpublished (1997)  
JOURNAL Tumor Gene Index  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.  
cDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: [www-bio.llnl.gov/bbrp/image/image.html](http://www-bio.llnl.gov/bbrp/image/image.html)

Trace considered overall poor quality  
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 Seq primer: -40ml3 fwd. ET from Amersham  
 High quality sequence stop: 1.

# FEATURES

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  /mol_type="mRNA"
  /db_xref="taxon:9606"
  /clone="IMAGE:1644268"
  /sex="male"
  /lab_host="DH10B"
  /note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
was prepared from mRNA obtained from Clontech
Laboratories, Inc., and primed with a Not I - oligo(dT)
primer [5'
TGTATCAATCTGAAGTGGGCGCGCCCAATTTTTTTTTTTT 3'].
Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT73 vector. Library
went through one round of normalization to Cot5, and was
constructed by Bento Soares and M. Fatima Bonaldo. "
```

# ORIGIN

```

Query Match      100.0%; Score 20; DB 9; Length 115;
Best Local Similarity 55.0%; Pred. NO. 9.7;
Matches 11; Conservative 9; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCUUCUCCUCCUCCUCCUUG 20
Db 34 CCTTCTCTCCTGCTCTTGG 53

AV303548 195 bp mRNA linear EST 10-NOV-1999
AV303548 RIKEN full-length enriched, 8 days embryo Mus musculus
cDNA clone 5730513J17 3', mRNA sequence.
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AV303548 1 GI:6336062

EST.

Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 195)

Konno,H., Aizawa,K., Akahira,S., Akiyama,J., Carninci,P., Endo,T.,  
 Fukuda,S., Fukunishi,Y., Hara,A., Hayatsu,N., Hirozane,T., Hori,F.,  
 Ishii,Y., Ishikawa,T., Itoh,M., Izawa,M., Kadota,K., Kagawa,I.,  
 Kai,C., Kawai,J., Kikuchi,N., Kojima,Y., Koya,S., Kusakabe,M.,  
 Matsuyama,T., Miki,R., Mizuno,Y., Nakamura,M., Oda,H., Okazaki,Y.,  
 Owa,C., Ozawa,Y., Saito,H., Sano,M., Sato,K., Shibata,K.,  
 Shibata,Y., Shigemoto,Y., Shiraki,T., Sogabe,Y., Sugahara,Y.,  
 Suzuki,H., Suzuki,H., Takahashi,F., Tateno,M., Tominaga,N.,  
 Tsunoda,Y., Watahiki,A., Watanabe,S., Yamamura,T., Yasunishi,A.,  
 Yokota,T., Yoshiki,A., Yoshino,M., Muramatsu,M. and Hayashizaki,Y.  
 RIKEN Mouse ESTs (Konno,H., et al. 1999)

Unpublished (1999)

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The Institute of Physical and Chemical Research (RIKEN)

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Tel: 81-45-503-9222

Fax: 81-45-503-9216

Email: genome-res@sc.riken.go.jp,

URL: http://genome.gsc.riken.go.jp/

Sasaki,N., Izawa,M., Watahiki,M., Ozawa,K., Tanaka,T., Yoneda,Y.,

Matsuura,S., Carninci,P., Muramatsu,M., Okazaki,Y. and

Hayashizaki,Y.

Transcriptional sequencing: A method for DNA sequencing using RNA

polymerase. Proc. Natl. Acad. Sci. U.S.A. 95 (7), 3455-3460 (1998)  
 Itoh,M., Kitsuunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,  
 Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M.,  
 Okazaki,Y. and Hayashizaki,Y.  
 Automated filtration-based high-throughput plasmid preparation  
 system. Genome Res. 9 (5), 463-470 (1999)  
 Carninci,P. and Hayashizaki,Y.  
 High-efficiency full-length cDNA cloning. Methods Enzymol. 303,  
 19-44 (1999)  
 Please visit our web site (<http://genome.rtc.riken.go.jp>) for  
 further details.

# FEATURES

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  /mol_type="mRNA"
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  /clone="5730513J17"
  /sex="mixed"
  /dev_stage="8 days embryo"
  /lab_host="DH10B"
  /clone_lib="RIKEN full-length enriched, 8 days embryo"
  /note="Site 1: SalI; Site 2: BamHI; cDNA library was
prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. 1st strand cDNA was
primed with a primer [5'
GAGAGAGAGAGATCCAGAGCTCTTTTTTTTTTTTNN 3'], cDNA was
prepared by using trehalose thermo-activated reverse
transcriptase and subsequently enriched for full-length by
cap-trapper. cDNA went through one round of subtraction to
Not = 100.0 Second strand cDNA was prepared with the
primer adapter of sequence [5'
GAGAGAGAGATTCGAGTTAAATAATTAATTCCTCCCCCCCC 3']. cDNA
was cloned into the XhoI and BamHI sites. Vector: a
modified pBluescript KS(+) after bulk excision from Lambda
FLC I. Cloning sites, 5' end: SalI; 3' end: BamHI."
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# ORIGIN

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QY 1 CCUUCUCCUCCUCCUCCUUG 20
Db 53 CCTTCTCTCCTGCTCTTGG 34
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# RESULT 3

BB047102/c

LOCUS

DEFINITION

Mus musculus cDNA clone 6330581K13 3', mRNA sequence.

ACCESSION

BB047102

VERSION

BB047102.1 GI:8454278

KEYWORDS

SOURCE

Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 196)

Konno,H., Aizawa,K., Akahira,S., Akiyama,J., Arakawa,T.,

Carninci,P., Endo,T., Fukuda,S., Fukunishi,Y., Hara,A., Hayatsu,N.,

Hirozane,T., Hori,F., Ishii,Y., Ishikawa,J., Ishikawa,T., Itoh,M.,

Izawa,M., Kadota,K., Kagawa,I., Kai,C., Kawai,J., Kikuchi,N.,

Kiyosawa,H., Kojima,Y., Kondo,S., Koya,S., Kurihara,C.,

Kusakabe,M., Matsuyama,T., Miki,R., Mizuno,Y., Nakamura,M., Oda,H.,

Okazaki,Y., Owa,C., Saito,H., Sakai,C., Sato,K.,

Shibata,K., Shibata,Y., Shigemoto,Y., Shinagawa,A., Shiraki,T.,

Sogabe,Y., Sugahara,Y., Suzuki,H., Suzuki,H., Tagawa,A.,

Takahashi,F., Tominaga,N., Toya,T., Tsunoda,Y., Watahiki,A.,



Genome Science Laboratory  
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Fax: 81-298-36-9098

Email: genome-res@sc.riken.go.jp

Thermolabile and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA (Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))  
Transcriptional sequencing: A method for DNA sequencing using RNA polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))  
Please visit our web site (<http://genome.rtc.riken.go.jp>) for further details.

## FEATURES Location/Qualifiers

1..209  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="5730405E02"  
/sex="mixed"  
/dev\_stage="8-day embryo"  
/clone\_lib="Mus musculus C57BL/6J 8-day embryo"

## ORIGIN

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Best Local Similarity 55.0%; Pred. No. 11;  
Matches 11; Conservative 9; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCUUCUCCGUCGUCUUCUUG 20

Db 55 CCTTCTCCCTGCTCTTTG 36

## RESULT 6

BB132800/c

LOCUS BB132800 RIKEN full-length enriched, adult male bone Mus musculus  
DEFINITION CDNA clone 9830003E19 3', mRNA sequence.

ACCESSION BB132800

VERSION BB132800.1 GI:8787190

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 220)

Konno, H., Aizawa, K., Akahira, S., Akiyama, J., Arakawa, T., Carninci, P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., Hirozane, T., Hori, F., Ishii, Y., Ishikawa, J., Ishikawa, T., Itoh, M., Izawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N., Kiyosawa, H., Kojima, Y., Kondo, S., Koya, S., Kurihara, C., Kusakabe, M., Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y., Ono, T., Owa, C., Saito, H., Sakai, C., Sato, K., Shibata, K., Shibata, Y., Shigemoto, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Sugahara, Y., Suzuki, H., Tagawa, A., Takahashi, F., Tominaga, N., Toya, T., Tsunoda, Y., Watahiki, A., Watanabe, S., Yamamura, I., Yamana, I., Yano, K., Yasunishi, A., Yokota, T., Yoshida, K., Yoshiki, A., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.  
RIKEN Mouse ESTs (Konno, H., et al.)  
Unpublished (2000)

## TITLE

JOURNAL

COMMENT

Contact: Yoshihide Hayashizaki  
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute  
The Institute of Physical and Chemical Research (RIKEN)

1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan

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Email: genome-res@sc.riken.go.jp

URL: <http://genome.gsc.riken.go.jp/>

Carninci, P., Nishiyama, Y., Westover, A., Itoh, M., Nagaoka, S., Sasaki, N., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.

Thermolabile and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)  
Itoh, M., Kiteunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J., Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y.  
Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)

High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)

Please visit our web site (<http://genome.rtc.riken.go.jp>) for further details.

## FEATURES

source

Location/Qualifiers

1..220  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/db\_xref="taxon:10090"  
/clone="9830003E19"  
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/dev\_stage="adult"  
/lab\_host="DH10B"  
/clone\_lib="RIKEN full-length enriched, adult male bone"  
/note="Site 1: SalI; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5'  
GAGAGAGAGAGATCCAGAGCTCTTTTTTTTTTNN 3']. cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 10.0 and subtraction to Rot = 185.0. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGATCTCGAGTTAATAATTAATCCCCCCCCCC 3']. cDNA was cleaved with XhoI and BamHI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I."

## ORIGIN

Query Match 100.0%; Score 20; DB 10; Length 220;  
Best Local Similarity 55.0%; Pred. No. 11;  
Matches 11; Conservative 9; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCUUCUCCGUCGUCUUCUUG 20

Db 78 CCTTCTCCCTGCTCTTTG 59

## RESULT 7

AV104236/c

LOCUS AV104236

DEFINITION

CDNA clone 2510003K19, mRNA sequence.

ACCESSION AV104236

VERSION AV104236.1 GI:5251784

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

## ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 233)

Carninci, P., Shibata, K., Ozawa, Y., Konno, H., Itoh, M., Aizawa, K., Akahira, S., Akiyama, J., Fukuda, S., Fukunishi, Y., Funayama, T., Hara, A., Hayatsu, N., Hori, F., Ishikawa, T., Itoh, M., Izawa, M., Kawai, J., Kikuchi, N., Kojima, Y., Matsuyama, T., Naitsumu, H., Oda, H., Owa, C., Sato, K., Shibata, Y., Shigemoto, Y., Shiraki, T., Sogabe, Y., Sugahara, Y., Suzuki, H., Taten, M., Tomaru, Y., Tominaga, N., Watanabe, S., Yagame, M., Yamamura, T., Yokota, T., Yoshino, M., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y.







encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)  
 cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.  
 Please visit our web site (<http://genome.gsc.riken.go.jp>) for further details.

## FEATURES

source

Location/Qualifiers

1..249  
 /organism="Mus musculus"  
 /mol\_type="mRNA"  
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## ORIGIN

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 Matches 11; Conservative 9; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCUUCUCCGUCUCCUUG 20

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Db 108 CTTCTCTCCCTGCTCTTTG 89

## RESULT 11

AV136928/c

LOCUS

AV136928 Mus musculus C57BL/6J 10-11 day embryo Mus musculus cDNA  
 Clone 2810029G21, mRNA sequence.

ACCESSION

AV136928

VERSION

EST.

SOURCE

Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 250)

Carninci, P., Shibata, K., Ozawa, Y., Konno, H., Itoh, M., Aizawa, K.,

Akahira, S., Akiyama, J., Fukuda, S., Fukunishi, Y., Funayama, T.,

Hara, A., Hayatsu, N., Hori, F., Ishikawa, T., Itoh, M., Izawa, M.,

Kawai, J., Kikuchi, N., Kojima, Y., Matsuyama, T., Niitsuma, H., Oda, H.,

Owa, C., Sato, K., Shibata, Y., Shigemoto, Y., Shiraki, T., Sogabe, Y.,

Sugahara, Y., Suzuki, H., Suzuki, H., Tateno, M., Tomaru, Y.,

Tomimaga, N., Watanabe, S., Yagane, M., Yamamura, T., Yokota, T.,

Yoshino, M., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y.

RIKEN Mouse ESTs

Unpublished (1999)

Contact: Chie Owa

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Fax: 81-298-36-9098

Email: [genome-res@rtc.riken.go.jp](mailto:genome-res@rtc.riken.go.jp)

Thermostabilization and thermostabilization of thermolabile enzymes by

trehalose and its application for the synthesis of full length cDNA

(Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))

Transcriptional sequencing: A method for DNA sequencing using RNA

polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))

Please visit our web site (<http://genome.rtc.riken.go.jp>) for

further details.

## FEATURES

source

Location/Qualifiers

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 /clone\_lib="Mus musculus C57BL/6J 10-11 day embryo"

## ORIGIN

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QY 1 CCUUCUCCGUCUCCUUG 20

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Db 109 CTTCTCTCCCTGCTCTTTG 90

## RESULT 12

AV215533/c

LOCUS

AV215533 RIKEN full-length enriched, ES cells Mus musculus cDNA  
 Clone 2410149G15 3', mRNA sequence.

ACCESSION

AV215533.1

VERSION

EST.

SOURCE

Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 250)

Konno, H., Aizawa, K., Akahira, S., Akiyama, J., Carninci, P., Endo, T.,

Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., Hirozane, T., Hori, F.,

Ishii, Y., Ishikawa, T., Itoh, M., Izawa, M., Kadota, K., Kagawa, I.,

Kai, C., Kawai, J., Kikuchi, N., Kojima, Y., Koya, S., Kusakabe, M.,

Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y.,

Owa, C., Ozawa, Y., Saito, H., Sano, M., Sato, K., Shibata, K.,

Shibata, Y., Shigemoto, Y., Shiraki, T., Sogabe, Y., Sugahara, Y.,

Suzuki, H., Suzuki, H., Takahashi, F., Tateno, M., Tomimaga, N.,

Tsunoda, Y., Watanabe, S., Yamamura, T., Yasunishi, A.,

Yokota, T., Yoshiki, A., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.

RIKEN Mouse ESTs (Konno, H., et al. 1999)

Unpublished (1999)

Contact: Yoshihide Hayashizaki

Laboratory for Genome Exploration Research Group, RIKEN Genomic

Sciences Center (GSC), Yokohama Institute

The Institute of Physical and Chemical Research (RIKEN)

1-7-22 Suehiro-cho, Teurumi-ku, Yokohama, Kanagawa 230-0045, Japan

Tel: 81-45-503-9222

Fax: 81-45-503-9216

Email: [genome-res@rtc.riken.go.jp](mailto:genome-res@rtc.riken.go.jp)URL: <http://genome.gsc.riken.go.jp/>

Sasaki, N., Izawa, M., Watahiki, M., Ozawa, K., Tanaka, T., Yoneda, Y.,

Matsura, S., Carninci, P., Muramatsu, M., Okazaki, Y. and

Hayashizaki, Y.

Transcriptional sequencing: A method for DNA sequencing using RNA

polymerase. Proc. Natl. Acad. Sci. U.S.A. 95 (7), 3455-3460 (1998)

Itoh, M., Katsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J.,

Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M.,

Okazaki, Y. and Hayashizaki, Y.

Automated filtration-based high-throughput plasmid preparation

system. Genome Res. 9 (5), 463-470 (1999)

Carninci, P. and Hayashizaki, Y.

High-efficiency full-length cDNA cloning. Methods Enzymol. 303,

19-44 (1999)

Please visit our web site (<http://genome.rtc.riken.go.jp>) for

further details.

Location/Qualifiers

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/organism="Mus musculus"

/mol\_type="mRNA"

/strain="C57BL/6J"

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/clone="2410149G15"





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Search completed: May 26, 2004, 22:44:29  
Job time : 706.154 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 26, 2004, 16:00:31 ; Search time 510.783 Seconds  
(without alignments)  
2036.547 Million cell updates/sec

Title: US-09-121-239-16

Perfect score: 24

Sequence: 1 GTGGAACATGAAGCCCTTCAGCGG 24

Scoring table: OLIGO NUC

Gapop 60.0 , Gapext 60.0

Searched: 3470272 seqs, 21671516995 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

GenEmbl.\*

1: gb\_ba.\*

2: gb\_hg.\*

3: gb\_in.\*

4: gb\_om.\*

5: gb\_ov.\*

6: gb\_pat.\*

7: gb\_ph.\*

8: gb\_pl.\*

9: gb\_pr.\*

10: gb\_ro.\*

11: gb\_sts.\*

12: gb\_sy.\*

13: gb\_un.\*

14: gb\_vl.\*

15: em\_ba.\*

16: em\_fun.\*

17: em\_hum.\*

18: em\_in.\*

19: em\_mu.\*

20: em\_om.\*

21: em\_or.\*

22: em\_ov.\*

23: em\_pat.\*

24: em\_ph.\*

25: em\_pl.\*

26: em\_ro.\*

27: em\_sts.\*

28: em\_un.\*

29: em\_vi.\*

30: em\_hg\_hum.\*

31: em\_hg\_inv.\*

32: em\_hg\_other.\*

33: em\_hg\_mus.\*

34: em\_hg\_pln.\*

35: em\_hg\_rtd.\*

36: em\_hg\_mam.\*

37: em\_hg\_vrt.\*

38: em\_sy.\*

39: em\_hgo\_hum.\*

40: em\_hgo\_mus.\*

41: em\_hgo\_other.\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
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C 4	24	100.0	24	6	BD222541	BD222541 Methods f
C 5	24	100.0	299	6	BD222547	BD222547 Methods f
C 6	18	75.0	34125	14	AT12CGA	XJ3487 Adenovirus
C 7	18	75.0	238483	2	AC132177	AC132177 Rattus no
C 8	17	70.8	60456	2	AC087634	AC087634 Homo sapi
C 9	17	70.8	104244	10	AL805925	AL805925 Mouse DNA
C 10	17	70.8	138152	10	AL954170	AL954170 Mouse DNA
C 11	17	70.8	152804	2	BX248232	BX248232 Danio rer
C 12	17	70.8	162077	2	AC109200	AC109200 Mus muscu
C 13	17	70.8	184317	10	AL606494	AL606494 Mouse DNA
C 14	17	70.8	215356	10	AC096363	AC096363 Rattus no
C 15	17	70.8	215958	2	AC102091	AC102091 Mus muscu
C 16	17	70.8	256703	2	AC114076	AC114076 Rattus no
C 17	17	70.8	259220	2	AC097694	AC097694 Rattus no
C 18	16	66.7	404	8	AF082605	AF082605 Leavenwor
C 19	16	66.7	415	8	AF082606	AF082606 Leavenwor
C 20	16	66.7	556	11	G85739	G85739 S209P6356RA
C 21	16	66.7	688	11	G97604	G97604 S209P6432PF
C 22	16	66.7	751	6	BD018368	BD018368 Novel gen
C 23	16	66.7	751	6	BD098306	BD098306 Novel gen
C 24	16	66.7	760	8	AF082603	AF082603 Leavenwor
C 25	16	66.7	1050	10	AF039216	AF039216 Mus muscu
C 26	16	66.7	1109	10	BC005636	BC005636 Mus muscu
C 27	16	66.7	1454	8	AY266141	AY266141 Setaria i
C 28	16	66.7	1599	8	ZMA430386	AJ430386 Zea mays
C 29	16	66.7	2233	8	AY166887	AY166887 Cryphonc
C 30	16	66.7	2370	8	ZMA430205	AJ430205 Zea mays
C 31	16	66.7	2577	9	BC028075	BC028075 Homo sapi
C 32	16	66.7	3335	5	AY422997	AY422997 Danio rer
C 33	16	66.7	3337	9	HSA295142	AJ295142 Homo sapi
C 34	16	66.7	3398	5	BC045427	BC045427 Danio rer
C 35	16	66.7	3398	5	BC047178	BC047178 Danio rer
C 36	16	66.7	3460	6	AR079398	AR079398 Sequence
C 37	16	66.7	3460	9	HSU94333	U94333 Human Clq/M
C 38	16	66.7	4194	10	MUSCTNC	J04971 M.musculus
C 39	16	66.7	14652	1	AE004799	AE004799 Pseudomon
C 40	16	66.7	48139	9	AC109827	AC109827 Homo sapi
C 41	16	66.7	50436	9	AL391258	AL391258 Human DNA
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C 43	16	66.7	67542	9	AC026422	AC026422 Homo sapi
C 44	16	66.7	70305	1	YPCD1	AL117189 Yersinia
C 45	16	66.7	70504	1	AF053946	AF053946 Yersinia

ALIGNMENTS

RESULT 1  
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LOCUS BD222538 24 bp DNA linear PAT 17-JUL-2003  
DEFINITION Methods for detecting and measuring spliced nucleic acids.  
ACCESSION BD222538  
VERSION BD222538.1 GI:33032308  
KEYWORDS JP 2002521037-A/16.  
SOURCE synthetic construct  
ORGANISM synthetic sequences  
REFERENCE 1 (bases 1 to 24)  
AUTHORS Harvey, R.C. and Eastman, P.S.  
TITLE Methods for detecting and measuring spliced nucleic acids  
JOURNAL Patent: JP 2002521037-A 16 16-JUL-2002;  
GEN PROBE INC

```

COMMENT      OS      Artificial Sequence
              PN      JP 2002521037-A/16
              PD      16-JUL-2002
              PF      23-JUL-1999 JP 2000561364
              PR      23-JUL-1998 US 09/121239
              PI      RICHARD C HARVEY, PAUL S EASTMAN
              PC      C12Q1/68, C12N15/09, C12N15/00
              CC      Description of Artificial Sequence: Probe for abl sequence PH
              Key source      1. .24      Location/Qualifiers
              FT      source      1. .24      /organism='Artificial Sequence'.
              FT      source      1. .24      /organism="synthetic construct"
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Query Match      100.0%; Score 24; DB 6; Length 24;
Best Local Similarity      100.0%; Pred. No. 0.0025;
Matches      24; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

QY      1 GTGGAACATGAAGCCCTTCAGCGG 24
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Db      1 GTGGAACATGAAGCCCTTCAGCGG 24

RESULT 2
BD222539
LOCUS      24 bp      RNA      linear      PAT 17-JUL-2003
DEFINITION      Methods for detecting and measuring spliced nucleic acids.
ACCESSION      BD222539
VERSION      BD222539.1 GI:33032309
KEYWORDS      JP 2002521037-A/17.
SOURCE      synthetic construct
ORGANISM      artificial sequences.
REFERENCE      1 (bases 1 to 24)
AUTHORS      Harvey, R.C. and Eastman, P.S.
TITLES      Methods for detecting and measuring spliced nucleic acids
JOURNAL      Patent: JP 2002521037-A 17 16-JUL-2002;
GEN PROBE INC
COMMENT      OS      Artificial Sequence
              PN      JP 2002521037-A/17
              PD      16-JUL-2002
              PF      23-JUL-1999 JP 2000561364
              PR      23-JUL-1998 US 09/121239
              PI      RICHARD C HARVEY, PAUL S EASTMAN
              PC      C12Q1/68, C12N15/09, C12N15/00
              CC      Description of Artificial Sequence: RNA version of SEQ ID NO:
              Key source      16      Location/Qualifiers
              FT      source      1. .24      /organism='Artificial Sequence'.
              FT      source      1. .24      /organism="synthetic construct"
              FT      source      /mol_type="genomic RNA"
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ORIGIN
Query Match      100.0%; Score 24; DB 6; Length 24;
Best Local Similarity      100.0%; Pred. No. 0.0025;
Matches      24; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

QY      1 GTGGAACATGAAGCCCTTCAGCGG 24
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Db      1 GTGGAACATGAAGCCCTTCAGCGG 24

RESULT 3
BD222540/c
LOCUS      24 bp      DNA      linear      PAT 17-JUL-2003
DEFINITION      Methods for detecting and measuring spliced nucleic acids.
ACCESSION      BD222540
VERSION      BD222540.1 GI:33032310
KEYWORDS      JP 2002521037-A/18.
SOURCE      synthetic construct
ORGANISM      artificial sequences.
REFERENCE      1 (bases 1 to 24)
AUTHORS      Harvey, R.C. and Eastman, P.S.
TITLES      Methods for detecting and measuring spliced nucleic acids
JOURNAL      Patent: JP 2002521037-A 18 16-JUL-2002;
GEN PROBE INC
COMMENT      OS      Artificial Sequence
              PN      JP 2002521037-A/18
              PD      16-JUL-2002
              PF      23-JUL-1999 JP 2000561364
              PR      23-JUL-1998 US 09/121239
              PI      RICHARD C HARVEY, PAUL S EASTMAN
              PC      C12Q1/68, C12N15/09, C12N15/00
              CC      Description of Artificial Sequence: Reverse complement of SEQ
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              FT      source      1. .24      /organism="synthetic construct"
              FT      source      /mol_type="genomic RNA"
              FT      source      /db_xref="taxon:32630"

ORIGIN
Query Match      100.0%; Score 24; DB 6; Length 24;
Best Local Similarity      100.0%; Pred. No. 0.0025;
Matches      24; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

QY      1 GTGGAACATGAAGCCCTTCAGCGG 24
      |||||||
Db      1 GTGGAACATGAAGCCCTTCAGCGG 24

RESULT 4
BD222541/c
LOCUS      24 bp      RNA      linear      PAT 17-JUL-2003
DEFINITION      Methods for detecting and measuring spliced nucleic acids.
ACCESSION      BD222541
VERSION      BD222541.1 GI:33032311
KEYWORDS      JP 2002521037-A/19.
SOURCE      synthetic construct
ORGANISM      artificial sequences.
REFERENCE      1 (bases 1 to 24)
AUTHORS      Harvey, R.C. and Eastman, P.S.
TITLES      Methods for detecting and measuring spliced nucleic acids
JOURNAL      Patent: JP 2002521037-A 19 16-JUL-2002;
GEN PROBE INC
COMMENT      OS      Artificial Sequence
              PN      JP 2002521037-A/19
              PD      16-JUL-2002
              PF      23-JUL-1999 JP 2000561364
              PR      23-JUL-1998 US 09/121239
              PI      RICHARD C HARVEY, PAUL S EASTMAN
              PC      C12Q1/68, C12N15/09, C12N15/00
              CC      Description of Artificial Sequence: RNA version of SEQ ID NO:
              Key source      18      Location/Qualifiers
              FT      source      1. .24      /organism='Artificial Sequence'.
              FT      source      1. .24      /organism="synthetic construct"
              FT      source      /mol_type="genomic RNA"
              FT      source      /db_xref="taxon:32630"

ORIGIN
Query Match      100.0%; Score 24; DB 6; Length 24;
Best Local Similarity      100.0%; Pred. No. 0.0025;
Matches      24; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

QY      1 GTGGAACATGAAGCCCTTCAGCGG 24
      |||||||
Db      24 GTGGAACATGAAGCCCTTCAGCGG 1

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DEFINITION      Methods for detecting and measuring spliced nucleic acids.
ACCESSION      BD222540
VERSION      BD222540.1 GI:33032310
KEYWORDS      JP 2002521037-A/18.
SOURCE      synthetic construct
ORGANISM      artificial sequences.
REFERENCE      1 (bases 1 to 24)
AUTHORS      Harvey, R.C. and Eastman, P.S.
TITLES      Methods for detecting and measuring spliced nucleic acids
JOURNAL      Patent: JP 2002521037-A 18 16-JUL-2002;
GEN PROBE INC
COMMENT      OS      Artificial Sequence
              PN      JP 2002521037-A/18
              PD      16-JUL-2002
              PF      23-JUL-1999 JP 2000561364
              PR      23-JUL-1998 US 09/121239
              PI      RICHARD C HARVEY, PAUL S EASTMAN
              PC      C12Q1/68, C12N15/09, C12N15/00
              CC      Description of Artificial Sequence: Reverse complement of SEQ
              Key source      18      Location/Qualifiers
              FT      source      1. .24      /organism='Artificial Sequence'.
              FT      source      1. .24      /organism="synthetic construct"
              FT      source      /mol_type="genomic DNA"
              FT      source      /db_xref="taxon:32630"

ORIGIN
Query Match      100.0%; Score 24; DB 6; Length 24;
Best Local Similarity      100.0%; Pred. No. 0.0025;
Matches      24; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

QY      1 GTGGAACATGAAGCCCTTCAGCGG 24
      |||||||
Db      24 GTGGAACATGAAGCCCTTCAGCGG 1

RESULT 4
BD222541/c
LOCUS      24 bp      RNA      linear      PAT 17-JUL-2003
DEFINITION      Methods for detecting and measuring spliced nucleic acids.
ACCESSION      BD222541
VERSION      BD222541.1 GI:33032311
KEYWORDS      JP 2002521037-A/19.
SOURCE      synthetic construct
ORGANISM      artificial sequences.
REFERENCE      1 (bases 1 to 24)
AUTHORS      Harvey, R.C. and Eastman, P.S.
TITLES      Methods for detecting and measuring spliced nucleic acids
JOURNAL      Patent: JP 2002521037-A 19 16-JUL-2002;
GEN PROBE INC
COMMENT      OS      Artificial Sequence
              PN      JP 2002521037-A/19
              PD      16-JUL-2002
              PF      23-JUL-1999 JP 2000561364
              PR      23-JUL-1998 US 09/121239
              PI      RICHARD C HARVEY, PAUL S EASTMAN
              PC      C12Q1/68, C12N15/09, C12N15/00
              CC      Description of Artificial Sequence: RNA version of SEQ ID NO:
              Key source      18      Location/Qualifiers
              FT      source      1. .24      /organism='Artificial Sequence'.
              FT      source      1. .24      /organism="synthetic construct"
              FT      source      /mol_type="genomic RNA"
              FT      source      /db_xref="taxon:32630"

ORIGIN
Query Match      100.0%; Score 24; DB 6; Length 24;
Best Local Similarity      100.0%; Pred. No. 0.0025;
Matches      24; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

QY      1 GTGGAACATGAAGCCCTTCAGCGG 24
      |||||||
Db      24 GTGGAACATGAAGCCCTTCAGCGG 1

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Query Match      100.0%; Score 24; DB 6; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.0025;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGGAACATGAAGCCCTTCAGCGG 24
Db 24 GTGGAACATGAAGCCCTTCAGCGG 1

RESULT 5
LOCUS BD222547 299 bp DNA linear PAT 17-JUL-2003
DEFINITION Methods for detecting and measuring spliced nucleic acids.
ACCESSION BD222547
VERSION BD222547.1 GI:33032317
KEYWORDS JP 2002521037-A/25.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 299)
AUTHORS Harvey,R.C. and Eastman,P.S.
TITLE Methods for detecting and measuring spliced nucleic acids
JOURNAL Patent: JP 2002521037-A 25 16-JUL-2002;
COMMENT GEN PROBE INC
OS Homo sapiens (human)
PN JP 2002521037-A/25
PD 16-JUL-2002
PR 23-JUL-1999 JP 2000561364
PF 23-JUL-1998 US 09/121239
PI RICHARD C HARVEY, PAUL S EASTMAN
PC C12Q1/68,C12N15/09,C12N15/00
CC Methods for detecting and measuring spliced nucleic acids FH
KEY Location/Qualifiers
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ORIGIN
Query Match      100.0%; Score 24; DB 6; Length 299;
Best Local Similarity 100.0%; Pred. No. 0.002;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGGAACATGAAGCCCTTCAGCGG 24
Db 142 GTGGAACATGAAGCCCTTCAGCGG 165

RESULT 6
AT12CGA/c
LOCUS Adenovirus type 12 DNA, complete genome.
DEFINITION Adenovirus type 12 DNA, complete genome.
ACCESSION X73487
VERSION X73487.1 GI:313361
KEYWORDS complete genome; core protein; DNA polymerase; DNA-binding protein;
endoprotease; fiber protein; hexon protein; large T-antigen;
maturation protein; minor core protein; penton protein;
peripentonal hexon-associated protein; promoter; repeat region;
small t-antigen; transcriptional activation.
SOURCE Human adenovirus type 12
ORGANISM Human adenovirus type 12
Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
REFERENCE 1 (bases 1 to 3957)
AUTHORS Tolun,A., Alestrom,P. and Pettersson,U.
TITLE Sequence of inverted terminal repetitions from different
adenoviruses: demonstration of conserved sequences and homology
between SA7 termini and SV40 DNA
JOURNAL Cell 17 (3), 705-713 (1979)

MEDLINE 80001962
PUBMED 225041
REFERENCE 2 (bases 1 to 3957)
AUTHORS Sugisaki,H., Sugimoto,K., Takamami,M., Shiroki,K., Saito,I.,
Shimojo,H., Sawada,Y., Uemizu,Y., Uesugi,S. and Fujinaga,K.
TITLE Structure and gene organization in the transformed Hind III-G
fragment of Ad12
JOURNAL Cell 20 (3), 777-786 (1980)
MEDLINE 81022638
PUBMED 6251973
REFERENCE 3 (bases 1 to 3957)
AUTHORS Shinagawa,M. and Padmanabhan,R.
TITLE Comparative sequence analysis of the inverted terminal repetitions
from different adenoviruses
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 77 (7), 3831-3835 (1980)
MEDLINE 81054665
PUBMED 6253991
REFERENCE 4
AUTHORS Kimura,T., Sawada,Y., Shinawawa,M., Shimizu,Y., Shiroki,K.,
Shimojo,H., Sugisaki,H., Takamami,M., Uemizu,Y. and Fujinaga,K.
TITLE Nucleotide sequence of the transforming early region E1b of
adenovirus type 12 DNA: structure and gene organization, and
comparison with those of adenovirus type 5 DNA
JOURNAL Nucleic Acids Res. 9 (23), 6571-6589 (1981)
MEDLINE 82105565
PUBMED 6275367
REMARK (sites)
REFERENCE 5 (bases 24334 to 24703)
AUTHORS Engler,J.A. and van Bree,M.P.
TITLE The nucleotide sequence of the gene encoding protein IVa2 in human
adenovirus type 7
JOURNAL Gene 19 (1), 71-80 (1982)
MEDLINE 83054637
PUBMED 6292051
REFERENCE 6 (bases 1488 to 3861)
AUTHORS Kimura,T.
TITLE Structure and sequence analysis of the transforming region E1b of
human adenovirus type 12
JOURNAL Sapporo Igaku Zasshi 52, 253-267 (1983)
REFERENCE 7 (bases 20966 to 22966)
AUTHORS Kruijer,W., van Schaik,F.M., Speijer,J.G. and Sussenbach,J.S.
TITLE Structure and function of adenovirus DNA binding protein:
comparison of the amino acid sequences of the Ad5 and Ad12 proteins
derived from the nucleotide sequence of the corresponding genes
JOURNAL Virology 128 (1), 140-153 (1983)
MEDLINE 83277521
PUBMED 6308889
REFERENCE 8 (bases 1 to 3957)
AUTHORS van Ormondt,H. and Galibert,F.
TITLE Nucleotide sequences of adenovirus DNAs
JOURNAL Curr. Top. Microbiol. Immunol. 110, 73-142 (1984)
MEDLINE 85002829
PUBMED 6383725
REFERENCE 9 (bases 4831 to 10470)
AUTHORS Shu,L.M., Hong,J.S., Wei,Y.F. and Engler,J.A.
TITLE Nucleotide sequence of the genes encoded in early region 2b of
human adenovirus type 12
JOURNAL Gene 46 (2-3), 187-195 (1986)
MEDLINE 87106854
PUBMED 8303925
REFERENCE 10 (bases 1 to 530)
AUTHORS Shibata,H., Zheng,J.H., Koikeda,S., Masamune,Y. and Nakanishi,Y.
TITLE Cis- and trans-acting factors for transcription of the adenovirus
12 E1A gene
JOURNAL Biochim. Biophys. Acta 1007 (2), 184-191 (1989)
MEDLINE 89150250
PUBMED 2522011
REFERENCE 11
AUTHORS Juttermann,R., Weyer,U. and Doerfler,W.
TITLE Defect of adenovirus type 12 replication in hamster cells: absence
of transcription of viral virus-associated and L1 RNAs
JOURNAL J. Virol. 63 (8), 3535-3540 (1989)
MEDLINE 89311650

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PUBMED 2746738
REFERENCE (sites)
AUTHORS Zock, C., Iselt, A. and Doerfler, W.
TITLE A unique mitigator sequence determines the species specificity of
the major late promoter in adenovirus type 12 DNA
JOURNAL J. Virol. 67 (2), 682-693 (1993)
MEDLINE 93124560
PUBMED 8419643
REMARK (sites)
REFERENCE 13
AUTHORS Sprengel, J., Schmitz, B., Heuss-Neitzel, D., Zock, C. and Doerfler, W.
TITLE Nucleotide sequence of human adenovirus type 12 DNA: comparative
functional analysis
JOURNAL J. Virol. 68 (1), 379-389 (1994)
MEDLINE 94076430
PUBMED 8254750
REFERENCE 14 (bases 1 to 34125)
AUTHORS Sprengel, J.
TITLE Direct Submission
JOURNAL Submitted (21-JUN-1993) J. Sprengel, Institute of Genetics/Dept.
Virology, Weyertal 121, 50931 Cologne 41, FRG
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1029..1628
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Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 7
AC132177 238483 bp DNA linear HTG 10-OCT-2002
LOCUS Rattus norvegicus clone CH230-165B1, WORKING DRAFT SEQUENCE, 6
DEFINITION unordered pieces.
ACCESSION AC132177
VERSION AC132177.4 GI:23683197
KEYWORDS HTG; HTGS PHASE1; HTGS DRAFT; HTGS FULLTOP.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 238483)
AUTHORS Muzny, D. Marie., Metzker, M. Lee., Abramson, S., Adams, C., Alder, J.,
Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D.,
Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H.,
Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F.,
Biswal, N., Blair, J., Blankenburg, K., Blyth, P., Brown, M.,
Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E.,
Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A.,
Chacko, J., Chavez, D., Chen, R., Chen, Y., Chen, Z., Chu, J.,
Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L.,
Davila, M. L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D.,
Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K.,
Draper, H., Dugan-Kocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K.,
Egan, A., Escotto, M., Eugene, C., Evans, C. A., Falls, T., Fan, G.,

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Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P., Frazer, C.M., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Garza, M., Gregor, E., Geer, K., Gill, R., Grady, M., Guerra, W., Guevara, W., Gunaratne, P., Haaland, W., Hamill, C., Hamilton, C., Hamilton, K., Harvey, Y., Haylak, P., Hawes, A., Henderson, N., Hernandez, J., Hernandez, R., Hines, S., Hladun, S.L., Hodgson, A., Hogues, M., Hollins, B., Howells, S., Hulyk, S., Hume, J., Idlebird, D., Jackson, A., Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jolivet, A., Karpathy, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C., Kowis, C., Kratt, C.L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J., Liu, J., Liu, Y., Liu, Y., London, P., Longacre, S., Lopez, J., Lorensu, L., Louise, H., Lozano, R., Lu, X., Ma, J., Maheshwari, M., Mahindaratne, M., Mahmoud, M., Malloy, K., Mangum, A., Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, E., Manthey, S., McLeod, M.P., McNeill, T.Z., Meenen, E., Milosavljevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S., Morgan, M., Morris, K., Morris, S., Munidasa, M., Murphy, J., Nair, L., Nankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S., Nwakaeme, O., Okunolu, G., Olarnpunagoon, A., Pal, S., Parks, K., Pasternak, S., Paul, H., Perez, A., Perez, L., Prankoch, C., Plopper, F., Poindexter, A., Popovic, D., Primus, E., Pu, L., Puzo, M., Quirroz, J., Rachlin, E., Reeves, K., Regier, M.A., Reigh, R., Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, P., Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S.J., Sanders, W., Savery, G., Scherer, S., Scott, G., Shatsman, S., Shen, H., Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smajs, D., Speed, A., Sodergren, E., Song, X.-Z., Sorelle, R., Sosa, J., Steidle, M., Strong, R., Sutton, A., Svatek, A., Tabor, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Umani, K., Valas, R., Vera, V., Villasana, D., Waldron, L., Walker, B., Wang, J., Wang, Q., Wang, S., Warren, J., Warren, R., Wei, X., White, F., Williams, G., Willson, R., Wlezyk, R., Wooden, H., Worley, K., Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von Niederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O., Weinstock, G. and Gibbs, R.A.

Direct Submission  
Unpublished  
2 (bases 1 to 238483)  
Rat Genome Sequencing Consortium.  
Submitted (30-AUG-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA  
3 (bases 1 to 238483)  
Rat Genome Sequencing Consortium.  
Submitted (10-OCT-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA  
On Oct 10, 2002 this sequence version replaced gi:22725823.  
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.

----- Genome Center  
Center: Baylor College of Medicine  
Center code: BCM  
Web site: http://www.hgsc.bcm.tmc.edu/  
Contact: hgsc-help@bcm.tmc.edu  
----- Project Information  
Center project name: GOVP  
Center clone name: CH230-165B1  
----- Summary Statistics  
Assembly program: Phrap; version 0.990329

Consensus quality: 22924 bases at least Q40  
Consensus quality: 22513 bases at least Q30  
Consensus quality: 226732 bases at least Q20  
Estimated insert size: 226330; sum-of-contigs estimation  
Quality coverage: 7x in Q20 bases; sum-of-contigs estimation

-----  
\* NOTE: Estimated insert size may differ from sequence length  
(see http://www.hgsc.bcm.tmc.edu/docs/genbank\_draft\_data.html).  
\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 6 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.

1 3207: contig of 3207 bp in length  
3208 3307: gap of unknown length  
3308 184048: contig of 180741 bp in length  
184049 184148: gap of unknown length  
184149 197235: contig of 13087 bp in length  
197236 197335: gap of unknown length  
197336 227086: contig of 29751 bp in length  
227087 227186: gap of unknown length  
227187 228436: contig of 1250 bp in length  
228437 228536: gap of unknown length  
228537 238483: contig of 9947 bp in length.

FEATURES  
Location/Qualifiers  
1..238483  
/organism="Rattus norvegicus"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:10116"  
/clone="CH230-165B1"  
194764..195895  
misc\_feature  
/note="wgs\_contig"  
195946..137235  
misc\_feature  
/note="wgs\_contig"

ORIGIN  
Query Match 75.0%; Score 18; DB 2; Length 238483;  
Best Local Similarity 100.0%; Pred. No. 3.8;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TGAACATGAGGCCCTTC 19  
DB 13348 TGAACATGAGGCCCTTC 13365

RESULT 8  
AC087634/c  
LOCUS  
DEFINITION  
AC087634 Homo sapiens chromosome 15 clone RP11-302D8 map 15, LOW-PASS  
SEQUENCE SAMPLING.  
AC087634 AC087634.1 GI:12229409  
VERSION  
AC087634.1 HTGS\_PHASE0.  
KEYWORDS  
HTG; HTGS\_PHASE0.  
SOURCE  
Homo sapiens (human)  
ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE  
1 (bases 1 to 60456)  
Birken, B., Linton, L., Nusbaum, C. and Lander, E.  
AUTHORS  
Homo sapiens chromosome 15, clone RP11-302D8  
TITLE  
Unpublished  
REFERENCE  
2 (bases 1 to 60456)  
Birken, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, S., Barna, N., Baetien, V., Boguslavsky, L., Boukhalter, B., Brown, A., Camarata, J., Campopiano, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArrellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Headford, A., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Karatas, A., Lamazares, R., Landers, T.,

Lehoczyk, J., Levine, R., Liu, G., MacClean, C., Macdonald, P.,  
 Marquis, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K.,  
 McPheeters, R., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V.,  
 Murphy, T., Naylor, J., Nguyen, C., Norbu, C., Norman, C.H.,  
 O'Connor, T., O'Donnell, P., O'Neill, P., Oliver, J., Peterson, K.,  
 Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Ratta, R.,  
 Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M.,  
 Roy, A., Santos, R., Schauer, S., Schupbach, R., Seaman, S., Severy, P.,  
 Sougne, C., Spencer, B., Stange-Thomann, N., Stojanovic, N.,  
 Straus, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J.,  
 Travers, N., Travis, N., Trigglio, J., Vassiliev, H., Viel, R., Vo, A.,  
 Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G., Zainoun, J.,  
 Zemek, L., Zimmer, A. and Zody, M.

# Direct Submission

Submitted (15-JAN-2001) Whitehead Institute/MIT Center for Genome  
 Research, 320 Charles Street, Cambridge, MA 02141, USA  
 All repeats were identified using RepeatMasker:

Smit, A.F.A. & Green, P. (1996-1997)  
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

----- Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIBR

Web site: <http://www-seq.wi.mit.edu>

Contact: [sequence\\_submissions@genome.wi.mit.edu](mailto:sequence_submissions@genome.wi.mit.edu)

----- Project Information

Center project name: L11917

Center clone name: 302\_D\_8

-----

\* NOTE: This record contains 72 individual  
 \* sequencing reads that have not been assembled into  
 \* contigs. Runs of N are used to separate the reads  
 \* and the order in which they appear is completely  
 \* arbitrary. Low-pass sequence sampling is useful for  
 \* identifying clones that may be gene-rich and allows  
 \* overlap relationships among clones to be deduced.  
 \* However, it should not be assumed that this clone  
 \* will be sequenced to completion. In the event that  
 \* the record is updated, the accession number will  
 \* be preserved.

\* 1 785: contig of 785 bp in length  
 \* 786 885: gap of 100 bp  
 \* 886 1621: contig of 736 bp in length  
 \* 1622 1721: gap of 100 bp  
 \* 1722 2493: contig of 772 bp in length  
 \* 2494 2593: gap of 100 bp  
 \* 2594 3335: contig of 742 bp in length  
 \* 3336 3435: gap of 100 bp  
 \* 3436 4147: contig of 712 bp in length  
 \* 4148 4247: gap of 100 bp  
 \* 4248 4982: contig of 735 bp in length  
 \* 4983 5082: gap of 100 bp  
 \* 5083 5805: contig of 723 bp in length  
 \* 5806 5905: gap of 100 bp  
 \* 5906 6636: contig of 730 bp in length  
 \* 6636 6735: gap of 100 bp  
 \* 6736 7460: contig of 725 bp in length  
 \* 7461 7560: gap of 100 bp  
 \* 7561 8283: contig of 723 bp in length  
 \* 8284 8383: gap of 100 bp  
 \* 8384 9142: contig of 759 bp in length  
 \* 9143 9242: gap of 100 bp  
 \* 9243 9975: contig of 733 bp in length  
 \* 9976 10075: gap of 100 bp  
 \* 10076 10813: contig of 738 bp in length  
 \* 10814 10913: gap of 100 bp  
 \* 10914 11649: contig of 736 bp in length  
 \* 11650 11749: gap of 100 bp  
 \* 11750 12481: contig of 732 bp in length  
 \* 12482 12581: gap of 100 bp  
 \* 12582 13315: contig of 734 bp in length  
 \* 13316 13415: gap of 100 bp  
 \* 14151: contig of 736 bp in length  
 \* 14152 14251: gap of 100 bp

14252 14975: contig of 724 bp in length  
 14976 15075: gap of 100 bp  
 15076 15814: contig of 739 bp in length  
 15815 15914: gap of 100 bp  
 15915 16662: contig of 748 bp in length  
 16663 16762: gap of 100 bp  
 16763 17532: contig of 770 bp in length  
 17533 17632: gap of 100 bp  
 17633 18362: contig of 730 bp in length  
 18363 18462: gap of 100 bp  
 18463 19220: contig of 758 bp in length  
 19221 19320: gap of 100 bp  
 19322 20051: contig of 731 bp in length  
 20052 20151: gap of 100 bp  
 20152 20880: contig of 729 bp in length  
 20881 20980: gap of 100 bp  
 20982 21750: contig of 770 bp in length  
 21751 21850: gap of 100 bp  
 21852 22606: contig of 756 bp in length  
 22607 22706: gap of 100 bp  
 22707 23469: contig of 763 bp in length  
 23470 23569: gap of 100 bp  
 23570 24318: contig of 749 bp in length  
 24319 24418: gap of 100 bp  
 24419 25159: contig of 741 bp in length  
 25160 25259: gap of 100 bp  
 25260 26093: contig of 734 bp in length  
 26094 26946: contig of 753 bp in length  
 26947 27651: contig of 705 bp in length  
 27652 27751: gap of 100 bp  
 27752 28487: contig of 736 bp in length  
 28488 29324: contig of 737 bp in length  
 29325 29424: gap of 100 bp  
 29425 30193: contig of 769 bp in length  
 30194 30293: gap of 100 bp  
 30294 31035: contig of 742 bp in length  
 31036 31135: gap of 100 bp  
 31136 31889: contig of 754 bp in length  
 31890 32731: contig of 742 bp in length  
 32732 32831: gap of 100 bp  
 32832 33569: contig of 738 bp in length  
 33570 33669: gap of 100 bp  
 33670 34415: contig of 746 bp in length  
 34416 34515: gap of 100 bp  
 34516 35272: contig of 757 bp in length  
 35273 35372: gap of 100 bp  
 35373 36095: contig of 723 bp in length  
 36096 36195: gap of 100 bp  
 36196 36912: contig of 717 bp in length  
 36913 37012: gap of 100 bp  
 37013 37770: contig of 758 bp in length  
 37771 37870: gap of 100 bp  
 37871 38611: contig of 741 bp in length  
 38612 39462: contig of 751 bp in length  
 39463 39562: gap of 100 bp  
 39563 40324: contig of 762 bp in length  
 40325 40424: gap of 100 bp  
 40425 41225: contig of 801 bp in length  
 41226 41325: gap of 100 bp  
 41326 42063: contig of 738 bp in length  
 42064 42163: gap of 100 bp  
 42164 42879: contig of 716 bp in length  
 42880 42979: gap of 100 bp  
 42980 43712: contig of 733 bp in length  
 43713 43812: gap of 100 bp  
 43813 44509: contig of 697 bp in length  
 44510 44609: gap of 100 bp  
 44610 45341: contig of 732 bp in length

## TITLE JOURNAL

## COMMENT

```

* 45342 45441: gap of 100 bp
* 45442 46168: contig of 727 bp in length
* 46169 46268: gap of 100 bp
* 46269 47020: contig of 752 bp in length
* 47021 47120: gap of 100 bp
* 47121 47867: contig of 747 bp in length
* 47868 47967: gap of 100 bp
* 47968 48112: contig of 745 bp in length
* 48113 48812: gap of 100 bp
* 48813 49531: contig of 719 bp in length
* 49532 49631: gap of 100 bp
* 49632 50374: contig of 743 bp in length
* 50375 51198: gap of 100 bp
* 51199 51298: contig of 724 bp in length
* 51299 52022: contig of 724 bp in length
* 52023 52122: gap of 100 bp
* 52123 52888: contig of 766 bp in length
* 52889 52988: gap of 100 bp
* 52989 53725: contig of 737 bp in length
* 53726 54566: gap of 100 bp
* 54567 54666: contig of 741 bp in length
* 54667 55445: gap of 100 bp
* 55446 55445: contig of 779 bp in length
* 55446 56281: gap of 100 bp
* 56282 56381: gap of 100 bp
* 56382 57126: contig of 745 bp in length
* 57127 57226: gap of 100 bp
* 57227 57965: contig of 739 bp in length
* 57966 58065: gap of 100 bp

Query Match 70.8%; Score 17; DB 2; Length 60456;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TCGACATGAGCCCTT 18
Db 9941 TCGACATGAGCCCTT 9925

RESULT 9
AL805925 104244 bp DNA linear ROD 24-AUG-2002
LOCUS Mouse DNA sequence from clone RP23-210E20 on chromosome X, complete
DEFINITION
ACCESSION AL805925
VERSION AL805925.6 GI:22531408
KEYWORDS HTG.
SOURCE Mus musculus (house mouse)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 104244)
Direct Submission
Submitted (24-AUG-2002) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Aug 27, 2002 this sequence version replaced gi:22416054.
----- Genome Center
Center: Wellcome Trust Sanger Institute
Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
-----
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence was finished as follows otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such

```

```

regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest. The following
abbreviations are used to associate primary accession numbers given
in the feature table with their source databases: Em:, EMBL; Sw:,
SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP
database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP23-210E20 is
from the RPCI-23 Mouse PAC Library
constructed by the group of Pieter de Jong.
For further details see http://www.chori.org/bacpac/home.htm
VECTOR: pBACE3.6.

FEATURES
Location/Qualifiers
source
1..104244
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
/chromosome="X"
/clone="RP23-210E20"
/clone_lib="RPCI-23"

ORIGIN
Query Match 70.8%; Score 17; DB 10; Length 104244;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 AACATGAGCCCTTCAG 21
Db 2162 AACATGAGCCCTTCAG 2178

RESULT 10
AL954170 138152 bp DNA linear ROD 13-AUG-2003
LOCUS Mouse DNA sequence from clone RP23-467H15 on chromosome 2, complete
DEFINITION
ACCESSION AL954170
VERSION AL954170.4 GI:33636222
KEYWORDS HTG.
SOURCE Mus musculus (house mouse)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 138152)
Direct Submission
Submitted (13-AUG-2003) Mouse Sequencing Group, HGMP-RC, Hinxton,
Cambridge, CB10 1SB, UK. E-mail enquiries:- mrbotche@hgmp.mrc.ac.uk
or pnoth@hgmp.mrc.ac.uk
HGMP-RC part of the UK Mouse Sequencing Consortium
On Aug 13, 2003 this sequence version replaced gi:32567581.
----- Genome Center
Center: UK Medical Research Council
Center code: UK-MRC
Web site: http://mrcseq.har.mrc.ac.uk
Contact: mouseq@har.mrc.ac.uk
-----
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence was finished as follows otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such

```

as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em., EMBL; Sw., SWISSPROT; Tr., TREMBL; Wp., WORMPEP; Information on the WORMPEP database can be found at [http://www.sanger.ac.uk/projects/C\\_elegans/wormpep](http://www.sanger.ac.uk/projects/C_elegans/wormpep) RP23-467H15 is from the RPCI-23 Mouse BAC Library

constructed by the group of Pieter de Jong.

VECTOR: pBACE3.6

Sequence from the Mouse Genome Sequencing Consortium whole genome shotgun may have been used to confirm this sequence. Sequence data from the whole genome shotgun alone has only been used where it has a phred quality of at least 30.

## FEATURES

source

```
1. .138152
   Location/Qualifiers
     /organism="Mus musculus"
     /mol_type="genomic DNA"
     /db_xref="taxon:10090"
     /chromosomes="2"
     /clone="RP23-467H15"
     /clone_lib="RPCI-23"
```

## ORIGIN

```
Query Match      70.8%; Score 17; DB 10; Length 138152;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY 4 GAACATGAAGCCCTTCA 20

Db 137169 GAACATGAAGCCCTTCA 137153

## RESULT 11

BX248232

LOCUS

DEFINITION BX248232 152804 bp DNA linear HTG 07-NOV-2003 Danio rerio clone CH211-23215, WORKING DRAFT SEQUENCE, 3 unordered pieces.

ACCESSION BX248232.6

VERSION HTG; HTGS PHASE1; HTGS ACTIVEFIN; HTGS\_DRAFT; HTGS\_FULLTOP.

KEYWORDS Danio rerio (zebrafish)

SOURCE Danio rerio

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Actinopterygii; Neopterygii; Teleostei; Ostariophysi;

Cypriniformes; Cyprinidae; Danio.

REFERENCE 1 (bases 1 to 152804)

AUTHORS Giselle H.

TITLE Direct Submission

JOURNAL Submitted (06-NOV-2003) Wellcome Trust Sanger Institute, Hinxton,

Cambridgeshire, CB10 1SA, UK. E-mail enquiries:

zfish-help@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk

On Nov 7, 2003 this sequence version replaced gi:38141652.

COMMENT ----- Genome Center

Center: Wellcome Trust Sanger Institute

Center code: SC

Web site: <http://www.sanger.ac.uk>

Contact: zfish-help@sanger.ac.uk

----- Project Information

Center project name: zC23215

----- Summary Statistics

Assembly program: XGAP4; version 4.5

Chemistry: Dye-terminator; 100% of reads

Consensus quality: 152578 bases at least Q40

Consensus quality: 152597 bases at least Q30

Consensus quality: 152598 bases at least Q20

Insert size: 152604; sum-of-contigs

Insert size: 161454; 2.1% error; agarose-fp

Quality coverage: 10.26x in Q20 bases; sum-of-contigs Quality

Coverage: 9.69x in Q20 bases; agarose-fp

-----

\* NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

```
1. 86810: contig of 86810 bp in length
* 86811 86910: gap of 100 bp
* 86911 138019: contig of 51109 bp in length
* 138020 138119: gap of 100 bp
* 138120 152804: contig of 14685 bp in length.
```

## FEATURES

source

```
1. .152804
   Location/Qualifiers
     /organism="Danio rerio"
     /mol_type="genomic DNA"
     /db_xref="taxon:7955"
     /clone="CH211-23215"
     /clone_lib="CHORI-211"
     /note="assembly_fragment:02232"
     /fragment_chain:1
```

misc\_feature

```
1. .86810
   /note="assembly_fragment:00979"
   /fragment_chain:1
```

misc\_feature

```
86911. .138019
   /note="assembly_fragment:01208"
   /fragment_chain:1
```

misc\_feature

```
138120. .152804
   /note="assembly_fragment:01208"
   /fragment_chain:1
```

## ORIGIN

```
Query Match      70.8%; Score 17; DB 2; Length 152804;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY 5 AACATGAAGCCCTTCAG 21

Db 137360 AACATGAAGCCCTTCAG 137376

## RESULT 12

AC109200

LOCUS

DEFINITION AC109200 162077 bp DNA linear HTG 19-NOV-2003 Mus musculus chromosome 8 clone RP23-26G21 map 8, WORKING DRAFT SEQUENCE, 6 ordered pieces.

ACCESSION AC109200

VERSION AC109200.5

KEYWORDS HTG; HTGS PHASE2; HTGS\_DRAFT; HTGS\_FULLTOP.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 162077)

AUTHORS Birren,B., Nusbaum,C. and Lander,E.

TITLE Mus musculus chromosome 8, clone RP23-26G21

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 162077)

AUTHORS Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,

Anderson,S., Barna,N., Bastien,V., Boguslavsky,L., Boukhgaiter,B.,

Brown,A., Camarata,J., Campotiano,A., Chang,J., Chazaro,B.,

Choepel,Y., Collangelo,M., Collins,S., Collymore,A., Cook,A.,

Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S.,

Ferreira,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S.,

Ginde,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N.,

Hagos,B., Horton,L., Hulme,W., Illiev,I., Johnson,R., Jones,C.,

Kamat,A., Karatas,A., Kells,C., LaRoque,K., Lamazares,R.,

Landers,T., Lehoczy,J., Levine,N., Liu,G., MacLean,C.,

Macdonald,P., Major,J., Marquis,N., Matthews,C., McCarthy,M.,

McEwan,P., McKernan,K., Meldrum,J., Meneus,L., Mihova,T.,

Mlenga,V., Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C.,

Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D., Oliver,J.,

Peterson,K., Phunkhang,P., Pierre,N., Pollara,V., Raymond,C.,

Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupbach, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Travis, N., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

Direct Submission  
Submitted (03-FEB-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA  
3 (bases 1 to 162077)

Birren, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N., Anderson, M., Arachchi, H. M., Barna, N., Bastien, V., Bloom, T., Boguslavsky, L., Boukhgalter, B., Camarata, J., Chang, J., Choepel, Y., Collumore, A., Cook, A., Cooke, P., Corum, B., DeArellano, K., Diaz, J. S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Graham, L., Grand-Pierre, N., Hafez, N., Hagopian, D., Hagos, B., Hall, J., Horton, L., Hulne, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Keller, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., Lui, X., Mabbitt, R., MacLean, C., MacDonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Rachupka, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schupbach, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Venkataraman, V. S., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

Direct Submission  
Submitted (19-NOV-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA  
On Nov 19, 2003 this sequence version replaced gi:21313786.  
All repeats were identified using RepeatMasker:  
Smit, A.F.A. & Green, P. (1996-1997)  
http://ftp.genome.washington.edu/RN/RepeatMasker.html

TITLE  
JOURNAL  
COMMENT

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIBR  
Web site: <http://www-seq.wi.mit.edu>  
Contact: [sequence\\_submissions@genome.wi.mit.edu](mailto:sequence_submissions@genome.wi.mit.edu)  
----- Project Information  
Center project name: L20459  
Center clone name: 26 G 21

----- Summary Statistics  
Sequencing vector: Plasmid; n/a; 100% of reads  
Chemistry: Dye-terminator Big Dye; 100% of reads  
Assembly program: Phrap; version 0.960731  
Consensus quality: 160977 bases at least Q40  
Consensus quality: 161390 bases at least Q30  
Consensus quality: 161524 bases at least Q20  
Insert size: 157000; agarose-fp  
Insert size: 161577; sum-of-contigs  
Quality coverage: 13.8 in Q20 bases; agarose-fp  
Quality coverage: 13.4 in Q20 bases; sum-of-contigs

\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 6 contigs. Gaps between the contigs  
\* are represented as runs of N. The order of the pieces  
\* is believed to be correct as given, however the sizes  
\* of the gaps between them are based on estimates that have  
\* provided by the submitter.  
\* This sequence will be replaced  
\* by the finished sequence as soon as it is available and  
\* the accession number will be preserved.  
\* 1 53642: contig of 53642 bp in length  
\* 53643 53742: gap of 100 bp  
\* 53743 54202: contig of 460 bp in length  
\* 54203 54302: gap of 100 bp  
\* 54303 55174: contig of 872 bp in length  
\* 55175 55274: gap of 100 bp

\* 55275 127105: contig of 71831 bp in length  
\* 127106 127205: gap of 100 bp  
\* 127206 152575: contig of 25370 bp in length  
\* 152576 162077: gap of 100 bp  
\* 152676 162077: contig of 9402 bp in length.

FEATURES  
source

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/chromosome="8"  
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/clone\_RP23-26G21"  
/clone\_lib="RPCI-23 Female Mouse BAC"  
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clone end:SP6  
vector\_side:left"  
53743..54202  
/note="assembly\_fragment"  
54303..55174  
/note="assembly\_fragment"  
55275..127105  
/note="assembly\_fragment"  
127206..152575  
/note="assembly\_fragment"  
152676..162077  
/note="assembly\_fragment"  
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vector\_side:right"

ORIGIN

Query Match 70.8%; Score 17; DB 2; Length 162077;  
Best Local Similarity 100.0%; Pred. No. 16;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGGAACATGAAGCCCT 17  
|||||

DB 95197 GTGGAACATGAAGCCCT 95213  
|||||

RESULT 13  
AL606494/c

LOCUS AL606494 184317 bp DNA linear ROD 12-JUL-2003  
DEFINITION Mouse DNA sequence from clone RP23-198B6 on chromosome 2, complete  
sequence.

ACCESSION AL606494

VERSION AL606494.3 GI:32567580

KEYWORDS HTG.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 184317)

REFERENCE

AUTHORS

TITLE

JOURNAL

REMARK

COMMENT

Submitted (12-JUL-2003) Mouse Sequencing Group, HGMP-RC, Hinxton,  
Cambridge, CB10 1SB, UK. E-mail enquiries:- [mrbotche@hgmp.mrc.ac.uk](mailto:mrbotche@hgmp.mrc.ac.uk)  
or [pnoth@hgmp.mrc.ac.uk](mailto:pnoth@hgmp.mrc.ac.uk)  
HGMP-RC part of the UK Mouse Sequencing Consortium  
On Jul 12, 2003 this sequence version replaced gi:15723837.

----- Genome Center

Center: UK Medical Research Council

Center code: UK-MRC

Web site: <http://mrcseq.har.mrc.ac.uk>

Contact: [mouseq@har.mrc.ac.uk](mailto:mouseq@har.mrc.ac.uk)

-----

During sequence assembly data is compared from overlapping clones.  
Where differences are found these are annotated as variations  
together with a note of the overlapping clone name. Note that the

variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em: EMBL; Sw: SWISSPROT; Tr: TREMBL; Wp: WORMPEP; Information

on the WORMPEP database can be found at

[http://www.sanger.ac.uk/Projects/C\\_elegans/wormpep](http://www.sanger.ac.uk/Projects/C_elegans/wormpep) RP23-198B6 is

from the RPCI-23 Mouse BAC library

constructed by the group of Pieter de Jong.

For further details see <http://www.chori.org/bacpac/home.htm>

VECTOR: pBACE3.6

Sequence from the Mouse Genome Sequencing Consortium whole genome shotgun may have been used to confirm this sequence. Sequence data from the whole genome shotgun alone has only been used where it has a phred quality of at least 30.

#### FEATURES

source

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#### ORIGIN

Query Match 70.8%; Score 17; DB 10; Length 184317;

Best Local Similarity 100.0%; Pred. No. 15;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GAACATGAAGCCCTTCA 20

Db 1748 GAACATGAAGCCCTTCA 1732

#### RESULT 14

AC096363/c

LOCUS

DEFINITION Rattus norvegicus 1 BAC CH230-54P17 (Children's Hospital Oakland

Research Institute) complete sequence.

AC096363

AC096363.8 GI:32362332

HTG.

SOURCE Rattus norvegicus (Norway rat)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;

Rattus.

REFERENCE 1 (bases 1 to 215356)

Muzny, D. Marie, Metzker, M. Lee, Abramson, S., Adams, C., Alder, J., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguitano, D., Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Biswal, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E., Cardenas, V., Carter, K., Cavazos, I., Caesar, H., Center, A., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Davila, M. L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K., Egan, A., Escoto, M., Eugene, C., Evans, C. A., Falls, T., Fan, G., Fernandez, S., Finley, M., Flegg, N., Forbes, L., Foster, M., Foster, P., Fraser, C. M., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Garza, M., Gebregeorgis, E., Geer, K., Gill, R., Grady, M., Guerra, W., Guevara, W.,

Gunaratne, P., Haaland, W., Hamil, C., Hamilton, C., Hamilton, K., Harvey, Y., Haylak, P., Hawes, A., Henderson, N., Hernandez, J., Hernandez, R., Hines, S., Hladun, S. L., Hodgson, A., Hoques, M., Hollins, B., Howells, S., Hulyk, S., Hume, J., Idlebird, D., Jackson, A., Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jolivet, A., Karpathy, S., Kelly, S., Khan, Z., King, D., Kovar, C., Kowis, C., Kraft, C. L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J., Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J., Lorensheva, L., Loulsegged, H., Lozado, R. J., Lu, X., Ma, J., Maheshwari, M., Mahindartne, M., Mahmoud, M., Malloy, K., Mangum, A., Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, E., Mathew, S., McLeod, M., McNeill, T., Meenen, E., Milosavljevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S., Morgan, M., Morris, K., Morris, S., Munidasa, M., Murphy, M., Nair, L., Nankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S., Nwaokemele, O., Okwuonu, G., Olarunsgoon, A., Pal, S., Parks, K., Pasternak, S., Paul, H., Perez, A., Perez, L., Pfannkuch, C., Plopper, F., Poindexter, A., Popovic, D., Primus, E., Pu, L.-L., Puazo, M., Quiroz, J., Rachlin, E., Reeves, K., Regier, M. A., Reigh, R., Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F., Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S. J., Sanders, W., Savary, G., Scherer, S., Scott, G., Shatsman, S., Shen, H., Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C. D., Smajls, D., Sneed, A., Sodergren, E., Song, X.-Z., Sorelle, R., Sosa, J., Steimle, M., Strong, R., Sutton, A., Svatek, A., Tabor, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Usmani, K., Valas, R., Vera, V., Villaseana, D., Waldron, L., Walker, B., Wang, J., Wang, Q., Wang, S., Warren, J., Warren, R., Wei, X., White, F., Williams, G., Willson, R., Wlezyk, R., Wooden, H., Worley, K., Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von Niederhausern, A., Weiss, R., Smith, D. R., Holt, R. A., Smith, H. O., Weinstock, G. and Gibbs, R. A.

Direct Submission

Unpublished

2 (bases 1 to 215356)

Worley, K. C.

Direct Submission

Submitted (17-SEP-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

3 (bases 1 to 215356)

Rat Genome Sequencing Consortium.

Direct Submission

Submitted (10-MAY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

4 (bases 1 to 215356)

Worley, K. C.

Direct Submission

Submitted (01-JUL-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

#### COMMENT

On Jul 1, 2003 this sequence version replaced gi:30521822. Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality does not meet this standard, it will be indicated in the annotation.

#### FEATURES

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805. .1138

repeat\_region

1148. .1232

repeat\_region

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repeat\_region

1507. .1734

repeat\_region



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Best Local Similarity 100.0%; Pred. No. 15;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ACATGAAGCCCTTCAGC 22
|||||
Db 34030 ACATGAAGCCCTTCAGC 34014

RESULT 15
AC102091 215958 bp DNA linear HTG 24-JAN-2003
LOCUS Mus musculus clone RP23-9K20, WORKING DRAFT SEQUENCE, 5 unordered
pieces.
AC102091
AC102091.3 GI:27884970
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
KEYWORDS Mus musculus (house mouse)
SOURCE Mus musculus
ORGANISM Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 215958)
AUTHORS Birren,B., Nusbaum,C. and Lander,E.
TITLE Mus musculus, clone RP23-9K20
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 215958)
AUTHORS Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
Anderson,S., Barna,N., Bastien,V., Boguslavskiy,L., Boukhgalter,B.,
Brown,A., Camarata,J., Campopiano,A., Chang,J., Chazaro,B.,
Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cook,A.,
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Ferreira,P., FitzHugh,W., Gage,D., Galagan,J., Gaidyna,S.,
Ginde,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N.,
Hagos,B., Heaford,A., Horton,L., Hulme,W., Illiev,I., Johnson,R.,
Jones,C., Kamat,A., Karatas,A., Kells,C., LaRocque,K.,
Lamazares,R., Landers,T., Lehoczy,J., Levine,R., Liu,G.,
MacLean,C., Macdonald,P., Major,J., Marquis,N., Matthews,C.,
McCarthy,M., McEwan,P., McKernan,K., McPheeters,R., Meldrim,J.,
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Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D.,
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Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schuback,R.,
Seaman,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N.,
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Topham,K., Travers,M., Travis,N., Trigilio,J., Vassiliev,H.,

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TITLE  
JOURNAL  
REFERENCE  
AUTHORS

Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.  
Submitted (23-NOV-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA  
3 (bases 1 to 215958)

Anderson, S., Arachchi, H. M., Barna, N., Bastien, V., Bloom, T., Boguslavskiy, L., Boukhalter, B., Camarata, J., Chang, J., Choepel, Y., Collymore, A., Cook, A., Cooke, P., Corum, B., DeArrellano, K., Diaz, J. S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Faro, S., Ferreira, P., Fitzgerald, M., Gage, D., Galagan, J., Gardyna, S., Graham, L., Grand-Pierre, N., Hafez, N., Hagopian, B., Hagos, B., Hall, J., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., Lui, A., Mabbitt, R., MacLean, C., Macdonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M., Melgrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Rachupka, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M., Talamas, J., Teefaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Venkataraman, V. S., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.  
Submitted (24-JAN-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA  
On Jan 24, 2003 this sequence version replaced gi:22381287.  
All repeats were identified using RepeatMasker:  
Smit, A. F. A. & Green, P. (1996-1997)  
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

TITLE  
JOURNAL  
COMMENT

misc\_feature  
misc\_feature  
misc\_feature  
misc\_feature  
misc\_feature

misc\_feature  
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misc\_feature

ORIGIN

Query Match 70.8%; Score 17; DB 2; Length 215958;  
Best Local Similarity 100.0%; Pred. No. 15;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ACATGAAGCCCTTCAGC 22  
|||||||  
DB 106575 ACATGAAGCCCTTCAGC 106591

Search completed: May 27, 2004, 02:16:49  
Job time : 514.783 secs

Center: Whitehead Institute/ MIT Center for Genome Research  
Center code: WIBR  
Web site: <http://www-seq.wi.mit.edu>  
Contact: [sequence\\_submissions@genome.wi.mit.edu](mailto:sequence_submissions@genome.wi.mit.edu)  
----- Project Information  
Center project name: L18028  
Center clone name: 9\_K\_20  
----- Summary Statistics  
Sequencing vector: Plasmid; n/a; 100% of reads  
Chemistry: Dye-terminator Big Dye; 100% of reads  
Assembly program: Phrap; version 0.960731  
Consensus quality: 214869 bases at least Q40  
Consensus quality: 215183 bases at least Q30  
Consensus quality: 215314 bases at least Q20  
Insert size: 220000; agarose-fp  
Insert size: 215558; sum-of-contigs  
Quality coverage: 11.4 in Q20 bases; agarose-fp  
Quality coverage: 11.6 in Q20 bases; sum-of-contigs  
-----  
\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 5 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.  
\* 1 16300: contig of 16300 bp in length  
\* 16301 16400: gap of 100 bp  
\* 16401 122337: contig of 105937 bp in length  
\* 122338 122437: gap of 100 bp  
\* 122438 139749: contig of 17312 bp in length  
\* 139750 139849: gap of 100 bp  
\* 139850 211515: contig of 71666 bp in length  
\* 211516 211615: gap of 100 bp  
\* 211616 215958: contig of 4343 bp in length.  
Location/Qualifiers  
1. .215958  
/organism="Mus musculus"

FEATURES  
source

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: May 26, 2004, 14:55:11 ; Search time 107.037 Seconds  
(without alignments)  
952.539 Million cell updates/sec

Title: US-09-121-239-16

Perfect score: 24

Sequence: 1 GTGGAACATGAAGCCCTTCAGCG 24

Scoring table: OLIGO\_NUC

Gapop 60.0 , Gapext 60.0

Searched: 3373863 seqs, 2124099041 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : N\_Geneseq\_29Jan04:\*

- 1: Geneseqn1980s:\*
- 2: Geneseqn1990s:\*
- 3: Geneseqn2000s:\*
- 4: Geneseqn2001as:\*
- 5: Geneseqn2001bs:\*
- 6: Geneseqn2002as:\*
- 7: Geneseqn2003as:\*
- 8: Geneseqn2003bs:\*
- 9: Geneseqn2003cs:\*
- 10: Geneseqn2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	24	100.0	24	3	AAZ60857 Oligonucle
C 2	24	100.0	24	3	AAZ60855 Oligonucle
C 3	24	100.0	24	3	AAZ60858 Oligonucle
C 4	24	100.0	24	3	AAZ60856 Oligonucle
C 5	24	100.0	299	3	AAZ60864 Region su
C 6	24	100.0	3380	7	ABZ18520 Group III
C 7	18	75.0	34125	6	ABSE69903 Human ade
C 8	16	66.7	65	6	ABN54940 Mouse spl
C 9	16	66.7	751	4	AAI94531 Human neu
C 10	16	66.7	1044	4	AAZ54224 Pseudomon
C 11	16	66.7	1044	7	ACA42504 Prokaryot
C 12	16	66.7	2278	3	AAZ89962 Corn ADA2
C 13	16	66.7	2599	3	AAZ56382 Escherich
C 14	16	66.7	3460	2	AAV36957 Nucleotid
C 15	16	66.7	3460	3	AAZ34989 Human cel
C 16	16	66.7	3460	6	ABK84482 Human cDN
C 17	16	66.7	6699	7	ABX08804 Angiogene
C 18	16	66.7	6699	7	ABX76302 Lung canc
C 19	16	66.7	185035	6	ABT10147 Human bre
C 20	16	66.7	185035	7	ACA64951 Human PBN
C 21	15	62.5	23	2	AAZ56765 Human bcr
C 22	15	62.5	23	2	AAZ56766 Human bcr
C 23	15	62.5	33	2	AAZ10497 ABL onco

24	15	62.5	33	2	AAZ10495	AAZ10495
C 25	15	62.5	40	2	AAQ57147	AAQ57147 Chromosom
C 26	15	62.5	47	2	AAQ66785	AAQ66785 Ribozyme
C 27	15	62.5	52	2	AAZ12637	AAZ12637 T7 promot
C 28	15	62.5	60	2	AAZ29713	AAZ29713 Chronic m
C 29	15	62.5	62	2	AAQ66774	AAQ66774 L6(1)31 r
C 30	15	62.5	63	6	ABS73178	ABS73178 DNA encod
C 31	15	62.5	80	2	AAQ34631	AAQ34631 Human Phl
C 32	15	62.5	80	2	AAV20460	AAV20460 Human bcr
C 33	15	62.5	205	6	ABL87455	ABL87455 Human ova
C 34	15	62.5	257	2	AAQ34625	AAQ34625 Human bcr
C 35	15	62.5	257	2	AAV20458	AAV20458 Human bcr
C 36	15	62.5	423	6	ABS73179	ABS73179 DNA encod
C 37	15	62.5	436	7	ABX40048	ABX40048 Bovine ES
C 38	15	62.5	483	7	ADA71111	ADA71111 Rice gene
C 39	15	62.5	549	6	ABS73314	ABS73314 DNA encod
C 40	15	62.5	729	7	ABZ66719	ABZ66719 Orthosomy
C 41	15	62.5	921	5	AAZ85025	AAZ85025 DNA encod
C 42	15	62.5	922	6	ABS73180	ABS73180 DNA encod
C 43	15	62.5	1024	7	ABZ82900	ABZ82900 Toxicolog
C 44	15	62.5	1079	5	AAZ85026	AAZ85026 DNA encod
C 45	15	62.5	1079	6	ABS73181	ABS73181 DNA encod

ALIGNMENTS

RESULT 1  
AAZ60857/c  
ID AAZ60857 standard; DNA; 24 BP.  
XX  
AC AAZ60857;  
XX  
DT 16-MAY-2000 (first entry)  
XX  
DE Oligonucleotide used to detect bcr b3-abl fusion transcripts.  
XX  
KW Fusion transcript; translocation; bcr b3 region; abl gene;  
KW amplification assay; detection assay; medical diagnosis;  
KW clinical monitoring; chimeric RNA; fusion RNA; condition marker;  
KW disease marker; cancer; leukemia; ss.  
XX  
OS Synthetic.  
XX  
PN WO200005418-A1.  
XX  
PD 03-FEB-2000.  
XX  
PF 23-JUL-1999; 99WO-US016832.  
XX  
PR 23-JUL-1998; 98US-00121239.  
XX  
(GENP-) GEN-PROBE INC.  
XX  
PI Harvey RC, Eastman PS;  
XX  
DR WPI; 2000-182730/16.  
XX  
PT Novel methods for preparing RNA from biological samples, used for the  
PT detection and measurement of nucleic acids and fusion nucleic acids.  
XX  
XX Claim 19; Page 43; 49pp; English.

Oligonucleotides AAZ60840-62 and AAZ60865-66 are used in the method of the invention to detect fusion transcripts produced from a translocation between the bcr b3 region and the abl gene. The specification describes a method for detecting a fusion nucleic acid (particularly chimeric mRNA species), in a biological sample. The method comprises contacting a sample of fusion nucleic acid with primers, amplifying the hybridized fusion nucleic acid, and detecting the target hybrid. The method is used for the simple and rapid preparation of RNA from a biological sample, particularly from the cytoplasm of eukaryotic cells, which is suitable for use in an amplification and detection assay. The methods are used for

CC the analysis and detection of nucleic acids in biological samples. The  
 CC methods are useful in the human medical and veterinary fields, for  
 CC medical diagnoses and clinical monitoring of a patient's response to  
 CC therapy where a disease or medical condition is associated with a  
 CC particular type and/or level of mRNA present in the sample. The methods  
 CC are also useful for detecting or quantifying fusion or chimeric RNA  
 CC species, and for detecting a translocation as a marker for a given  
 CC condition or disease, e.g. translocations associate with cancers,  
 CC particularly forms of leukemia

XX Sequence 24 BP; 4 A; 8 C; 6 G; 6 T; 0 U; 0 Other;

Query Match 100.0%; Score 24; DB 3; Length 24;  
 Best Local Similarity 100.0%; Pred. No. 0.00026;  
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGGAACATGAAGCCCTTCAGCGG 24  
 DB 24 GTGGAACATGAAGCCCTTCAGCGG 1

RESULT 2  
 AAZ60855  
 ID AAZ60855 standard; DNA; 24 BP.  
 AC AAZ60855;  
 XX  
 DT 16-MAY-2000 (first entry)  
 XX  
 DE Oligonucleotide used to detect bcr b3-abl fusion transcripts.  
 XX Fusion transcript; translocation; bcr b3 region; abl gene;  
 KW amplification assay; detection assay; medical diagnosis;  
 KW clinical monitoring; chimeric RNA; fusion RNA; condition marker;  
 KW disease marker; cancer; leukemia; ss.

XX Synthetic.

OS WO200005418-A1.

PN 03-FEB-2000.

XX 23-JUL-1999; 99WO-US016832.

PR 23-JUL-1998; 98US-00121239.

PA (GENP-) GEN-PROBE INC.

XX Harvey RC, Eastman PS;

DR WPI; 2000-182730/16.

XX Novel methods for preparing RNA from biological samples, used for the  
 PT detection and measurement of nucleic acids and fusion nucleic acids.

XX Claim 19; Page 42; 49pp; English.

XX Oligonucleotides AAZ60840-62 and AAZ60865-66 are used in the method of  
 CC the invention to detect fusion transcripts produced from a translocation  
 CC between the bcr b3 region and the abl gene. The specification describes a  
 CC method for detecting a fusion nucleic acid (particularly chimeric mRNA  
 CC species), in a biological sample. The method comprises contacting a  
 CC sample of fusion nucleic acid with primers, amplifying the hybridized  
 CC fusion nucleic acid, and detecting the target hybrid. The method is used  
 CC for the simple and rapid preparation of RNA from a biological sample,  
 CC particularly from the cytoplasm of eukaryotic cells, which is suitable  
 CC for use in an amplification and detection assay. The methods are used for  
 CC the analysis and detection of nucleic acids in biological samples. The  
 CC methods are useful in the human medical and veterinary fields, for  
 CC medical diagnoses and clinical monitoring of a patient's response to  
 CC therapy where a disease or medical condition is associated with a  
 CC particular type and/or level of mRNA present in the sample. The methods  
 CC are also useful for detecting or quantifying fusion or chimeric RNA

CC species, and for detecting a translocation as a marker for a given  
 CC condition or disease, e.g. translocations associate with cancers,  
 CC particularly forms of leukemia

XX Sequence 24 BP; 6 A; 6 C; 8 G; 4 T; 0 U; 0 Other;

Query Match 100.0%; Score 24; DB 3; Length 24;  
 Best Local Similarity 100.0%; Pred. No. 0.00026;  
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGGAACATGAAGCCCTTCAGCGG 24  
 DB 1 GTGGAACATGAAGCCCTTCAGCGG 24

RESULT 3  
 AAZ60858/c  
 ID AAZ60858 standard; RNA; 24 BP.  
 AC AAZ60858;  
 XX  
 DT 16-MAY-2000 (first entry)  
 XX  
 DE Oligonucleotide used to detect bcr b3-abl fusion transcripts.  
 XX Fusion transcript; translocation; bcr b3 region; abl gene;  
 KW amplification assay; detection assay; medical diagnosis;  
 KW clinical monitoring; chimeric RNA; fusion RNA; condition marker;  
 KW disease marker; cancer; leukemia; ss.

OS Synthetic.

PN WO200005418-A1.

XX 03-FEB-2000.

XX 23-JUL-1999; 99WO-US016832.

PR 23-JUL-1998; 98US-00121239.

XX (GENP-) GEN-PROBE INC.

PA Harvey RC, Eastman PS;

DR WPI; 2000-182730/16.

XX Novel methods for preparing RNA from biological samples, used for the  
 PT detection and measurement of nucleic acids and fusion nucleic acids.

XX Claim 19; Page 43; 49pp; English.

XX Oligonucleotides AAZ60840-62 and AAZ60865-66 are used in the method of  
 CC the invention to detect fusion transcripts produced from a translocation  
 CC between the bcr b3 region and the abl gene. The specification describes a  
 CC method for detecting a fusion nucleic acid (particularly chimeric mRNA  
 CC species), in a biological sample. The method comprises contacting a  
 CC sample of fusion nucleic acid with primers, amplifying the hybridized  
 CC fusion nucleic acid, and detecting the target hybrid. The method is used  
 CC for the simple and rapid preparation of RNA from a biological sample,  
 CC particularly from the cytoplasm of eukaryotic cells, which is suitable  
 CC for use in an amplification and detection assay. The methods are used for  
 CC the analysis and detection of nucleic acids in biological samples. The  
 CC methods are useful in the human medical and veterinary fields, for  
 CC medical diagnoses and clinical monitoring of a patient's response to  
 CC therapy where a disease or medical condition is associated with a  
 CC particular type and/or level of mRNA present in the sample. The methods  
 CC are also useful for detecting or quantifying fusion or chimeric RNA  
 CC species, and for detecting a translocation as a marker for a given  
 CC condition or disease, e.g. translocations associate with cancers,  
 CC particularly forms of leukemia

XX Sequence 24 BP; 4 A; 8 C; 6 G; 0 T; 6 U; 0 Other;

Query Match 100.0%; Score 24; DB 3; Length 24;  
 Best Local Similarity 100.0%; Pred. No. 0.00026;  
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGGAACATGAAGCCCTTCAGCGG 24.  
 DB 24 GTGGAACATGAAGCCCTTCAGCGG 1

RESULT 4  
 ID AAZ60856 standard; RNA; 24 BP.  
 AC AAZ60856;  
 DT 16-MAY-2000 (first entry)  
 DE Oligonucleotide used to detect bcr b3-abl fusion transcripts.  
 KW Fusion transcript; translocation; bcr b3 region; abl gene;  
 KW amplification assay; detection assay; medical diagnosis;  
 KW clinical monitoring; chimeric RNA; fusion RNA; condition marker;  
 KW disease marker; cancer; leukemia; ss.  
 OS Synthetic.  
 PN WO200005418-A1.  
 PD 03-FEB-2000.  
 PF 23-JUL-1999; 99WO-US016832.  
 PR 23-JUL-1998; 98US-00121239.  
 PA (GENP-) GEN-PROBE INC.  
 PI Harvey RC, Eastman PS;  
 XX WPI; 2000-182730/16.  
 XX Novel methods for preparing RNA from biological samples, used for the  
 PT detection and measurement of nucleic acids and fusion nucleic acids.  
 PS Claim 19; Page 42; 49pp; English.  
 CC Oligonucleotides AAZ60840-62 and AAZ60865-66 are used in the method of  
 CC the invention to detect fusion transcripts produced from a translocation  
 CC between the bcr b3 region and the abl gene. The specification describes a  
 CC method for detecting a fusion nucleic acid (particularly chimeric mRNA  
 CC species), in a biological sample. The method comprises contacting a  
 CC sample of fusion nucleic acid with primers, amplifying the hybridized  
 CC fusion nucleic acid, and detecting the target hybrid. The method is used  
 CC for the simple and rapid preparation of RNA from a biological sample,  
 CC particularly from the cytoplasm of eukaryotic cells, which is suitable  
 CC for use in an amplification and detection assay. The methods are used for  
 CC the analysis and detection of nucleic acids in biological samples. The  
 CC methods are useful in the human medical and veterinary fields, for  
 CC medical diagnoses and clinical monitoring of a patient's response to  
 CC therapy where a disease or medical condition is associated with a  
 CC particular type and/or level of mRNA present in the sample. The methods  
 CC are also useful for detecting or quantifying fusion or chimeric RNA  
 CC species, and for detecting a translocation as a marker for a given  
 CC condition or disease, e.g. translocations associate with cancers,  
 CC particularly forms of leukemia  
 XX Sequence 24 BP; 6 A; 6 C; 8 G; 0 T; 4 U; 0 Other;

Query Match 100.0%; Score 24; DB 3; Length 24;  
 Best Local Similarity 83.3%; Pred. No. 0.00026;  
 Matches 20; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGGAACATGAAGCCCTTCAGCGG 24  
 [:|||||:|||||:|||||:]

Db 1 GUGGAACAUGAAGCCCTTCAGCGG 24

RESULT 5  
 ID AAZ60864 standard; DNA; 299 BP.  
 AC AAZ60864;  
 DT 16-MAY-2000 (first entry)  
 DE Region surrounding a splice junction in a normal abl transcript.  
 KW Fusion transcript; translocation; bcr b3 region; abl gene;  
 KW amplification assay; detection assay; medical diagnosis;  
 KW clinical monitoring; chimeric RNA; fusion RNA; condition marker;  
 KW disease marker; cancer; leukemia; ss.  
 OS Unidentified.  
 PN WO200005418-A1.  
 PD 03-FEB-2000.  
 PF 23-JUL-1999; 99WO-US016832.  
 PR 23-JUL-1998; 98US-00121239.  
 PA (GENP-) GEN-PROBE INC.  
 PI Harvey RC, Eastman PS;  
 XX WPI; 2000-182730/16.  
 XX Novel methods for preparing RNA from biological samples, used for the  
 PT detection and measurement of nucleic acids and fusion nucleic acids.  
 PS Disclosure; Fig 3; 49pp; English.  
 CC The present sequence represents a region surrounding a potential splice  
 CC junction in a normal abl transcript. The specification describes  
 CC oligonucleotides which are used to detect fusion transcripts produced  
 CC from a translocation between the bcr b3 region and the abl gene. The  
 CC specification also describes a method for detecting a fusion nucleic acid  
 CC (particularly chimeric mRNA species), in a biological sample. The method  
 CC comprises contacting a sample of fusion nucleic acid with primers,  
 CC amplifying the hybridized fusion nucleic acid, and detecting the target  
 CC hybrid. The method is used for the simple and rapid preparation of RNA  
 CC from a biological sample, particularly from the cytoplasm of eukaryotic  
 CC cells, which is suitable for use in an amplification and detection assay.  
 CC The methods are used for the analysis and detection of nucleic acids in  
 CC biological samples. The methods are useful in the human medical and  
 CC veterinary fields, for medical diagnoses and clinical monitoring of a  
 CC patient's response to therapy where a disease or medical condition is  
 CC associated with a particular type and/or level of mRNA present in the  
 CC sample. The methods are also useful for detecting or quantifying fusion  
 CC or chimeric RNA species, and for detecting a translocation as a marker  
 CC for a given condition or disease, e.g. translocations associate with  
 CC cancers, particularly forms of leukemia  
 XX Sequence 299 BP; 77 A; 70 C; 81 G; 71 T; 0 U; 0 Other;

Query Match 100.0%; Score 24; DB 3; Length 299;  
 Best Local Similarity 100.0%; Pred. No. 0.00028;  
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGGAACATGAAGCCCTTCAGCGG 24  
 DB 142 GTGGAACATGAAGCCCTTCAGCGG 165

RESULT 6  
 ABZ18520

ID ABZ18520 standard; cDNA; 3380 BP.  
 AC ABZ18520;  
 XX  
 XX 23-JAN-2003 (first entry)  
 DT  
 XX Group III cDNA cancer related clone SEQ ID NO:946.  
 DE  
 XX Human; cancer; tumour; therapy; diagnosis; CT antigen; CP antigen;  
 KW humane response; virology; immunology; microbiology; molecular biology;  
 KW recombinant DNA technology; gene; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO200278516-A2.  
 PN  
 XX 10-OCT-2002.  
 PD  
 XX 28-MAR-2002; 2002WO-US010421.  
 PF  
 XX 30-MAR-2001; 2001US-0280255P.  
 PR  
 XX 28-AUG-2001; 2001US-0315563P.  
 PR  
 XX 09-JAN-2002; 2002US-0347313P.  
 XX  
 XX (CORI-) CORIXA CORP.  
 PA  
 XX Wang T, Wang S, Bangur CS, Gaiger A;  
 PI  
 XX WPI; 2003-058387/05.  
 DR  
 XX  
 XX New immunogenic polynucleotides or polypeptides useful for diagnosing,  
 PT preventing and treating cancer expressing CT or CP mRNA antigens, and in  
 PT virology, immunology, microbiology, molecular biology and recombinant DNA  
 PT techniques.  
 XX  
 PS Claim 1; SEQ ID NO 946; 207pp; English.  
 XX  
 CC ABQ17575 to ABQ20506 represent isolated polynucleotide (I) sequences, and  
 CC ABP54446 to ABP54472 represent protein (II) sequences, from the present  
 CC invention. (I) and (II) have cytostatic activity and can be used in gene  
 CC therapy and vaccines. (I), (II), antibodies and compositions from the  
 CC present invention are useful for diagnosing, preventing and treating  
 CC cancer, which expresses CT or CP mRNA antigens. They are useful for  
 CC stimulating immune response. They can also be useful in virology,  
 CC immunology, microbiology, molecular biology and recombinant DNA  
 CC techniques. N.B. The sequence data for this patent did not form part of  
 CC the printed specification, but was obtained in electronic format directly  
 CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 3380 BP; 819 A; 1005 C; 989 G; 567 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 24; DB 7; Length 3380;  
 Best Local Similarity 100.0%; Pred. No. 0.00029;  
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 GTGGACATGAGCCCTTCAGCGG 24  
 Db 57 GTGGACATGAGCCCTTCAGCGG 80  
 RESULT 7  
 ABS69903/c  
 ID ABS69903 standard; DNA; 34125 BP.  
 XX  
 AC ABS69903;  
 XX  
 XX 21-NOV-2002 (first entry)  
 DT  
 XX Human adenovirus type 12 genome sequence.  
 DE  
 XX Vector; adenovirus; adeno-associated; adenosine deaminase gene; receptor;  
 KW adenosine deaminase deficiency; severe combined immune deficiency; PAH;  
 KW beta-chain; haemoglobin gene; beta-thalassaemia; sickle cell disease;

KW low density lipoprotein gene; familial hypercholesterolaemia;  
 KW hypoxanthine-guanine phosphoribosyltransferase; Lesch-Nyhan syndrome;  
 KW phenylalanine hydroxylase gene; gene therapy; phenylketonuria;  
 KW dystrophin gene; muscular dystrophy; cystic fibrosis; immunostimulant;  
 KW human cystic fibrosis transmembrane conductance regulator gene;  
 KW antianemic; antilipemic; nootropic; cytostatic; dermatological;  
 KW human adenovirus genome; ds.  
 XX  
 OS Human adenovirus type 12.  
 XX  
 XX US2002102731-A1.  
 PN  
 XX 01-AUG-2002.  
 PD  
 XX 12-FEB-2001; 2001US-00782378.  
 PF  
 XX 02-OCT-2000; 2000US-0237747P.  
 PR  
 XX (UYNV) UNIV NEW YORK STATE RES FOUND.  
 PA  
 XX Hearing P, Bahou WF, Sandalon Z, Gnatenko DV;  
 PI  
 XX WPI; 2002-690619/74.  
 XX  
 PT Producing vector, by introducing vector having nucleotide sequence,  
 PT adenovirus inverted terminal repeats and packaging sequence, and adeno-  
 PT associated virus terminal repeat, into cell, and culturing cell.  
 XX  
 PS Disclosure; Page 135-150; 191pp; English.  
 XX  
 CC The present invention relates to a new method of producing a vector. The  
 CC method involves introducing recombinant vector having nucleotide sequence  
 CC (NS) having 5' and 3' end, left and right inverted terminal repeats of  
 CC adenovirus flanking NS, adenovirus packaging sequence linked to inverted  
 CC terminal repeat, and adeno-associated virus terminal repeat linked to 3'  
 CC end of NS, into cell expressing adenovirus early gene lacking from vector  
 CC ; and culturing cell to produce another vector. The method is useful for  
 CC generating vectors, especially mAd vectors. The method is useful in  
 CC transferring nucleotide sequences of interest into a cell, for gene  
 CC transfer applications (e.g. gene therapy) in vitro, ex vivo and in vivo.  
 CC The nucleotide sequences are useful for treating diseases associated with  
 CC it, i.e. adenosine deaminase gene associated with adenosine deaminase  
 CC deficiency with severe combined immune deficiency, beta-chain of  
 CC haemoglobin gene associated with beta-thalassaemia and sickle cell  
 CC disease, receptor for low density lipoprotein gene associated with  
 CC familial hypercholesterolaemia, hypoxanthine-guanine  
 CC phosphoribosyltransferase associated with Lesch-Nyhan syndrome,  
 CC phenylalanine hydroxylase (PAH) gene associated with phenylketonuria,  
 CC dystrophin gene associated with muscular dystrophy, and human cystic  
 CC fibrosis transmembrane conductance regulator gene associated with cystic  
 CC fibrosis. The present nucleic acid sequence represents a human adenovirus  
 CC genome sequence that was used in the methods of the invention  
 XX  
 SQ Sequence 34125 BP; 9330 A; 8012 C; 7864 G; 8919 T; 0 U; 0 Other;  
 Query Match 75.0%; Score 18; DB 6; Length 34125;  
 Best Local Similarity 100.0%; Pred. No. 0.95;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 3 GGAAACATGAAGCCCTTCA 20  
 Db 4015 GGAAACATGAAGCCCTTCA 3998  
 RESULT 8  
 ABN54940  
 ID ABN54940 standard; DNA; 65 BP.  
 XX  
 AC ABN54940;  
 XX  
 XX 15-JUL-2002 (first entry)  
 DT  
 XX Mouse spliced transcript detection oligonucleotide SEQ ID NO:27688.

```

XX Human; mouse; rat; splice transcript; detection; RNA transcript;
KW splice variant; transcriptome; oligonucleotide library; ss.
XX
XX Mus musculus.
XX
XX WO200210449-A2.
XX
XX 07-FEB-2002.
XX
XX 20-JUL-2001; 2001WO-IB001903.
XX
XX 28-JUL-2000; 2000US-0221607P.
XX
XX 02-MAY-2001; 2001US-0287724P.
XX
XX (COMP-) COMPUGEN INC.
XX
XX Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;
XX
XX WPI; 2002-257383/30.
XX
XX New oligonucleotide libraries comprising oligonucleotides which
PT selectively hybridize to mRNAs transcribed from a transcription unit of a
PT genome, useful for detecting tissue-, pathology-, and developmental-
PT specific genes.
XX
XX Example 1; SEQ ID NO 27688; 47pp; English.
XX
XX The present invention describes oligonucleotide libraries for detecting
CC messenger RNAs that populate a (sub-)transcriptome, where the (sub-)
CC transcriptome comprises messenger RNAs transcribed from multiple
CC transcription units that populate a genome. The library comprises several
CC oligonucleotides, each capable of hybridising selectively to a set of
CC messenger RNAs transcribed from a given transcription unit of the genome,
CC which encodes one or more messenger RNA splice variants. The
CC oligonucleotide libraries are useful for detecting mRNAs from a
CC biological sample, in expression profiling studies, in qualitatively or
CC quantitatively characterising the corresponding transcriptome, and in
CC detecting RNA transcripts and splice variants of human or animal
CC transcriptomes. The libraries may also be used as specialised mini
CC libraries to detect transcripts of a sub-transcriptome under a particular
CC biological or pathological state, and so allowing the detection of tissue
CC - and pathology-specific genes such as those genes only expressed in
CC specific tissue under a specific pathological condition; to detect
CC developmental specific genes; and to detect RNA transcripts and splice
CC variants of a transcriptome of a patient suffering from a particular
CC disorder. ABN27253 to ABN59589 represent oligonucleotide sequences from
CC rats, humans and mice, which are used in the exemplification of the
CC present invention. N.B. The sequence data for this patent did not form
CC part of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 65 BP; 18 A; 16 C; 19 G; 12 T; 0 U; 0 Other;
XX
XX Query Match 66.7%; Score 16; DB 6; Length 65;
XX Best Local Similarity 100.0%; Pred. No. 12;
XX Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 GTGGAAACATGAAGCCC 16
XX
XX DB 7 GTGGAAACATGAAGCCC 22
XX
XX RESULT 9
XX AA194531/c
XX ID AA194531 standard; cDNA; 751 BP.
XX
XX AC AA194531;
XX
XX 13-NOV-2001 (first entry)
XX
XX Human neuroblastoma expressed polynucleotide SEQ ID NO 606.
XX

```

```

KW Human; neuroblastoma; malignancy; cancer; tumour marker; N-myc; TrkA; ss.
XX
XX Homo sapiens.
XX
XX PN WO200166719-A1.
XX
XX PD 13-SEP-2001.
XX
XX 02-MAR-2001; 2001WO-JP001629.
XX
XX 07-MAR-2000; 2000JP-00159195.
XX
XX (CHIB-) CHIBA PREFECTURE.
XX
XX (HISM) HISAMITSU PHARM CO LTD.
XX
XX Nakagawara A;
XX
XX WPI; 2001-565584/63.
XX
XX Nucleic acids originating in gene expressed in human neuroblastoma,
PT useful as probe or primer in diagnosing prognosis of human neuroblastoma,
PT malignancy and susceptibility indicator or tumor marker for anti-cancer
PT agents.
XX
XX Claim 1; Page 485; 2979pp; Japanese.
XX
XX The invention relates to novel genes (AA193926-AA197963) expressed in
CC human neuroblastoma. The nucleic acids are applicable as a probe or
CC primer in diagnosing the prognosis of human neuroblastoma, malignancy and
CC susceptibility indicators or tumour markers for anti-cancer agents. The
CC gene information for diagnosing prognosis is related to factors similar
CC to that for N-myc and TrkA genes
XX
XX Sequence 751 BP; 176 A; 176 C; 215 G; 157 T; 0 U; 27 Other;
XX
XX Query Match 66.7%; Score 16; DB 4; Length 751;
XX Best Local Similarity 100.0%; Pred. No. 12;
XX Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 7 CATGAAGCCCTTCAGC 22
XX
XX DB 563 CATGAAGCCCTTCAGC 548
XX
XX RESULT 10
XX AAS54224
XX ID AAS54224 standard; DNA; 1044 BP.
XX
XX AC AAS54224;
XX
XX 13-FEB-2002 (first entry)
XX
XX Pseudomonas aeruginosa DNA for cellular proliferation protein #355.
XX
XX Antisense; ds; prokaryotic cellular proliferation gene; antibiotic;
KW antibacterial; drug design.
XX
XX OS Pseudomonas aeruginosa.
XX
XX PN WO200170955-A2.
XX
XX PD 27-SEP-2001.
XX
XX 21-MAR-2001; 2001WO-US009180.
XX
XX 21-MAR-2000; 2000US-0191078P.
XX
XX 23-MAY-2000; 2000US-0206848P.
XX
XX 26-MAY-2000; 2000US-0207727P.
XX
XX 23-OCT-2000; 2000US-0242578P.
XX
XX 27-NOV-2000; 2000US-0253625P.
XX
XX 22-DEC-2000; 2000US-0257931P.
XX
XX 16-FEB-2001; 2001US-0269308P.
XX

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PA (ELIT-) ELITRA PHARM INC.
XX
PI Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;
PI Yamamoto RT, Xu HH;
XX
XX WPI; 2001-611495/70.
DR P-PSDB; AAU36365.
XX
XX New polynucleotides for the identification and development of
PT antibiotics, comprise sequences of antisense nucleic acids.
PT
XX
XX Claim 27; SEQ ID NO 7861; 511bp; English.
PS
XX The invention relates to antisense inhibitors of genes essential to
XX prokaryotic cellular proliferation, their use in identifying the genes,
XX themselves and the encoded proteins. The prokaryotes used are Escherichia
XX coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae,
XX Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also
XX useful for the identification of potential new targets for antibiotic
XX development. The antisense nucleic acids can also be used to identify
XX proteins used in proliferation, to express these proteins, and to obtain
XX antibodies capable of binding to the expressed proteins. The proteins can
XX be used to screen compounds in rational drug discovery programmes. The
XX antisense nucleic acid sequence is also useful to screen for homologous
XX nucleic acids which are required for cell proliferation in a wide variety
XX of organisms. The present sequence encodes an essential prokaryotic
XX cellular proliferation protein. Note: The sequence data for this patent
XX did not form part of the printed specification, but was obtained in
XX electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 1044 BP; 159 A; 373 C; 334 G; 178 T; 0 U; 0 Other;
XX
Query Match 66.7%; Score 16; DB 4; Length 1044;
Best Local Similarity 100.0%; Pred. NO. 13;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 9 TGAAGCCCTTCAGCGG 24
Db |||||
797 TGAAGCCCTTCAGCGG 812

RESULT 11
ACA42504
ID ACA42504 standard; DNA; 1044 BP.
XX
XX ACA42504;
XX
XX 19-JUN-2003 (first entry)
XX
XX Prokaryotic essential gene #24161.
XX
XX Antisense; ds; prokaryotic essential gene; cell proliferation;
XX drug design; gene.
XX
XX Pseudomonas aeruginosa.
XX
XX WO200277183-A2.
XX
XX 03-OCT-2002.
XX
XX 21-MAR-2002; 2002WO-US009107.
XX
XX 21-MAR-2001; 2001US-00815242.
XX 06-SEP-2001; 2001US-00948993.
XX 25-OCT-2001; 2001US-0342923P.
XX 08-FEB-2002; 2002US-00072851.
XX 06-MAR-2002; 2002US-0362699P.
XX
XX (ELIT-) ELITRA PHARM INC.
XX
XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
PI

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PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
XX
XX WPI; 2003-029926/02.
DR P-PSDB; ABU38634.
XX
XX New antisense nucleic acids, useful for identifying proteins or screening
PT for homologous nucleic acids required for cellular proliferation to
PT isolate candidate molecules for rational drug discovery programs.
PT
XX
XX Claim 14; SEQ ID NO 30374; 1766bp; English.
XX
XX The invention relates to an isolated nucleic acid comprising any one of
XX the 6213 antisense sequences given in the specification where expression
XX of the nucleic acid inhibits proliferation of a cell. Also included are:
XX (1) a vector comprising a promoter operably linked to the nucleic acid
XX encoding a polypeptide whose expression is inhibited by the antisense
XX nucleic acid; (2) a host cell containing the vector; (3) an isolated
XX polypeptide or its fragment whose expression is inhibited by the
XX antisense nucleic acid; (4) an antibody capable of specifically binding
XX the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
XX proliferation or the activity of a gene in an operon required for
XX proliferation; (7) identifying a compound that influences the activity of
XX the gene product or that has an activity against a biological pathway
XX required for proliferation, or that inhibits cellular proliferation; (8)
XX identifying a gene required for cellular proliferation or the biological
XX pathway in which a proliferation-required gene or its gene product lies
XX or a gene on which the test compound that inhibits proliferation of an
XX organism acts; (9) manufacturing an antibiotic; (10) profiling a
XX compound's activity; (11) a culture comprising strains in which the gene
XX product is overexpressed or underexpressed; (12) determining the extent
XX to which each of the strains is present in a culture or collection of
XX strains; or (13) identifying the target of a compound that inhibits the
XX proliferation of an organism. The antisense nucleic acids are useful for
XX identifying proteins or screening for homologous nucleic acids required
XX for cellular proliferation to isolate candidate molecules for rational
XX drug discovery programs, or for screening homologous nucleic acids
XX required for proliferation in cells other than S. aureus, S. typhimurium,
XX K. pneumoniae or P. aeruginosa. The present sequence is one of the target
XX prokaryotic essential genes. Note: The sequence data for this patent did
XX not form part of the printed specification, but was obtained in
XX electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 1044 BP; 159 A; 373 C; 334 G; 178 T; 0 U; 0 Other;
XX
Query Match 66.7%; Score 16; DB 7; Length 1044;
Best Local Similarity 100.0%; Pred. NO. 13;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 9 TGAAGCCCTTCAGCGG 24
Db |||||
797 TGAAGCCCTTCAGCGG 812

RESULT 12
AAZ89962
ID AAZ89962 standard; cDNA; 2278 BP.
XX
XX AAZ89962;
XX
XX 05-MAY-2000 (first entry)
XX
XX Corn ADA2 transcription co-activator nucleotide sequence.
XX
XX ADA2; transcription co-activator; adaptor; plant breeding; corn; ss;
XX transgenic plant.
XX
XX Zea mays.
XX
XX WO200003026-A2.
XX
XX 20-JAN-2000.
XX

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PF 12-JUL-1999; 99WO-US015664.
XX
PR 13-JUL-1998; 98US-0092659P.
XX
PA (DUPO ) DU PONT DE NEMOURS & CO E I.
XX
PI Cahoon RE, Liu Z, Odell JT, Sakai H;
XX
XX WPI; 2000-160931/14.
DR P-PSDB; AAY78518.
XX
XX New isolated nucleic acid fragment encoding a transcription coactivator
PT in plants and seeds useful as a probe to isolate genes encoding
PT homologous proteins from other plant species, and as a primer.
XX
PS Claim 3; Page 29-30; 42pp; English.
XX
XX This sequence represents an ADA2 transcription adaptor/co-activator. In
CC yeast ADA2 functionally interacts with the acidic activation domain of
CC transcriptional activators. The invention relates to ADA2 nucleotide and
CC protein sequences, and also to a chimeric gene comprising of the ADA2
CC nucleotide sequence operably linked to a suitable regulatory sequence.
CC The ADA2 nucleotide sequence can be used as a DNA hybridization probe to
CC screen libraries from any desired plant and to isolate cDNAs and genes
CC encoding other ADA2 transcription adaptors, either as cDNAs or genomic
CC DNAs from the same or other plant species. The ADA2 nucleotide sequence
CC is also used as a primer to amplify longer nucleic acid fragments
CC encoding homologous genes from DNA or RNA. The ADA2 nucleotide and
CC peptide sequences are used in the immunological screening of cDNA
CC expression libraries. The nucleotide sequence is used to create
CC transgenic plants in which the protein is present at higher or lower
CC levels than normal or in cell types or developmental stages in which they
CC are not normally found. This would have the effect of altering the level
CC of transcription initiation in those cells. The ADA2 protein is used to
CC prepare antibodies which are useful for detecting them in situ in cells
CC or in vitro in cell extracts. All or a substantial portion of the ADA2
CC nucleotide sequence is used as probes for genetically and physically
CC mapping the genes that they are a part of, and as markers of traits
CC linked to those genes. Such information may be useful in plant breeding
CC in order to develop lines with desired phenotypes. In addition, they are
CC used to probe southern blots containing restriction endonuclease-treated
CC genomic DNAs of a set of individuals representing parent and progeny of a
CC defined genetic cross. Loss of function mutant phenotypes for the cDNA
CC clones identified by target gene disruption or by identifying specific
CC mutants for the genes contained in maize population carrying mutations in
CC all possible genes, are used for producing a plant containing a mutation
CC in the endogenous gene encoding ADA2. This mutant plant can then be used
CC to determine or confirm the natural function of ADA2
XX
SQ Sequence 2278 BP; 669 A; 451 C; 590 G; 561 T; 0 U; 7 Other;
Query Match 66.7%; Score 16; DB 3; Length 2278;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GGAACATGAGCCCTT 18
Db 1274 GGAACATGAGCCCTT 1289

RESULT 13
AAZ56382
ID AAZ56382 standard; DNA; 2599 BP.
XX
AC AAZ56382;
XX
XX 17-MAR-2000 (first entry)
XX
XX Escherichia coli flagellin protein nucleotide sequence SEQ ID NO:52.
XX
XX Flagellin; fliC; antigen; detection; ds.
XX
XX Escherichia coli.

PF 12-JUL-1999; 99WO-US015664.
XX
PR 13-JUL-1998; 98US-0092659P.
XX
PA (DUPO ) DU PONT DE NEMOURS & CO E I.
XX
PI Cahoon RE, Liu Z, Odell JT, Sakai H;
XX
XX WPI; 2000-160931/14.
DR P-PSDB; AAY78518.
XX
XX New isolated nucleic acid fragment encoding a transcription coactivator
PT in plants and seeds useful as a probe to isolate genes encoding
PT homologous proteins from other plant species, and as a primer.
XX
PS Claim 3; Page 29-30; 42pp; English.
XX
XX This sequence represents an ADA2 transcription adaptor/co-activator. In
CC yeast ADA2 functionally interacts with the acidic activation domain of
CC transcriptional activators. The invention relates to ADA2 nucleotide and
CC protein sequences, and also to a chimeric gene comprising of the ADA2
CC nucleotide sequence operably linked to a suitable regulatory sequence.
CC The ADA2 nucleotide sequence can be used as a DNA hybridization probe to
CC screen libraries from any desired plant and to isolate cDNAs and genes
CC encoding other ADA2 transcription adaptors, either as cDNAs or genomic
CC DNAs from the same or other plant species. The ADA2 nucleotide sequence
CC is also used as a primer to amplify longer nucleic acid fragments
CC encoding homologous genes from DNA or RNA. The ADA2 nucleotide and
CC peptide sequences are used in the immunological screening of cDNA
CC expression libraries. The nucleotide sequence is used to create
CC transgenic plants in which the protein is present at higher or lower
CC levels than normal or in cell types or developmental stages in which they
CC are not normally found. This would have the effect of altering the level
CC of transcription initiation in those cells. The ADA2 protein is used to
CC prepare antibodies which are useful for detecting them in situ in cells
CC or in vitro in cell extracts. All or a substantial portion of the ADA2
CC nucleotide sequence is used as probes for genetically and physically
CC mapping the genes that they are a part of, and as markers of traits
CC linked to those genes. Such information may be useful in plant breeding
CC in order to develop lines with desired phenotypes. In addition, they are
CC used to probe southern blots containing restriction endonuclease-treated
CC genomic DNAs of a set of individuals representing parent and progeny of a
CC defined genetic cross. Loss of function mutant phenotypes for the cDNA
CC clones identified by target gene disruption or by identifying specific
CC mutants for the genes contained in maize population carrying mutations in
CC all possible genes, are used for producing a plant containing a mutation
CC in the endogenous gene encoding ADA2. This mutant plant can then be used
CC to determine or confirm the natural function of ADA2
XX
SQ Sequence 2278 BP; 669 A; 451 C; 590 G; 561 T; 0 U; 7 Other;
Query Match 66.7%; Score 16; DB 3; Length 2278;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GGAACATGAGCCCTT 18
Db 1274 GGAACATGAGCCCTT 1289

RESULT 13
AAZ56382
ID AAZ56382 standard; DNA; 2599 BP.
XX
AC AAZ56382;
XX
XX 17-MAR-2000 (first entry)
XX
XX Escherichia coli flagellin protein nucleotide sequence SEQ ID NO:52.
XX
XX Flagellin; fliC; antigen; detection; ds.
XX
XX Escherichia coli.

XX PN WO9961458-A1.
XX PD 02-DEC-1999.
XX PF 21-MAY-1999; 99WO-AU000385.
XX PR 21-MAY-1998; 98AU-00003634.
XX PA (UNSY ) UNIV SYDNEY.
XX PI Reeves PR, Wang L;
XX XX WPI; 2000-072598/06.
XX XX Novel nucleic acid molecule useful for the detection of flagellated
XX bacterial strains in food, feces, etc.
XX PS Claim 3; Page 226-227; 245pp; English.
XX CC AAZ56331 to AAZ56398 represent nucleic acid molecules (I) encoding all or
CC part of an Escherichia coli flagellin protein except a protein expressed
CC by E. coli H1, H7, H12 or H48 type strains. The present invention also
CC describes a method of detecting the presence of E. coli of a particular H
CC serotype in a sample, comprising specifically hybridising a nucleic acid,
CC preferably at least a pair, derived from a flagellating gene, specific
CC for a particular flagellin gene associated with the H serotype, to any
CC E. coli in the sample which contain the gene, and detecting any hybridised
CC molecules, identifying the presence of that serotype in the sample. (I)
CC are useful for: (1) detecting the presence of E. coli of H serotype in a
CC sample by hybridising at least one or a pair of (I) to any E. coli in the
CC sample and detecting the hybridised nucleic acid molecules; and (2) for
CC detecting the presence of both O and H-serotypes of E. coli by
CC hybridising at least one or a pair of (I) to any E. coli present in the
CC sample and detecting the hybridised nucleic acid molecules. (I) is
CC particularly useful for detecting the combination of O and H antigen.
CC Hybridised (I) when using at least one (I) is detected by southern blot
CC analysis and, when using a pair of (I), is detected by polymerase chain
CC reaction (PCR). AAZ56399 to AAZ56420 represent primers used in the
CC exemplification of the present invention
XX
SQ Sequence 2599 BP; 708 A; 651 C; 615 G; 625 T; 0 U; 0 Other;
Query Match 66.7%; Score 16; DB 3; Length 2599;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 AACATGAAGCCCTTCA 20
Db 1057 AACATGAAGCCCTTCA 1072

RESULT 14
AAV36957/C
ID AAV36957 standard; cDNA; 3460 BP.
XX
AC AAV36957;
XX
XX 26-OCT-1998 (first entry)
XX
XX Nucleotide sequence of human C1qR gene.
XX
XX Human; C1q receptor protein; C1qR; phagocytosis; complement;
XX immune system; inflammation; prophylactic; genetic immune deficiency;
XX HIV; cancer; chemotherapy; inhibition; vasculitis; sepsis; Fragment;
XX primer; probe; antibody; ss.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX FT CDS 149..2107
XX FT /*tag= a
XX FT /product= "C1qR gene product"

```

```
XX WO9822584-A1.
XX
XX PD
XX
XX PD
XX
XX PF 12-NOV-1997; 97WO-US021205.
XX
XX PR 18-NOV-1996; 96US-00751305.
XX
XX PA (REGC ) UNIV CALIFORNIA.
XX
XX PI Tenner AJ, Nepomuceno RR;
XX
XX WPI; 1998-312470/27.
XX
XX DR P-PSDB; AAW49879.
XX
XX PT New complement Clq receptor - and methods for identifying modulators,
XX useful for controlling phagocytosis, e.g. to prevent infection or to
XX treat sepsis.
XX
XX PS Claim 3; Fig 3A-3C; 99pp; English.
XX
XX CC This is the nucleotide sequence of the novel human Clq receptor (ClqR)
XX gene, used in the method of the invention to identify modulators useful
XX for the control of phagocytosis. Delivering the ClqR nucleic acid to a
XX cell (in vivo, in vitro or ex vivo) alters the level of ClqR mRNA. ClqR
XX stimulates the complement component of the immune system, particularly
XX phagocytosis, without simultaneous increase in inflammation. ClqR
XX regulation is used for prophylactic treatment of subjects at risk of
XX infection (e.g. those with genetic immune deficiency, human immune
XX deficiency virus infection, undergoing cancer chemotherapy or high risk
XX surgery), also for treating cancer. Antisense or similar sequences are
XX used to inhibit phagocytosis or the complement component of immunity,
XX e.g. in cases of vasculitis or sepsis. Fragments of ClqR are useful as
XX primers and probes for detecting ClqR and related nucleic acids. ClqR
XX polypeptides and antibodies are all useful for treating disorders
XX involving the complement component or immune deficiencies
XX
XX SQ Sequence 3460 BP; 764 A; 943 C; 996 G; 757 T; 0 U; 0 Other;

Query Match 66.7%; Score 16; DB 2; Length 3460;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 TGAAGCCCTTCAGCGG 24
DB 491 TGAAGCCCTTCAGCGG 476

RESULT 15
AAZ34989/c
ID AAZ34989 standard; cDNA; 3460 BP.
XX
XX AC AAZ34989;
XX
XX DT 28-FEB-2000 (first entry)
XX
XX DE Human cell surface receptor ClqR cDNA.
XX
XX KW ClqR; receptor; cell surface; transmembrane; glycoprotein; human;
XX host defence; infection; HIV; therapy; immunodeficiency; immunostimulant;
XX phagocytosis; signal transduction; ss.
XX
XX OS Homo sapiens.
XX
XX FH Key Location/Qualifiers
XX CDS 149..2107
XX FT /*tag= a
XX FT sig_peptide 149..211
XX FT /*tag= b
XX FT mat_peptide 212..2104
XX FT /*tag= b
XX
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PN WO9955839-A1.
XX
XX PD 04-NOV-1999.
XX
XX PF 29-APR-1999; 99WO-US009335.
XX
XX PR 30-APR-1998; 98US-00071386.
XX
XX PA (REGC ) UNIV CALIFORNIA.
XX
XX PI Tenner AJ, Nepomuceno RR;
XX
XX WPI; 2000-062021/05.
XX
XX DR P-PSDB; AAY32345.
XX
XX PT A new cell surface receptor protein used as a prophylactic for
XX individuals at risk from infection, e.g. HIV.
XX
XX PS Claim 5; Fig 3; 49pp; English.
XX
XX CC This is the nucleotide sequence of isolated cDNA coding for a novel human
XX cell surface transmembrane glycoprotein receptor designated ClqR (see
XX AAY32345). The cDNA was obtained from a 937 library by PCR using primers
XX based on tryptic peptides of ClqR. The receptor plays a role in
XX stimulating the classic complement component of the immune system,
XX specifically in stimulating phagocytosis in cells without a concomitant
XX increase in inflammation. A method of hybridisation based on the ClqR
XX nucleic acid sequence is provided, as well as methods for detecting novel
XX ligands for ClqR, including those which function as agonists or
XX antagonists. ClqR nucleic acid or recombinant protein can be used to
XX effect the role of the classical complement component of the immune
XX system. Transgenic animals may be created to aid in the study of the role
XX of ClqR during growth and metabolism and as a model for disease states
XX in which the normal level of ClqR is effected. The ability to regulate
XX the phagocytic capacity of myeloid cells via the regulation of cell
XX surface expression and function of ClqR will be valuable as a
XX prophylactic treatment of individuals at risk from infection,
XX particularly those with genetic immunodeficiencies, HIV infection, or
XX undergoing cancer chemotherapy or high risk surgery
XX
XX SQ Sequence 3460 BP; 764 A; 943 C; 996 G; 757 T; 0 U; 0 Other;

Query Match 66.7%; Score 16; DB 3; Length 3460;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 TGAAGCCCTTCAGCGG 24
DB 491 TGAAGCCCTTCAGCGG 476

Search completed: May 26, 2004, 16:52:24
Job time : 109.037 secs
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OM nucleic - nucleic search, using sw model

Run on: May 26, 2004, 16:02:51 ; Search time 20.2274 Seconds  
(without alignments)  
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Gapop 60.0 , Gapext 60.0

Searched: 682709 seqs, 277475446 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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4: /cgn2\_6/ptodata/2/ina/6B\_COMB.seq.\*  
5: /cgn2\_6/ptodata/2/ina/PCTUS\_COMB.seq.\*  
6: /cgn2\_6/ptodata/2/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	16	66.7	306	4	US-09-252-991A-6328
2	16	66.7	897	4	US-09-252-991A-6056
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4	16	66.7	3460	2	US-08-751-305-1
5	15	62.5	23	1	US-08-363-233B-21
6	15	62.5	23	1	US-08-363-233B-22
7	15	62.5	33	3	US-08-793-408-9
8	15	62.5	33	3	US-08-793-408-11
9	15	62.5	33	3	US-09-139-762A-9
10	15	62.5	33	3	US-09-139-762A-11
11	15	62.5	47	3	US-08-448-446B-12
12	15	62.5	62	3	US-08-448-446B-1
13	15	62.5	80	1	US-08-152-621-7
14	15	62.5	80	1	US-08-306-691B-38
15	15	62.5	80	5	PCT-US92-05035-7
16	15	62.5	204	5	PCT-US93-06251-5
17	15	62.5	257	1	US-08-152-621-1
18	15	62.5	257	1	US-08-306-691B-36
19	15	62.5	257	5	PCT-US92-05035-1
20	15	62.5	1818	4	US-09-252-991A-3290
21	15	62.5	2115	4	US-09-252-991A-3388
22	15	62.5	3623	1	US-08-306-691B-35
23	15	62.5	30001	1	US-08-125-468-1
24	15	62.5	30001	2	US-08-474-933-1
25	14	58.3	23	1	US-08-152-621-34
26	14	58.3	23	1	US-08-363-233B-24
27	14	58.3	23	1	US-08-363-233B-25

28	14	58.3	23	5	PCT-US92-05035-34
29	14	58.3	25	4	US-09-168-947-31
30	14	58.3	26	1	US-08-152-621-29
31	14	58.3	26	1	US-08-152-621-33
32	14	58.3	26	1	US-08-306-691B-1
33	14	58.3	26	1	US-08-306-691B-2
34	14	58.3	26	3	US-09-341-955-1
35	14	58.3	26	4	US-09-779-881-1
36	14	58.3	26	5	PCT-US92-05035-29
37	14	58.3	26	5	PCT-US92-05035-33
38	14	58.3	26	5	PCT-US93-07541-12
39	14	58.3	26	5	PCT-US93-07541-25
40	14	58.3	42	2	US-08-768-177-3
41	14	58.3	42	3	US-08-991-675A-3
42	14	58.3	56	1	US-07-940-652-14
43	14	58.3	56	1	US-07-940-652-19
44	14	58.3	56	1	US-08-255-553-14
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ALIGNMENTS

RESULT 1

US-09-252-991A-6328  
; Sequence 6328, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 6328  
; LENGTH: 306  
; TYPE: DNA  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-6328

Query Match 66.7%; Score 16; DB 4; Length 306;  
Best Local Similarity 100.0%; Pred. No. 2.4;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	9	TGAAGCCCTTCAGCGG 24
DB	59	TGAAGCCCTTCAGCGG 74

RESULT 2

US-09-252-991A-6056/c  
; Sequence 6056, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 6056  
; LENGTH: 897  
; TYPE: DNA

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; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-6056

Query Match          66.7%; Score 16; DB 4; Length 897;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 TGAAGCCCTTCACGG 24
   |||||
Db 34 TGAAGCCCTTCACGG 19

RESULT 3
US-09-252-991A-6218/c
; Sequence 6218, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 6218
; LENGTH: 1536
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-6218

Query Match          66.7%; Score 16; DB 4; Length 1536;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 TGAAGCCCTTCACGG 24
   |||||
Db 1334 TGAAGCCCTTCACGG 1319

RESULT 4
US-08-751-305-1/c
; Sequence 1, Application US/08751305
; Patent No. 5965439
; GENERAL INFORMATION:
; APPLICANT: Tenner et al., Andrea J.
; TITLE OF INVENTION: HOST DEFENSE ENHANCEMENT
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/751,305
; FILING DATE: 18-NOV-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Wetherell, Jr., John R.
; REGISTRATION NUMBER: 31,678
; REFERENCE/DOCKET NUMBER: 07306/012001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
```

```
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3460 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 149..2105
US-08-751-305-1

Query Match          66.7%; Score 16; DB 2; Length 3460;
Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 TGAAGCCCTTCACGG 24
   |||||
Db 491 TGAAGCCCTTCACGG 476

RESULT 5
US-08-363-233B-21
; Sequence 21, Application US/08363233B
; Patent No. 5714383
; GENERAL INFORMATION:
; APPLICANT: Thompson, James D.
; TITLE OF INVENTION: METHOD AND REAGENT FOR TREATING CHRONIC
; TITLE OF INVENTION: MYELOGENOUS LEUKEMIA
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/363,233B
; FILING DATE: December 23, 1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION DATA: including application
; PRIOR APPLICATION DATA: described below: 2
; APPLICATION NUMBER: 07/882,822
; FILING DATE: May 14, 1992
; APPLICATION NUMBER: 08/193,922
; FILING DATE: February 7, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 209/165
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 23 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-363-233B-21

Query Match          62.5%; Score 15; DB 1; Length 23;
Best Local Similarity 86.7%; Pred. No. 9.1;
```

```

Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 10 GAAGCCCTTCAGCGG 24
    |||||:|||||
Db 4 GAAGCCCUACAGCGG 18

RESULT 6
US-08-363-233B-22
; Sequence 22, Application US/08363233B
; Patent No. 5714383
; GENERAL INFORMATION:
; APPLICANT: Thompson, James D.
; TITLE OF INVENTION: METHOD AND REAGENT FOR TREATING CHRONIC
; MYELOGENOUS LEUKEMIA
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Suite 4700
; STATE: Los Angeles
; COUNTRY: California
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; OPERATING SYSTEM: IBM Compatible
; SOFTWARE: FastSeq for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/363,233B
; FILING DATE: December 23, 1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION DATA: including application
; PRIOR APPLICATION DATA: described below:
; APPLICATION NUMBER: 07/882,822
; FILING DATE: May 14, 1992
; APPLICATION NUMBER: 08/193,922
; FILING DATE: February 7, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 209/165
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 23 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-363-233B-22

Query Match 62.5%; Score 15; DB 1; Length 23;
Best Local Similarity 86.7%; Pred. No. 9.1;
Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 10 GAAGCCCTTCAGCGG 24
    |||||:|||||
Db 3 GAAGCCCUACAGCGG 17

RESULT 7
US-08-793-408-9
; Sequence 9, Application US/08793408
; Patent No. 6007988
; GENERAL INFORMATION:
; APPLICANT: Choo, Yen
; APPLICANT: Klug, Aaron
; TITLE OF INVENTION: Improvements in or Relating to
; Binding Proteins for Recognition of DNA
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pillsbury Madison & Sutro, L.L.P.
; STREET: 1100 New York Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3918
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/793,408
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION DATA: PCT/GB95/01949
; FILING DATE: 17-AUG-1995
; APPLICATION NUMBER: GB 9514698.1
; FILING DATE: 18-JUL-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9422534.9
; FILING DATE: 08-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9416880.4
; FILING DATE: 20-AUG-1994
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 33 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-793-408-9

Query Match 62.5%; Score 15; DB 3; Length 33;
Best Local Similarity 100.0%; Pred. No. 9.1;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 GAAGCCCTTCAGCGG 24
    |||||:|||||
Db 16 GAAGCCCTTCAGCGG 30

RESULT 8
US-08-793-408-11
; Sequence 11, Application US/08793408
; Patent No. 6007988
; GENERAL INFORMATION:
; APPLICANT: Choo, Yen
; APPLICANT: Klug, Aaron
; TITLE OF INVENTION: Improvements in or Relating to
; Binding Proteins for Recognition of DNA
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pillsbury Madison & Sutro, L.L.P.
; STREET: 1100 New York Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3918
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/793,408
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION DATA: PCT/GB95/01949
; FILING DATE: 17-AUG-1995
; APPLICATION NUMBER: GB 9514698.1
; FILING DATE: 18-JUL-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9422534.9
; FILING DATE: 08-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9416880.4
; FILING DATE: 20-AUG-1994
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 33 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-793-408-9

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/ APPLICATION NUMBER: US/08/793,408
/ FILING DATE:
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA: PCT/GB95/01949
/ FILING DATE: 17-AUG-1995
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: GB 9514698.1
/ FILING DATE: 18-JUL-1995
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: GB 9422534.9
/ FILING DATE: 08-NOV-1994
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: GB 9416880.4
/ FILING DATE: 20-AUG-1994
/ INFORMATION FOR SEQ ID NO: 11:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 33 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ US-08-793-408-11

Query Match      62.5%; Score 15; DB 3; Length 33;
Best Local Similarity 100.0%; Pred. No. 9.1;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      10 GAAGCCCTTCAGCGG 24
Db      16 GAAGCCCTTCAGCGG 30

RESULT 9
US-09-139-762A-9
/ Sequence 9, Application US/09139762A
/ Patent No. 6013453
/ GENERAL INFORMATION:
/ APPLICANT: Choo, Yen
/ APPLICANT: Klug, Aaron
/ APPLICANT: Sanchez Garcia, Isidro
/ TITLE OF INVENTION: Improvements in or Relating to
/ TITLE OF INVENTION: Binding Proteins for Recognition of DNA
/ NUMBER OF SEQUENCES: 125
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Pillsbury Madison & Sutro, L.L.P.
/ STREET: 1100 New York Avenue, N.W.
/ CITY: Washington
/ STATE: D.C.
/ COUNTRY: USA
/ ZIP: 20005-3918
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Word Perfect
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/139,762A
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/793,408
/ FILING DATE: 02-JUN-1997
/ APPLICATION NUMBER: PCT/GB95/01949
/ FILING DATE: 17-AUG-1995
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: GB 9514698.1
/ FILING DATE: 18-JUL-1995
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: GB 9422534.9
/ FILING DATE: 08-NOV-1994
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: GB 9416880.4
/ FILING DATE: 20-AUG-1994
/ INFORMATION FOR SEQ ID NO: 11:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 33 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ US-09-139-762A-9

Query Match      62.5%; Score 15; DB 3; Length 33;
Best Local Similarity 100.0%; Pred. No. 9.1;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      10 GAAGCCCTTCAGCGG 24
Db      16 GAAGCCCTTCAGCGG 30
```

```
/ INFORMATION FOR SEQ ID NO: 9:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 33 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ US-09-139-762A-9

Query Match      62.5%; Score 15; DB 3; Length 33;
Best Local Similarity 100.0%; Pred. No. 9.1;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      10 GAAGCCCTTCAGCGG 24
Db      16 GAAGCCCTTCAGCGG 30

RESULT 10
US-09-139-762A-11
/ Sequence 11, Application US/09139762A
/ Patent No. 6013453
/ GENERAL INFORMATION:
/ APPLICANT: Choo, Yen
/ APPLICANT: Klug, Aaron
/ APPLICANT: Sanchez Garcia, Isidro
/ TITLE OF INVENTION: Improvements in or Relating to
/ TITLE OF INVENTION: Binding Proteins for Recognition of DNA
/ NUMBER OF SEQUENCES: 125
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Pillsbury Madison & Sutro, L.L.P.
/ STREET: 1100 New York Avenue, N.W.
/ CITY: Washington
/ STATE: D.C.
/ COUNTRY: USA
/ ZIP: 20005-3918
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Word Perfect
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/139,762A
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/793,408
/ FILING DATE: 02-JUN-1997
/ APPLICATION NUMBER: PCT/GB95/01949
/ FILING DATE: 17-AUG-1995
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: GB 9514698.1
/ FILING DATE: 18-JUL-1995
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: GB 9422534.9
/ FILING DATE: 08-NOV-1994
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: GB 9416880.4
/ FILING DATE: 20-AUG-1994
/ INFORMATION FOR SEQ ID NO: 11:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 33 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ US-09-139-762A-11

Query Match      62.5%; Score 15; DB 3; Length 33;
Best Local Similarity 100.0%; Pred. No. 9.1;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      10 GAAGCCCTTCAGCGG 24
Db      16 GAAGCCCTTCAGCGG 30
```

```

RESULT 11
US-08-448-446B-12
; Sequence 12, Application US/08448446B
; Patent No. 6080851
; GENERAL INFORMATION:
; APPLICANT: Pachuk et al.
; TITLE OF INVENTION: Compounds and Methods for the Treatment
; TITLE OF INVENTION: of Leukemias
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn
; ADDRESSEE: Kurtz Mackiewicz & No. 6080851Iris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/448,446B
; FILING DATE: July 10, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/989,852
; FILING DATE: December 4, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Doreen Yanko Trujillo
; REGISTRATION NUMBER: 35,719
; REFERENCE/DOCKET NUMBER: APOL-0020
; TELECOMMUNICATION INFORMATION: C
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 47
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; ANTI-SENSE:
; US-08-448-446B-12

Query Match 62.5%; Score 15; DB 3; Length 47;
Best Local Similarity 86.7%; Pred. No. 9.1;
Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 10 GAAGCCCTTCAGCGG 24
Db 16 GAAGCCCUUCAGCGG 30

RESULT 12
US-08-448-446B-1
; Sequence 1, Application US/08448446B
; Patent No. 6080851
; GENERAL INFORMATION:
; APPLICANT: Pachuk et al.
; TITLE OF INVENTION: Compounds and Methods for the Treatment
; TITLE OF INVENTION: of Leukemias
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn
; ADDRESSEE: Kurtz Mackiewicz & No. 6080851Iris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103

```

```

; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/448,446B
; FILING DATE: July 10, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/989,852
; FILING DATE: December 4, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Doreen Yanko Trujillo
; REGISTRATION NUMBER: 35,719
; REFERENCE/DOCKET NUMBER: APOL-0020
; TELECOMMUNICATION INFORMATION: C
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 62
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; ANTI-SENSE: No
; US-08-448-446B-1

Query Match 62.5%; Score 15; DB 3; Length 62;
Best Local Similarity 86.7%; Pred. No. 9;
Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 10 GAAGCCCTTCAGCGG 24
Db 31 GAAGCCCUUCAGCGG 45

RESULT 13
US-08-152-621-7
; Sequence 7, Application US/08152621
; Patent No. 5652222
; GENERAL INFORMATION:
; APPLICANT: Calabretta, Bruno
; APPLICANT: Gewirtz, Alan M.
; TITLE OF INVENTION: Selective Inhibition of
; TITLE OF INVENTION: Leukemic Cell Proliferation by bcr-abl
; TITLE OF INVENTION: Antisense Oligonucleotides
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEIDEL, GONDA, LAVORGNA
; ADDRESSEE: & MONACO, P.C.
; STREET: 1800 Two Penn Center
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: U.S.A.
; ZIP: 19102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 720 KB
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/152,621
; FILING DATE: No. 5652222ember 15, 1993
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/718,302
; FILING DATE: June 18, 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Monaco, Daniel A.
; REGISTRATION NUMBER: 30,480
; REFERENCE/DOCKET NUMBER: 6056-120 (CT.) 1
; TELECOMMUNICATION INFORMATION:

```

TELEPHONE: (215) 568-8383  
TELEFAX: (215) 568-5549  
TELEX: No. 5652222e  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 80 Nucleotides  
TYPE: nucleic acid  
STRANDEDNESS: single stranded  
TOPOLOGY: linear  
US-08-152-621-7

Query Match 62.5%; Score 15; DB 1; Length 80;  
Best Local Similarity 100.0%; Pred. No. 9;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GAAGCCCTTCAGCGG 24  
Db 31 GAAGCCCTTCAGCGG 45

## RESULT 14

US-08-306-691B-38  
Sequence 38, Application US/08306691B  
Patent No. 5734039  
GENERAL INFORMATION:  
APPLICANT: Calabretta, Bruno  
APPLICANT: Skorski, Tomasz  
TITLE OF INVENTION: ANTISENSE  
TITLE OF INVENTION: OLIGONUCLEOTIDES TARGETING COOPERATING ONCOGENES  
NUMBER OF SEQUENCES: 55  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Seigel, Gonda, Lavorgna & Monaco, P.C.  
STREET: Two Penn Center, Suite 1800  
CITY: Philadelphia  
STATE: Pennsylvania  
COUNTRY: U.S.A.  
ZIP: 19102

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb  
COMPUTER: IBM PS/2  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: WordPerfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/306,691B  
FILING DATE: September 15, 1994  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Monaco, Daniel A.

REGISTRATION NUMBER: 30,480  
REFERENCE/DOCKET NUMBER: 8321-8  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (215) 568-8383  
TELEFAX: (215) 568-5549  
TELEX: No. 5734039e  
INFORMATION FOR SEQ ID NO: 38:

SEQUENCE CHARACTERISTICS:  
LENGTH: 80 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-306-691B-38

Query Match 62.5%; Score 15; DB 1; Length 80;  
Best Local Similarity 100.0%; Pred. No. 9;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GAAGCCCTTCAGCGG 24  
Db 31 GAAGCCCTTCAGCGG 45

## RESULT 15

PCT-US92-05035-7  
Sequence 7, Application PC/TUS9205035  
GENERAL INFORMATION:  
APPLICANT: Calabretta, Bruno  
APPLICANT: Gewirtz, Alan M.  
TITLE OF INVENTION: Selective Inhibition of  
TITLE OF INVENTION: Leukemic Cell Proliferation by bcr-abl  
TITLE OF INVENTION: Antisense Oligonucleotides  
NUMBER OF SEQUENCES: 34  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Temple University - Of The Common-  
ADDRESSEE: wealth System of Higher Education  
STREET: 406 University Services Building  
CITY: Philadelphia  
STATE: Pennsylvania  
COUNTRY: U.S.A.  
ZIP: 19122

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb  
COMPUTER: IBM PS/2  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: WordPerfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US92/05035  
FILING DATE: 19920615  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/718,302  
FILING DATE: June 18, 1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/869,911  
FILING DATE: April 14, 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Monaco, Daniel A.  
REGISTRATION NUMBER: 30,480  
REFERENCE/DOCKET NUMBER: 6056-120 (CIP) 1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (215) 568-8383  
TELEFAX: (215) 568-5549  
TELEX: None  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 80 Nucleotides  
TYPE: NUCLEIC ACID  
STRANDEDNESS: single stranded  
TOPOLOGY: linear  
PCT-US92-05035-7

Query Match 62.5%; Score 15; DB 5; Length 80;  
Best Local Similarity 100.0%; Pred. No. 9;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GAAGCCCTTCAGCGG 24  
Db 31 GAAGCCCTTCAGCGG 45

Search completed: May 27, 2004, 02:25:15  
Job time : 21.2274 secs



GenCore version 5.1.1.6  
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OM nucleic - nucleic search, using sw model

Run on: May 27, 2004, 11:30:47 ; Search time 126.301 Seconds  
(without alignments)  
864.392 Million cell updates/sec

Title: US-09-121-239-16

Perfect score: 24

Sequence: 1 GTGGACATGAGCCCTTCAGCGG 24

Scoring table: OLIGO NUC

Gapop 60.0 , Gapext 60.0

Searched: 2960401 seqs, 2274450654 residues

Word size : 0

Total number of hits satisfying chosen parameters: 5920802

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published Applications NA.\*

- 1: /cgn2\_6/ptodata/2/pubpna/US07\_PUBCOMB.seq.\*
- 2: /cgn2\_6/ptodata/2/pubpna/PCT\_NEW\_PUB.seq.\*
- 3: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq.\*
- 4: /cgn2\_6/ptodata/2/pubpna/US06\_PUBCOMB.seq.\*
- 5: /cgn2\_6/ptodata/2/pubpna/US07\_NEW\_PUB.seq.\*
- 6: /cgn2\_6/ptodata/2/pubpna/PCTUS\_PUBCOMB.seq.\*
- 7: /cgn2\_6/ptodata/2/pubpna/US08\_NEW\_PUB.seq.\*
- 8: /cgn2\_6/ptodata/2/pubpna/US08\_PUBCOMB.seq.\*
- 9: /cgn2\_6/ptodata/2/pubpna/US09A\_PUBCOMB.seq.\*
- 10: /cgn2\_6/ptodata/2/pubpna/US09B\_PUBCOMB.seq.\*
- 11: /cgn2\_6/ptodata/2/pubpna/US09C\_PUBCOMB.seq.\*
- 12: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq.\*
- 13: /cgn2\_6/ptodata/2/pubpna/US10A\_PUBCOMB.seq.\*
- 14: /cgn2\_6/ptodata/2/pubpna/US10B\_PUBCOMB.seq.\*
- 15: /cgn2\_6/ptodata/2/pubpna/US10C\_PUBCOMB.seq.\*
- 16: /cgn2\_6/ptodata/2/pubpna/US10C\_PUBCOMB.seq.\*
- 17: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq.\*
- 18: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq.\*
- 19: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	24	100.0	3450	16	US-10-457-954-5
2	18	75.0	34125	9	US-09-782-378A-25
3	16	66.7	65	10	US-09-908-975-27688
4	16	66.7	310	15	US-10-029-386-26614
5	16	66.7	555	15	US-10-029-386-12914
6	16	66.7	1044	9	US-09-815-242-7861
7	16	66.7	1044	13	US-10-282-122A-30374
8	16	66.7	1424	13	US-10-425-114-523
9	16	66.7	1951	15	US-10-029-386-22997
10	16	66.7	6699	15	US-10-211-462-130
11	16	66.7	6699	15	US-10-021-660-15
12	16	66.7	85076	16	US-10-085-117-97
13	16	66.7	126413	13	US-10-087-132-1831
14	15	62.5	24	13	US-10-382-634-21

15	15	62.5	24	15	US-10-349-320-20	Sequence 20, Appl
16	15	62.5	205	9	US-09-867-701-10433	Sequence 10433, A
17	15	62.5	436	9	US-09-960-352-5213	Sequence 5213, Ap
18	15	62.5	489	13	US-10-424-599-43483	Sequence 43483, A
19	15	62.5	491	13	US-10-424-599-7082	Sequence 7082, Ap
20	15	62.5	499	13	US-10-027-632-85551	Sequence 85551, A
21	15	62.5	499	16	US-10-027-632-85551	Sequence 85551, A
22	15	62.5	729	13	US-10-107-431-100	Sequence 100, App
23	15	62.5	773	13	US-10-027-632-133705	Sequence 133705, A
24	15	62.5	773	16	US-10-027-632-133705	Sequence 133705, A
25	15	62.5	1133	13	US-10-425-114-4855	Sequence 4855, Ap
26	15	62.5	1163	13	US-10-027-632-118039	Sequence 118039, A
27	15	62.5	1163	13	US-10-027-632-118040	Sequence 118040, A
28	15	62.5	1163	16	US-10-027-632-118039	Sequence 118039, A
29	15	62.5	1590	16	US-10-027-632-118040	Sequence 118040, A
30	15	62.5	1749	13	US-10-369-493-27261	Sequence 27261, A
31	15	62.5	1765	13	US-10-282-122A-25460	Sequence 25460, A
32	15	62.5	1806	9	US-10-424-599-103532	Sequence 103532, A
33	15	62.5	1806	9	US-09-815-242-4015	Sequence 4015, Ap
34	15	62.5	2482	13	US-10-282-122A-7373	Sequence 7373, Ap
35	15	62.5	3393	15	US-10-363-616-49	Sequence 49, Appl
36	15	62.5	3606	16	US-10-263-480-1	Sequence 1, Appl
37	15	62.5	3840	15	US-10-214-529-6	Sequence 6, Appl
38	15	62.5	3840	15	US-10-204-041-3	Sequence 3, Appl
39	15	62.5	5527	9	US-09-880-107-3710	Sequence 3710, Ap
40	15	62.5	5744	16	US-10-439-703-5	Sequence 5, Appl
41	15	62.5	38734	10	US-09-373-658-30	Sequence 30, Appl
42	15	62.5	38734	11	US-09-989-687-30	Sequence 30, Appl
43	15	62.5	45055	13	US-10-107-431-277	Sequence 277, App
44	15	62.5	84539	9	US-09-962-436-36	Sequence 36, Appl
45	15	62.5	212231	13	US-10-087-132-1126	Sequence 1126, Ap

## ALIGNMENTS

### RESULT 1

US-10-457-954-5  
; Sequence 5, Application US/10457954  
; Publication No. US20040005623A1  
; GENERAL INFORMATION:  
; APPLICANT: Longley, B. Jack  
; TITLE OF INVENTION: Method of determining tumor sensitivities to therapeutic drugs  
; FILE REFERENCE: 960296.98890  
; CURRENT APPLICATION NUMBER: US/10/457,954  
; CURRENT FILING DATE: 2003-06-10  
; PRIOR APPLICATION NUMBER: 60/387,370  
; PRIOR FILING DATE: 2002-06-10  
; PRIOR APPLICATION NUMBER: 60/387,406  
; PRIOR FILING DATE: 2002-06-10  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 5  
; LENGTH: 3450  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(3447)  
; FEATURE:  
; NAME/KEY: misc\_structure  
; LOCATION: (730)..(765)  
; OTHER INFORMATION: encode amino acids 244-255 for forming the sides of the enzymatic pocket  
; OTHER INFORMATION: pocket  
; FEATURE:  
; NAME/KEY: misc\_structure  
; LOCATION: (931)..(1077)  
; OTHER INFORMATION: encode amino acids 311-359 for forming the sides of the enzymatic pocket  
; OTHER INFORMATION: pocket  
; FEATURE:  
; NAME/KEY: misc\_structure  
; LOCATION: (1141)..(1206)  
; OTHER INFORMATION: encode amino acids 381-402 for forming the enzymatic pocket's

OTHER INFORMATION: activation loop  
US-10-457-954-5

Query Match 100.0%; Score 24; DB 16; Length 3450;  
Best Local Similarity 100.0%; Pred. No. 0.00011;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGGAACATGAAGCCCTTCAGCGG 24  
DB 127 GTGGAACATGAAGCCCTTCAGCGG 150

RESULT 2

US-09-782-378A-25/c  
; Sequence 25, Application US/09782378A  
; Patent No. US20020102731A1  
; GENERAL INFORMATION:  
; APPLICANT: Hearing, Patrick  
; APPLICANT: Bahou, Wadie  
; APPLICANT: Sandalon, Ziv  
; APPLICANT: Gnatenko, Dmitri  
; TITLE OF INVENTION: Adenoviral Vectors  
; FILE REFERENCE: STONYB-04970  
; CURRENT APPLICATION NUMBER: US/09/782,378A  
; PRIOR FILING DATE: 2001-02-12  
; PRIOR APPLICATION NUMBER: 60/237,747  
; PRIOR FILING DATE: 2000-10-02  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: Patentin version 3.0  
; SEQ ID NO 25  
; LENGTH: 34125  
; TYPE: DNA  
; ORGANISM: Human adenovirus type 12  
US-09-782-378A-25

Query Match 75.0%; Score 18; DB 9; Length 34125;  
Best Local Similarity 100.0%; Pred. No. 0.41;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GGAACATGAAGCCCTTCA 20  
DB 4015 GGAACATGAAGCCCTTCA 3998

RESULT 3

US-09-908-975-27688  
; Sequence 27688, Application US/09908975  
; Publication No. US20030165843A1  
; GENERAL INFORMATION:  
; APPLICANT: SHOSHAN, Avi  
; APPLICANT: WASSERMAN, Alon  
; APPLICANT: MINTZ, Eli  
; APPLICANT: MINTZ, Liat  
; APPLICANT: FAIGLER, Simchon  
; TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICE  
; FILE REFERENCE: 36688-0005  
; CURRENT APPLICATION NUMBER: US/09/908,975  
; CURRENT FILING DATE: 2001-07-20  
; PRIOR APPLICATION NUMBER: US 60/287,724  
; PRIOR FILING DATE: 2001-05-02  
; PRIOR APPLICATION NUMBER: US 60/221,607  
; PRIOR FILING DATE: 2000-07-28  
; NUMBER OF SEQ ID NOS: 32337  
; SOFTWARE: Patentin version 3.0  
; SEQ ID NO 27688  
; LENGTH: 65  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-09-908-975-27688

Query Match 66.7%; Score 16; DB 10; Length 65;  
Best Local Similarity 100.0%; Pred. No. 7.9;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGGAACATGAAGCC 16  
DB 7 GTGGAACATGAAGCC 22

RESULT 4

US-10-029-386-26614  
; Sequence 26614, Application US/10029386  
; Publication No. US20030194704A1  
; GENERAL INFORMATION:  
; APPLICANT: Penn, Sharron G.  
; APPLICANT: Rank, David R.  
; APPLICANT: Hanzel, David K.  
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
; FILE REFERENCE: AEOMICA-X-2  
; CURRENT APPLICATION NUMBER: US/10/029,386  
; CURRENT FILING DATE: 2001-12-20  
; NUMBER OF SEQ ID NOS: 34288  
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1  
; SEQ ID NO 26614  
; LENGTH: 310  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: MAP TO CHR20.3  
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.2  
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 3.5  
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.5  
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.9  
; OTHER INFORMATION: SWISSPROT HIT: P07204, EVALUE 2.00e-08  
; OTHER INFORMATION: NT HIT: gil2742414, EVALUE 0.00e+00  
; OTHER INFORMATION: EST\_HUMAN HIT: BI907890.1, EVALUE 0.00e+00  
US-10-029-386-26614

Query Match 66.7%; Score 16; DB 15; Length 310;  
Best Local Similarity 100.0%; Pred. No. 7.5;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 TGAAGCCCTTCAGCGG 24  
DB 47 TGAAGCCCTTCAGCGG 62

RESULT 5

US-10-029-386-12914  
; Sequence 12914, Application US/10029386  
; Publication No. US20030194704A1  
; GENERAL INFORMATION:  
; APPLICANT: Penn, Sharron G.  
; APPLICANT: Rank, David R.  
; APPLICANT: Hanzel, David K.  
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
; FILE REFERENCE: AEOMICA-X-2  
; CURRENT APPLICATION NUMBER: US/10/029,386  
; CURRENT FILING DATE: 2001-12-20  
; NUMBER OF SEQ ID NOS: 34288  
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1  
; SEQ ID NO 12914  
; LENGTH: 555  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: MAP TO CHR20.3  
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.2  
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 3.5  
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.5  
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.9  
; OTHER INFORMATION: SWISSPROT HIT: P07204, EVALUE 4.00e-08  
; OTHER INFORMATION: NT HIT: gil2742414, EVALUE 0.00e+00

OTHER INFORMATION: EST\_HUMAN HIT: BI907890.1, EVALUATE 0.00e+00  
US-10-029-386-12914

Query Match 66.7%; Score 16; DB 15; Length 555;  
Best Local Similarity 100.0%; Pred. No. 7.3; Indels 0; Gaps 0;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 TGAAGCCCTTCAGCGG 24  
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DB 75 TGAAGCCCTTCAGCGG 90

## RESULT 6

US-09-815-242-7861  
; Sequence 7861, Application US/09815242  
; Patent No. US20020061569A1  
; GENERAL INFORMATION:  
; APPLICANT: Haselbeck, Robert  
; APPLICANT: Ohlsen, Kari L.  
; APPLICANT: Zyskind, Judith W.  
; APPLICANT: Wall, Daniel  
; APPLICANT: Trawick, John D.  
; APPLICANT: Carr, Grant J.  
; APPLICANT: Yamamoto, Robert T.  
; APPLICANT: Xu, H. Howard

TITLE OF INVENTION: Identification of Essential Genes in

FILE REFERENCE: ELITRA.011A  
CURRENT APPLICATION NUMBER: US/09/815,242  
CURRENT FILING DATE: 2001-03-21  
PRIOR APPLICATION NUMBER: 60/191,078  
PRIOR FILING DATE: 2000-03-21  
PRIOR APPLICATION NUMBER: 60/206,848  
PRIOR FILING DATE: 2000-05-23  
PRIOR APPLICATION NUMBER: 60/207,727  
PRIOR FILING DATE: 2000-05-26  
PRIOR APPLICATION NUMBER: 60/242,578  
PRIOR FILING DATE: 2000-10-23  
PRIOR APPLICATION NUMBER: 60/253,625  
PRIOR FILING DATE: 2000-11-27  
PRIOR APPLICATION NUMBER: 60/257,931  
PRIOR FILING DATE: 2000-12-22  
PRIOR APPLICATION NUMBER: 60/269,308  
PRIOR FILING DATE: 2001-02-16  
NUMBER OF SEQ ID NOS: 14110  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 7861  
LENGTH: 1044  
TYPE: DNA

ORGANISM: Pseudomonas aeruginosa

FEATURE:

NAME/KEY: CDS

LOCATION: (1)...(1044)

US-09-815-242-7861

Query Match 66.7%; Score 16; DB 9; Length 1044;  
Best Local Similarity 100.0%; Pred. No. 7.2;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 TGAAGCCCTTCAGCGG 24  
|||||  
DB 797 TGAAGCCCTTCAGCGG 812

## RESULT 7

US-10-282-122A-30374  
; Sequence 30374, Application US/10282122A  
; Publication No. US20040029129A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Liangsu  
; APPLICANT: Zamudio, Carlos  
; APPLICANT: Malone, Cheryl  
; APPLICANT: Haselbeck, Robert

APPLICANT: Ohlsen, Kari  
APPLICANT: Zyskind, Judith  
APPLICANT: Wall, Daniel  
APPLICANT: Trawick, John  
APPLICANT: Carr, Grant  
APPLICANT: Yamamoto, Robert  
APPLICANT: Forsyth, R.  
APPLICANT: Xu, H.  
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms  
FILE REFERENCE: ELITRA.034A  
CURRENT APPLICATION NUMBER: US/10/282,122A  
CURRENT FILING DATE: 2003-02-20  
PRIOR APPLICATION NUMBER: 60/191,078  
PRIOR FILING DATE: 2000-03-21  
PRIOR APPLICATION NUMBER: 60/206,848  
PRIOR FILING DATE: 2000-05-23  
PRIOR APPLICATION NUMBER: 60/207,727  
PRIOR FILING DATE: 2000-05-26  
PRIOR APPLICATION NUMBER: 60/230,335  
PRIOR FILING DATE: 2000-09-06  
PRIOR APPLICATION NUMBER: 60/230,347  
PRIOR FILING DATE: 2000-09-09  
PRIOR APPLICATION NUMBER: 60/242,578  
PRIOR FILING DATE: 2000-10-23  
PRIOR APPLICATION NUMBER: 60/253,625  
PRIOR FILING DATE: 2000-11-27  
PRIOR APPLICATION NUMBER: 60/257,931  
PRIOR FILING DATE: 2000-12-22  
PRIOR APPLICATION NUMBER: 60/267,636  
PRIOR FILING DATE: 2001-02-09  
PRIOR APPLICATION NUMBER: 60/269,308  
PRIOR FILING DATE: 2001-02-16  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 78614  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 30374  
LENGTH: 1044  
TYPE: DNA

ORGANISM: Pseudomonas aeruginosa

US-10-282-122A-30374

Query Match 66.7%; Score 16; DB 13; Length 1044;  
Best Local Similarity 100.0%; Pred. No. 7.2;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 TGAAGCCCTTCAGCGG 24  
|||||  
DB 797 TGAAGCCCTTCAGCGG 812

## RESULT 8

US-10-425-114-523  
; Sequence 523, Application US/10425114  
; Publication No. US20040034888A1  
; GENERAL INFORMATION:

APPLICANT: Liu, Jingdong  
APPLICANT: Zhou, Yihua  
APPLICANT: Kovalic, David K.  
APPLICANT: Screen, Steven E.  
APPLICANT: Tabaska, Jack E.  
APPLICANT: Cao, Yongwei  
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
FILE REFERENCE: 38-21(53313)B  
CURRENT APPLICATION NUMBER: US/10/425,114  
CURRENT FILING DATE: 2003-04-28  
NUMBER OF SEQ ID NOS: 73128  
SEQ ID NO 523  
LENGTH: 1424  
TYPE: DNA

ORGANISM: Zea mays

FEATURE:

OTHER INFORMATION: Clone ID: 700076886\_FLI

US-10-425-114-523

Query Match 66.7%; Score 16; DB 13; Length 1424;  
Best Local Similarity 100.0%; Pred. No. 7.1;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GGAACATGAAGCCCTT 18  
|||||  
Db 466 GGRACATGAAGCCCTT 481

RESULT 9

US-10-029-386-22997/c  
; Sequence 22997, Application US/10029386  
; Publication No. US20030194704A1  
; GENERAL INFORMATION:  
; APPLICANT: Penn, Sharron G.  
; APPLICANT: Rank, David R.  
; APPLICANT: Hanzel, David K.  
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
; TITLE OF INVENTION: EXPRESSION ANALYSIS TWO  
; FILE REFERENCE: AEOMICA-X-2  
; CURRENT APPLICATION NUMBER: US/10/029,386  
; CURRENT FILING DATE: 2001-12-20  
; NUMBER OF SEQ ID NOS: 34288  
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1  
; SEQ ID NO 22997  
; LENGTH: 1951  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: MAP TO AL118508.6  
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.4  
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.83  
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.3  
; OTHER INFORMATION: EXPRESSED IN SW620, SIGNAL = 1.00e-39  
; OTHER INFORMATION: NT HIT: g112742414, EVALUATE 0.00e+00  
; OTHER INFORMATION: EST\_HUMAN HIT: B1907890.1, EVALUATE 0.00e+00  
US-10-029-386-22997

Query Match 66.7%; Score 16; DB 15; Length 1951;  
Best Local Similarity 100.0%; Pred. No. 7;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 TGAAGCCCTTCAGCGG 24  
|||||  
Db 343 TGAAGCCCTTCAGCGG 328

RESULT 10

US-10-211-462-130/c  
; Sequence 130, Application US/10211462  
; Publication No. US20040033495A1  
; GENERAL INFORMATION:  
; APPLICANT: Murray, Richard  
; APPLICANT: Glynn, Richard  
; APPLICANT: Watson, Susan R.  
; APPLICANT: Aziz, Natasha  
; APPLICANT: Eos Biotechnology, Inc.  
; TITLE OF INVENTION: Methods of Diagnosis of Angiogenesis, Compositions and  
; TITLE OF INVENTION: Methods of Screening for Angiogenesis Modulators  
; FILE REFERENCE: 018501-006200US  
; CURRENT APPLICATION NUMBER: US/10/211,462  
; CURRENT FILING DATE: 2003-02-13  
; PRIOR APPLICATION NUMBER: US 09/784,356  
; PRIOR FILING DATE: 2001-02-14  
; PRIOR APPLICATION NUMBER: US 09/791,390  
; PRIOR FILING DATE: 2001-02-22  
; PRIOR APPLICATION NUMBER: US 60/310,025  
; PRIOR FILING DATE: 2001-08-03  
; PRIOR APPLICATION NUMBER: US 60/334,244  
; PRIOR FILING DATE: 2001-11-29  
; NUMBER OF SEQ ID NOS: 230

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 130  
; LENGTH: 6699  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-211-462-130

Query Match 66.7%; Score 16; DB 13; Length 6699;  
Best Local Similarity 100.0%; Pred. No. 6.7;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 TGAAGCCCTTCAGCGG 24  
|||||  
Db 491 TGAAGCCCTTCAGCGG 476

RESULT 11

US-10-021-660-15/c  
; Sequence 15, Application US/10021660  
; Publication No. US20030152926A1  
; GENERAL INFORMATION:  
; APPLICANT: Murray, Richard  
; APPLICANT: Glynn, Richard  
; APPLICANT: Watson, Susan R.  
; APPLICANT: Eos Biotechnology, Inc.  
; TITLE OF INVENTION: No. US20030152926A1 Methods of Diagnosis of Angiogenesis,  
; TITLE OF INVENTION: Compositions and Methods of Screening for Angiogenesis  
; TITLE OF INVENTION: Modulators  
; FILE REFERENCE: 018501-000710US  
; CURRENT APPLICATION NUMBER: US/10/021,660  
; CURRENT FILING DATE: 2001-12-06  
; PRIOR APPLICATION NUMBER: US/09/784,356  
; PRIOR FILING DATE: 2001-02-14  
; PRIOR APPLICATION NUMBER: US 09/637,977  
; PRIOR FILING DATE: 2000-08-11  
; NUMBER OF SEQ ID NOS: 135  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 15  
; LENGTH: 6699  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-021-660-15

Query Match 66.7%; Score 16; DB 15; Length 6699;  
Best Local Similarity 100.0%; Pred. No. 6.7;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 TGAAGCCCTTCAGCGG 24  
|||||  
Db 491 TGAAGCCCTTCAGCGG 476

RESULT 12

US-10-085-117-97  
; Sequence 97, Application US/10085117  
; Publication No. US2003023234A1  
; GENERAL INFORMATION:  
; APPLICANT: Morris, David W.  
; APPLICANT: Engelhard, Eric K.  
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER  
; FILE REFERENCE: 529452000121  
; CURRENT APPLICATION NUMBER: US/10/085,117  
; CURRENT FILING DATE: 2002-02-27  
; PRIOR APPLICATION NUMBER: US 09/798,586  
; PRIOR FILING DATE: 2001-03-02  
; NUMBER OF SEQ ID NOS: 361  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 97  
; LENGTH: 85076  
; TYPE: DNA  
; ORGANISM: Mus musculus  
; FEATURE:  
; NAME/KEY: variation

```
; LOCATION: (1)....(85076)
; OTHER INFORMATION: n = any nucleotide
US-10-085-117-97

Query Match
Best Local Similarity 66.7%; Score 16; DB 16; Length 85076;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 CATGAAGCCCTTCAGC 22
Db 30782 CATGAAGCCCTTCAGC 30797

RESULT 13
US-10-087-192-1831/c
; Sequence 1831, Application US/10087192
; Publication No. US20020182586A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
; FILE REFERENCE: 529452000122
; CURRENT APPLICATION NUMBER: US/10/087,192
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 2059
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1831
; LENGTH: 126413
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(126413)
; OTHER INFORMATION: n = A,T,C or G
US-10-087-192-1831

Query Match
Best Local Similarity 66.7%; Score 16; DB 13; Length 126413;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGGAACATGAAGCCC 16
Db 101496 GTGGAACATGAAGCCC 101481

RESULT 14
US-10-382-634-21
; Sequence 21, Application US/10382634
; Publication No. US20040038921A1
; GENERAL INFORMATION:
; APPLICANT: Kreutzer, Roalnd
; TITLE OF INVENTION: Composition and Method for Inhibiting Expression of a Target Gene
; FILE REFERENCE: 20200/2062
; CURRENT APPLICATION NUMBER: US/10/382,634
; CURRENT FILING DATE: 2003-03-07
; PRIOR APPLICATION NUMBER: DE 101 55 280.7
; PRIOR FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: DE 101 58 411.3
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: DE 101 60 151.4
; PRIOR FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: DE 102 30 996.5
; PRIOR FILING DATE: 2002-07-09
; PRIOR APPLICATION NUMBER: PCT/EP02/00152
; PRIOR FILING DATE: 2002-01-09
; PRIOR APPLICATION NUMBER: PCT/EP02/00151
; PRIOR FILING DATE: 2002-01-09
; PRIOR APPLICATION NUMBER: PCT/EP02/11971
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; PRIOR FILING DATE: 2002-10-25
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 21
; LENGTH: 24
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: PRIMER
US-10-382-634-21

Query Match
Best Local Similarity 62.5%; Score 15; DB 13; Length 24;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GAAGCCCTTCAGCGG 24
Db 9 GAAGCCCTTCAGCGG 23

RESULT 15
US-10-349-320-20
; Sequence 20, Application US/10349320
; Publication No. US20030190654A1
; GENERAL INFORMATION:
; APPLICANT: Heidenreich, Olaf
; TITLE OF INVENTION: DOUBLE-STRANDED RNA (dsRNA) AND METHOD OF USE
; FILE REFERENCE: 20200/2112
; CURRENT APPLICATION NUMBER: US/10/349,320
; CURRENT FILING DATE: 2003-01-22
; PRIOR APPLICATION NUMBER: DE 102 02 419.7
; PRIOR FILING DATE: 2002-01-22
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Taqman probe
US-10-349-320-20

Query Match
Best Local Similarity 62.5%; Score 15; DB 15; Length 24;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GAAGCCCTTCAGCGG 24
Db 9 GAAGCCCTTCAGCGG 23

Search completed: May 27, 2004, 14:58:30
Job time : 127.301 secs
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GenCore version 5.1.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 26, 2004, 15:22:41 ; Search time 847.385 Seconds  
(without alignments)  
845.770 Million cell updates/sec

Title: US-09-121-239-16

Perfect score: 24

Sequence: 1 GTGGAACATGAAGCCCTTCAGCGG 24

Scoring table: OLIGO NUC

Gapop 60.0 , Gapext 60.0

Searched: 27513289 seqs, 14931090276 residues

Word size : 0

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

EST:

- 1: em\_estba:\*
- 2: em\_esthum:\*
- 3: em\_estin:\*
- 4: em\_estmu:\*
- 5: em\_estov:\*
- 6: em\_estpl:\*
- 7: em\_estro:\*
- 8: em\_htc:\*
- 9: gb\_est1:\*
- 10: gb\_est2:\*
- 11: gb\_htc:\*
- 12: gb\_est3:\*
- 13: gb\_est4:\*
- 14: gb\_est5:\*
- 15: em\_estfun:\*
- 16: em\_estom:\*
- 17: em\_gss\_hum:\*
- 18: em\_gss\_inv:\*
- 19: em\_gss\_pln:\*
- 20: em\_gss\_vrt:\*
- 21: em\_gss\_fun:\*
- 22: em\_gss\_nam:\*
- 23: em\_gss\_mus:\*
- 24: em\_gss\_pro:\*
- 25: em\_gss\_rod:\*
- 26: em\_gss\_phg:\*
- 27: em\_gss\_vrl:\*
- 28: gb\_gsl:\*
- 29: gb\_gsl2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	24	100.0	404	14	H81820
2	24	100.0	421	12	BM832613
3	24	100.0	544	9	AL707819
C 4	24	100.0	781	13	BM832613 BX097261

C 5	18	75.0	525	14	CD848190
6	18	75.0	546	13	B0019091
C 7	18	75.0	573	13	BY243155
8	18	75.0	1110	12	BM917206
C 9	17	70.8	303	14	CD588643
C 10	17	70.8	317	14	CD585274
C 11	17	70.8	323	14	CD591703
C 12	17	70.8	324	14	CD601328
C 13	17	70.8	330	14	CD601373
C 14	17	70.8	330	14	CD602150
C 15	17	70.8	496	14	CD603852
C 16	17	70.8	500	14	CD585675
C 17	17	70.8	514	12	B0063595
C 18	17	70.8	705	13	BQ617441
19	17	70.8	925	10	BF120890
20	16	66.7	157	10	AW386252
21	16	66.7	191	10	AW420212
22	16	66.7	235	9	AT035445
23	16	66.7	256	9	AA881130
24	16	66.7	281	12	BG985652
C 25	16	66.7	288	10	B009502
C 26	16	66.7	322	14	CD166258
27	16	66.7	324	10	BB838010
C 28	16	66.7	325	10	BF148232
C 29	16	66.7	335	10	BF318395
C 30	16	66.7	339	12	BM211354
31	16	66.7	342	13	BY139003
32	16	66.7	344	10	BB869806
C 33	16	66.7	347	12	BM211586
34	16	66.7	348	13	BY175856
35	16	66.7	354	13	BY310701
36	16	66.7	356	9	AA268399
37	16	66.7	359	13	BY020770
38	16	66.7	361	28	AQ037986
39	16	66.7	362	28	AQ040284
C 40	16	66.7	363	12	BM195340
41	16	66.7	363	13	BY304103
42	16	66.7	364	9	AA119050
43	16	66.7	373	13	BY319051
C 44	16	66.7	377	13	BX636769
C 45	16	66.7	378	14	CD538683

## ALIGNMENTS

RESULT 1  
H81820/c  
LOCUS  
DEFINITION  
H81820  
Ys68e09.r1 Soares retina N2b4HR Homo sapiens cDNA clone  
IMAGE:219976 5', similar to gb:M14752 PROTO-ONCOGENE  
TYROSINE-PROTEIN KINASE ABL (HUMAN);, mRNA sequence.  
ACCESSION  
H81820  
VERSION  
H81820.1 GI:1059909  
KEYWORDS  
EST.  
SOURCE  
Homo sapiens (human)  
ORGANISM  
Homo sapiens  
REFERENCE  
H81820  
Ys68e09.r1 Soares retina N2b4HR Homo sapiens cDNA clone  
IMAGE:219976 5', similar to gb:M14752 PROTO-ONCOGENE  
TYROSINE-PROTEIN KINASE ABL (HUMAN);, mRNA sequence.  
AUTHORS  
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevas, E., Waterston, R., Williamson, A., Wohldmann, P. and Wilson, R.  
TITLE  
The WashU-Merck EST Project  
JOURNAL  
Unpublished (1995)  
COMMENT  
Contact: Wilson RK  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu

High quality sequence stops: 382

Source: IMAGE Consortium, LLNL  
This clone is available royalty-free through LLNL; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.

Insert length: 1427 Std Error: 0.00

Seq primer: M3RP1

High quality sequence stop: 382.

#### FEATURES

source  
Location/Qualifiers

1. 404

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="GDB:3847969"

/db\_xref="taxon:9606"

/clone="IMAGE:219976"

/sex="male"

/tissue\_type="retina"

/dev\_stage="55 year old"

/lab\_host="PH10B (ampicillin resistant)"

/clone\_lib="Soares retina N2b4HR"

/notes="Organ: eye; Vector: p7T73D (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCAATCTGAAGTGGAGCGCGCTTTTITTTTTTTTTT 3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT73 vector (Pharmacia). The retinas were obtained from a 55 year old Caucasian and total cellular poly(A)+ RNA was extracted 6 hrs after their removal. The retina RNA was kindly provided by Roderick R. McInnes M.D. Ph.D. from the University of Toronto. Library constructed by Bento Soares and M.Fatima Bonaldo."

#### ORIGIN

Query Match 100.0%; Score 24; DB 14; Length 404;

Best Local Similarity 100.0%; Pred. No. 0.0037;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGGAACATGAGCCCTTCAGCGG 24

Db 134 GTGGAACATGAGCCCTTCAGCGG 111

#### RESULT 2

BM832613

LOCUS 421 bp mRNA linear EST 06-MAR-2002

DEFINITION K-EST0107122 S11SNUI Homo sapiens cDNA clone S11SNUI-47-E02 5',

mRNA sequence.

BM832613

BM832613.1 GI:19189022

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 421)

AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,

Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and

Kim,Y.S.

21C Frontier Korean EST Project 2001

JOURNAL Unpublished (2002)

COMMENT Contact: Kim YS

Genome Research Center

Korea Research Institute of Bioscience & Biotechnology

52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea

Tel: +82-42-860-4470

Fax: +82-42-860-4409

Email: yongsung@mail.kribb.re.kr

Plate: 47 row: E column: 02

High quality sequence stop: 421.

Location/Qualifiers

1. 421

/organism="Homo sapiens"

#### FEATURES

source

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="S11SNUI-47-E02"

/sex="M"

/tissue\_type="Stomach"

/cell\_line="Lymphoblast-like"

/cell\_line="SNU-1"

/lab\_host="Top10F"

/clone\_lib="S11SNUI"

/note="Organ: Stomach; Vector: pME18-FL3; Site 1: XhoI; Site 2: XhoI; The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tobacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including SfiI site by treatment of T4 RNA ligase and the first strand cDNA was synthesized with Superscript II using SfiI oligo-dT primer. After first strand synthesis, RNA was degraded by NaOH treatment and cDNA was amplified by PCR reaction. The PCR products were digested with SfiI and cloned into DraIII- digested pME18S-FL3 vector. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10F' by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."

#### ORIGIN

Query Match 100.0%; Score 24; DB 12; Length 421;

Best Local Similarity 100.0%; Pred. No. 0.0037;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGGAACATGAGCCCTTCAGCGG 24

Db 247 GTGGAACATGAGCCCTTCAGCGG 270

#### RESULT 3

AL707819

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Contact: MIPS

MIPS

Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany

This is the 5' sequence of the clone insert

Clone from S. Wiemann, Molecular Genome Analysis, German Cancer

Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;

sequenced by AGOWA (Berlin/Germany) within the cDNA sequencing

consortium of the German Genome Project.

No sl sequence available.

This clone (DKFZp686L0149) is available at the RZPD in Berlin.

Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059

Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

#### FEATURES

source

Location/Qualifiers

1. 544

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="DKFZp686L0149"

/dev\_stage="adult"

/lab\_host="DH10B"

/clone\_lib="686 (synonym: hlccc3)"

/note="Vector: pTriplex2; Site\_1: SfiIA; Site\_2: SfiIB;



cdna-collection"

Query Match 100.0%; Score 24; DB 9; Length 544;  
Best Local Similarity 100.0%; Pred. No. 0.004;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGGAACATGAAGCCCTTCAGCGG 24  
|||||  
Db 114 GTGGAACATGAAGCCCTTCAGCGG 91  
|||||

RESULT 5  
CD848190 525 bp mRNA linear EST 11-JUL-2003  
LOCUS DH0AC002ZH02FM1 HaDevR2 Helianthus annuus cDNA clone HaDevR2002H02,  
DEFINITION mRNA sequence.  
ACCESSION CD848190  
VERSION CD848190.1 GI:32532012  
KEYWORDS Helianthus annuus (common sunflower)  
SOURCE EST.  
ORGANISM Helianthus annuus

REFERENCE  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
asterids; campanulids; Asterales; Asteraceae; Asteroideae;  
Heliantheae; Helianthus.  
1 (bases 1 to 525)  
Genopiante.  
Genopiante, a major partnership french program in plant genomics  
AUTHORS Unpublished (2003)  
TITLE Contact: Genopiante  
JOURNAL Genopiante  
COMMENT 93, rue Henri Rochefort 91025 EVRY CEDEX France  
Tel: 33 1 69 47 54 00  
Fax: 33 1 69 47 54 10  
This sequence has been generated in the framework of the french  
plant genomics programme 'Genopiante' (<http://www.genopiante.com>  
and <http://genopiante-info.infobiogen.fr>).

FEATURES  
source  
1..525  
/organism="Helianthus annuus"  
/mol\_type="mRNA"  
/cultivar="psc8"  
/db\_xref="taxon:4232"  
/clone="HaDevR2002H02"  
/tissue\_type="terminal bud"  
/clone\_lib="HaDevR2"

ORIGIN  
Query Match 75.0%; Score 18; DB 14; Length 525;  
Best Local Similarity 100.0%; Pred. No. 10;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGGAACATGAAGCCCTT 18  
|||||  
Db 228 GTGGAACATGAAGCCCTT 211  
|||||

RESULT 6  
BU019091 546 bp mRNA linear EST 23-AUG-2002  
LOCUS QHE20D24.yg.ab1 OH EFGHJ sunflower RHA280 Helianthus annuus CDNA  
DEFINITION clone QHE20D24, mRNA sequence.  
ACCESSION BU019091  
VERSION BU019091.1 GI:22454611  
KEYWORDS EST.  
SOURCE Helianthus annuus (common sunflower)  
ORGANISM Helianthus annuus

REFERENCE  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
asterids; campanulids; Asterales; Asteraceae; Asteroideae;  
Heliantheae; Helianthus.  
1 (bases 1 to 546)  
Kozik,A., Micheltore,R.W., Knapp,S., Matvienko,M., Rieseberg,L.,  
Lin,H., van Damme,M., Lavelle,D., Chevalier,P., Ziegler,J.,  
Ellison,P., Kolkman,J., Slabaugh,M.S., Livingston,K., Zhou,Y.,  
Lai,Z., Church,S., Jackson,L. and Bradford,K.  
Lettuce and Sunflower ESTs from the Composite Genome Project

TITLE

ORIGIN

cdna-collection"

Query Match 100.0%; Score 24; DB 9; Length 544;  
Best Local Similarity 100.0%; Pred. No. 0.004;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGGAACATGAAGCCCTTCAGCGG 24  
|||||  
Db 501 GTGGAACATGAAGCCCTTCAGCGG 524  
|||||

RESULT 4  
BX097261/c 781 bp mRNA linear EST 04-FEB-2003  
LOCUS BX097261 Soares retina N2b4HR Homo sapiens cDNA clone  
DEFINITION IMAGp998C17436 ; IMAGE:219976, mRNA sequence.  
ACCESSION BX097261  
VERSION BX097261.1 GI:27843159  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 781)  
Ebert,L., Heil,O., Hennig,S., Neubert,P., Partsch,E., Peters,M.,  
Radelof,U., Schneider,D. and Korn,B.  
Human UnigeneSet - RZPD3  
Unpublished (2003)  
Contact: Ina Rolfes  
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH  
Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany  
RZPD; IMAGp998C17436.  
RZPDLIB; I.M.A.G.E. cDNA Clone Collection;  
Human UnigeneSet - RZPD3 (RZPDLIB No.972)  
<http://www.rzpd.de/CloneCards/cgi-bin/showLib.pl.cgi?response?libNo=972> Contact: Ina Rolfes  
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH  
Heubnerweg 6, D-14059 Berlin, Germany  
Tel: +49 30 32639 101  
Fax: +49 30 32639 111  
[www.rzpd.de](http://www.rzpd.de)  
This clone is available royalty-free from RZPD;  
contact RZPD ([clone@rzpd.de](mailto:clone@rzpd.de)) for further information. Seq primer:  
M13r, Primer sequence: TTTCACACGAAACAGCTATGAC.  
Location/Qualifiers  
1..781  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGp998C17436 ; IMAGE:219976"  
/sex="male"  
/tissue\_type="retina"  
/dev\_stage="55 year old"  
/lab\_host="DH10B (ampicillin resistant)"  
/clone\_lib="Soares retina N2b4HR"  
/note="Organ: eye; Vector: pT7T3D (Pharmacia) with a modified polylinker; Site 1: Not 1; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCAATCGAAGTGGCGCCGCTTTTGTTTT 3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). The retinas were obtained from a 55 year old Caucasian and total cellular poly(A)+ RNA was extracted 6 hrs after their removal. The retina RNA was kindly provided by Roderick R. McInnes M.D. Ph.D. from the University of Toronto. Library constructed by Bento Soares and M.Fatima Bonaldo."

ORIGIN

Query Match 100.0%; Score 24; DB 13; Length 781;  
Best Local Similarity 100.0%; Pred. No. 0.0045;

http://compgenomics.ucdavis.edu/  
 Unpublished (2002)  
 Contact: Alexander Kozik [R.W.Michelmore]  
 Department of Vegetable Crops, R.W.Michelmore Lab  
 University of California at Davis (UCD)  
 Asmudson Hall, UCD, Davis, CA 95616, USA  
 Tel: 1-(530)-742-1742  
 Fax: 1-(530)-752-9659  
 Email: akozik@catc.org [michelmore@vegmail.ucdavis.edu]  
 singleton, see http://cpgdb.ucdavis.edu/ for details.  
 Plate: QHE20 row: D column: 24.

Location/Qualifiers  
 1. .546  
 /organism="Helianthus annuus"  
 /mol\_type="mRNA"  
 /cultivar="RHA280"  
 /db\_xref="taxon:4232"  
 /clone="QHE20D24"  
 /lab\_host="E.coli"  
 /clone\_lib="OH\_EFGHJ sunflower RHA280"  
 /note="Vector: pBRCNDASFIAB; The library was constructed from 11 different sources of RNA from a single genotype. Separate cDNAs were generated using primers that incorporated unique 5' and 3' tags to distinguish each source of RNA. cDNAs were then pooled, size-fractionated, directionally cloned into a custom medium-copy vector and transfections made with four size classes to minimize size bias. Details of each source of RNA and library construction can be obtained at http://cpgdb.ucdavis.edu/  
 TAG\_TISSUE=roots environmental stress  
 TAG\_LIB=OH\_EFGHJ sunflower RHA280  
 TAG\_SEQ=ATCTCGCGGG"

Query Match 75.0%; Score 18; DB 13; Length 546;  
 Best Local Similarity 100.0%; Pred. No. 10;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGGACATGAGCCCTT 18  
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 Db 292 GTGGAACATGAGCCCTT 309

RESULT 7  
 BY243155/c  
 LOCUS  
 DEFINITION  
 BY243155  
 ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
 1 (bases 1 to 573)  
 Okazaki.Y., Furuno.M., Kasukawa.T., Adachi.J., Bono.H., Kondo.S.,  
 Nikaide.I., Osato.N., Saito.R., Suzuki.H., Yamanaka.I.,  
 Kiyosawa.H., Yagi.K., Tomaru.Y., Hasegawa.Y., Nogami.A.,  
 Hume.D.A., Quackenbush.J., Baldarelli.R., Hill.D.P., Bult.C.,  
 Batalov.S., Beisel.K.W., Blake.J.A., Bradt.D., Brusic.V.,  
 Chothia.C., Corbani.L.E., Cousins.S., Dalla.E., Dragani.T.A.,  
 Fletcher.C.P., Forrest.A., Frazer.K.S., Gaasterland.T.,  
 Gariboldi.M., Gissi.C., Godzik.A., Gough.J., Grimmond.S.,  
 Gustincich.S., Hirokawa.N., Jackson.I.J., Jarvis.E.D., Kanai.A.,  
 Kawai.H., Kawasawa.Y., Kedierski.R.M., King.B.L., Konagaya.A.,  
 Kurochkin.I.V., Lee.Y., Lenhard.B., Lyons.P.A., Maglott.D.R.,  
 Maltais.L., Marchionni.L., McKenzie.L., Miki.H., Nagashima.T.,  
 Numata.K., Okido.T., Pavan.W.J., Perteau.G., Pesole.G.,  
 Petrovsky.N., Pillai.R., Pontius.J.U., Qi.D., Ramachandran.S.,  
 Ravasi.T., Reed.J.C., Reed.D.J., Reid.J., Ring.B.Z., Ringwald.M.,  
 Sandelin.A., Schneider.C., Sempile.C.A., Setou.M., Shimada.K.,

Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M.,  
 Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y.,  
 Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I.,  
 Yang,L., Yuan.Z., Zavolan.M., Zhu.Y., Zimmer,A., Carninci,P.,  
 Hayatsu,N., Hirozane-Kishikawa,T., Kono.H., Nakamura,M.,  
 Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K.,  
 Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y.,  
 Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K.,  
 Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S.,  
 Rogers,J., Birney,E. and Hayashizaki,Y.  
 Analysis of the mouse transcriptome based on functional annotation  
 of 60,770 full-length cDNAs  
 Nature 420, 563-573 (2002)  
 12466851  
 22354683  
 PUMED  
 COMMENT  
 Contact: Yoshihide Hayashizaki  
 Laboratory for Genome Exploration Research Group, RIKEN Genomic  
 Sciences Center (GSC), Yokohama Institute  
 The Institute of Physical and Chemical Research (RIKEN)  
 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan  
 Tel: 81-45-503-9222  
 Fax: 81-45-503-9216  
 Email: genome-res@gsc.riken.go.jp,  
 URL:http://genome.gsc.riken.go.jp/  
 Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S.,  
 Hirozane,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H.,  
 Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R.,  
 Ohno,M., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K.,  
 Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramatsu,M. and  
 Hayashizaki,Y. Direct Submission  
 Computational Analysis of Full-Length Mouse cDNAs Compared with  
 Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)  
 Normalization and subtraction of cap-trapper-selected cDNAs to  
 prepare full-length cDNA libraries for rapid discovery of new  
 genes. Genome Res. 10 (10), 1617-1630 (2000)  
 RIKEN integrated sequence analysis (RISA) system--384-format  
 sequencing pipeline with 384 multicapillary sequencer. Genome Res.  
 10 (11), 1757-1771 (2000)  
 Computer-based methods for the mouse full-length cDNA  
 encyclopedia: real-time sequence clustering for construction of a  
 nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)  
 cDNA library was prepared and sequenced in Mouse Genome  
 Encyclopedia Project of Genome Exploration Research Group in Riken  
 Genomic Sciences Center and Genome Science Laboratory in RIKEN.  
 Division of Experimental Animal Research in Riken contributed to  
 prepare mouse tissues.  
 Tissues were provided by Michela Fagiolini and Takao K. Hensch ( )  
 Laboratory for Neuronal Circuit Development Brain Science Institute  
 RIKEN 2-1 Hiroosawa,Wako-shi,Saitama 351-0198 Japan ) whose  
 assistance we gratefully acknowledge. Please visit our web site  
 (http://genome.gsc.riken.go.jp) for further details.

FEATURES  
 Location/Qualifiers  
 1. .573  
 /organism="Mus musculus"  
 /mol\_type="mRNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="K230039L14"  
 /tissue\_type="visual cortex"  
 /clone\_lib="RIKEN full-length enriched, visual cortex"

ORIGIN  
 Query Match 75.0%; Score 18; DB 13; Length 573;  
 Best Local Similarity 100.0%; Pred. No. 11;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 7 CATGAAGCCCTTCAGCGG 24  
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 Db 479 CATGAAGCCCTTCAGCGG 462

RESULT 8  
 BM917206

LOCUS BM917206 1110 bp mRNA linear EST 12-MAR-2002  
DEFINITION AGENCOURT\_6702147 NIH\_MGC\_106 Homo sapiens cDNA clone IMAGE:5483703  
5', mRNA sequence.  
ACCESSION BM917206  
VERSION BM917206.1 GI:19367585  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 1110)  
AUTHORS NIH-MGC <http://mgs.nci.nih.gov/>  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)  
COMMENT Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: [cgapsb@mail.nih.gov](mailto:cgapsb@mail.nih.gov)  
Tissue Procurement: Dr. Daniel McVicar, DBS/NCI  
CDNA Library Preparation: Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: LLCW2011 row: m column: 16  
High quality sequence stop: 651.  
location/Qualifiers  
1..1110  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:5483703"  
/tissue\_type="natural killer cells, cell line"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH MGC 106"  
/Note="Organ: blood; Vector: pOTB7; Site 1: XhoI; Site 2:  
EcoRI; cDNA made by oligo-dT priming. Directionally cloned  
into EcoRI/XhoI sites using the following 5' adaptor:  
GGCAGCAG(G). Library constructed by Ling Hong in the  
laboratory of Gerald M. Rubin (University of California,  
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and  
Superscript II RT (Life Technologies). Note: this is a  
NIH\_MGC Library."

ORIGIN  
Query Match 75.0%; Score 18; DB 12; Length 1110;  
Best Local Similarity 100.0%; Pred. No. 13;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 5 AACATGAGCCCTTCAGC 22  
DB 806 AACATGAGCCCTTCAGC 823

RESULT 9  
CD588643/c  
LOCUS  
DEFINITION RK047A3H04.T3 Zebrafish Kidney Marrow cDNA library Danio rerio cDNA  
clone RK047A3H04 5', mRNA sequence.  
ACCESSION CD588643  
VERSION CD588643.1 GI:31769995  
KEYWORDS EST.  
SOURCE Danio rerio (zebrafish)  
ORGANISM Danio rerio  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;  
Cypriniformes; Cyprinidae; Danio.  
REFERENCE 1 (bases 1 to 303)  
AUTHORS Song, H.D., Wu, X.Y., Sun, X.J., Zhou, Y., Liu, T.X., Zhang, G.W.,  
Sheng, Y., Chen, Y., Ruan, Z., Jiang, C.L., Fan, H.Y., Look, A.T.,  
Zou, L.I., and Chen, Z.  
TITLE Gene Expression Profiling in the Zebrafish Kidney Marrow Tissue  
JOURNAL Unpublished (2003)  
COMMENT Contact: Chen Z.

FEATURES  
source  
Location/Qualifiers  
1..303  
/organism="Danio rerio"  
/mol\_type="mRNA"  
/db\_xref="taxon:7955"  
/clone="RK047A3H04"  
/dev\_stages="mature"  
/Note="Organ: kidney; Vector: pBS-CMV; Site 1: XhoI;  
Site 2: EcoRI; Total RNA was extracted from the kidney  
tissues of mature zebrafish. The poly (A)+ RNA fraction  
was separated from total RNA by oligo (dT) cellulose  
chromatography. Library was initially constructed in the  
lambdaZAP Express vector (Stratagene) and in vivo excised  
into pBS-CMV vector."

ORIGIN  
Query Match 70.8%; Score 17; DB 14; Length 303;  
Best Local Similarity 100.0%; Pred. No. 32;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 5 AACATGAGCCCTTCAGC 21  
DB 127 AACATGAGCCCTTCAGC 111

RESULT 10  
CD585274/c  
LOCUS  
DEFINITION RK030A2C01.T3 Zebrafish Kidney Marrow cDNA library Danio rerio cDNA  
clone RK030A2C01 5', mRNA sequence.  
ACCESSION CD585274  
VERSION CD585274.1 GI:31766016  
KEYWORDS EST.  
SOURCE Danio rerio (zebrafish)  
ORGANISM Danio rerio  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;  
Cypriniformes; Cyprinidae; Danio.  
REFERENCE 1 (bases 1 to 317)  
AUTHORS Song, H.D., Wu, X.Y., Sun, X.J., Zhou, Y., Liu, T.X., Zhang, G.W.,  
Sheng, Y., Chen, Y., Ruan, Z., Jiang, C.L., Fan, H.Y., Look, A.T.,  
Zou, L.I., and Chen, Z.  
TITLE Gene Expression Profiling in the Zebrafish Kidney Marrow Tissue  
JOURNAL Unpublished (2003)  
COMMENT Contact: Chen Z.

FEATURES  
source  
Location/Qualifiers  
1..317  
/organism="Danio rerio"  
/mol\_type="mRNA"  
/db\_xref="taxon:7955"  
/clone="RK030A2C01"  
/dev\_stages="mature"  
/Note="Organ: kidney; Vector: pBS-CMV; Site 1: XhoI;  
Site 2: EcoRI; Total RNA was extracted from the kidney  
tissues of mature zebrafish. The poly (A)+ RNA fraction

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Tel: 86-21-64740490  
Fax: 86-21-64743206  
Email: [zchen@stn.sh.cn](mailto:zchen@stn.sh.cn)  
Seq primer: T3.  
Location/Qualifiers  
1..303  
/organism="Danio rerio"  
/mol\_type="mRNA"  
/db\_xref="taxon:7955"  
/clone="RK047A3H04"  
/dev\_stages="mature"  
/Note="Organ: kidney; Vector: pBS-CMV; Site 1: XhoI;  
Site 2: EcoRI; Total RNA was extracted from the kidney  
tissues of mature zebrafish. The poly (A)+ RNA fraction  
was separated from total RNA by oligo (dT) cellulose  
chromatography. Library was initially constructed in the  
lambdaZAP Express vector (Stratagene) and in vivo excised  
into pBS-CMV vector."

ORIGIN  
Query Match 70.8%; Score 17; DB 14; Length 303;  
Best Local Similarity 100.0%; Pred. No. 32;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 5 AACATGAGCCCTTCAGC 21  
DB 127 AACATGAGCCCTTCAGC 111

RESULT 10  
CD585274/c  
LOCUS  
DEFINITION RK030A2C01.T3 Zebrafish Kidney Marrow cDNA library Danio rerio cDNA  
clone RK030A2C01 5', mRNA sequence.  
ACCESSION CD585274  
VERSION CD585274.1 GI:31766016  
KEYWORDS EST.  
SOURCE Danio rerio (zebrafish)  
ORGANISM Danio rerio  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;  
Cypriniformes; Cyprinidae; Danio.  
REFERENCE 1 (bases 1 to 317)  
AUTHORS Song, H.D., Wu, X.Y., Sun, X.J., Zhou, Y., Liu, T.X., Zhang, G.W.,  
Sheng, Y., Chen, Y., Ruan, Z., Jiang, C.L., Fan, H.Y., Look, A.T.,  
Zou, L.I., and Chen, Z.  
TITLE Gene Expression Profiling in the Zebrafish Kidney Marrow Tissue  
JOURNAL Unpublished (2003)  
COMMENT Contact: Chen Z.

FEATURES  
source  
Location/Qualifiers  
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/organism="Danio rerio"  
/mol\_type="mRNA"  
/db\_xref="taxon:7955"  
/clone="RK030A2C01"  
/dev\_stages="mature"  
/Note="Organ: kidney; Vector: pBS-CMV; Site 1: XhoI;  
Site 2: EcoRI; Total RNA was extracted from the kidney  
tissues of mature zebrafish. The poly (A)+ RNA fraction

was separated from total RNA by oligo (dT) cellulose chromatography. Library was initially constructed in the lambdaZAP Express vector (Stratagene) and in vivo excised into pBS-CMV vector."

## ORIGIN

Query Match 70.8%; Score 17; DB 14; Length 317;  
Best Local Similarity 100.0%; Pred. No. 32;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 AACATGAGCCCTTCAG 21  
|||||  
Db 139 AACATGAGCCCTTCAG 123

## RESULT 11

CD591703/c  
LOCUS  
DEFINITION  
323 bp mRNA linear EST 16-JUN-2003  
clone RK065A4G05 T3 Zebrafish Kidney Marrow cDNA library Danio rerio cDNA  
clone RK065A4G05 5', mRNA sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

CD591703.1 GI:31773055  
EST.  
Danio rerio (zebrafish)  
Danio rerio  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;  
Cypriniformes; Cyprinidae; Danio.

REFERENCE  
AUTHORS  
Song, H.D., Wu, X.Y., Sun, X.J., Zhou, Y., Liu, T.X., Zhang, G.W.,  
Sheng, Y., Chen, Y., Ruan, Z., Jiang, C.L., Fan, H.Y., Look, A.T.,  
Zou, L.I. and Chen, Z.

TITLE  
JOURNAL  
COMMENT  
Gene Expression Profiling in the Zebrafish Kidney Marrow Tissue  
Unpublished (2003)  
Contact: Chen Z.

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Tel: 86-21-64740490  
Fax: 86-21-64743206  
Email: zchen@stn.sh.cn  
Seq primer: T3.

## FEATURES

source  
Location/Qualifiers  
1..323  
/organism="Danio rerio"  
/mol\_type="mRNA"  
/db\_xref="taxon:7955"  
/clone="RK065A4G05"  
/dev\_stage="mature"

/note="Organ: kidney; Vector: pBS-CMV; Site 1: XhoI;  
Site 2: EcoRI; Total RNA was extracted from the kidney  
tissues of mature zebrafish. The poly (A)+ RNA fraction  
was separated from total RNA by oligo (dT) cellulose  
chromatography. Library was initially constructed in the  
lambdaZAP Express vector (Stratagene) and in vivo excised  
into pBS-CMV vector."

## ORIGIN

Query Match 70.8%; Score 17; DB 14; Length 323;  
Best Local Similarity 100.0%; Pred. No. 32;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 AACATGAGCCCTTCAG 21  
|||||  
Db 136 AACATGAGCCCTTCAG 120

## RESULT 12

CD601328/c  
LOCUS  
DEFINITION  
324 bp mRNA linear EST 16-JUN-2003  
clone RK132A1C12 T3 Zebrafish Kidney Marrow cDNA library Danio rerio cDNA

clone RK132A1C12 5', mRNA sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

CD601328.1 GI:31782204  
EST.  
Danio rerio (zebrafish)  
Danio rerio  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;  
Cypriniformes; Cyprinidae; Danio.

REFERENCE  
AUTHORS  
Song, H.D., Wu, X.Y., Sun, X.J., Zhou, Y., Liu, T.X., Zhang, G.W.,  
Sheng, Y., Chen, Y., Ruan, Z., Jiang, C.L., Fan, H.Y., Look, A.T.,  
Zou, L.I. and Chen, Z.

TITLE  
JOURNAL  
COMMENT  
Gene Expression Profiling in the Zebrafish Kidney Marrow Tissue  
Unpublished (2003)  
Contact: Chen Z.

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197 Rui Jin Road II, Shanghai 200025, P. R. China  
Tel: 86-21-64740490  
Fax: 86-21-64743206  
Email: zchen@stn.sh.cn  
Seq primer: T3.

## FEATURES

source  
Location/Qualifiers  
1..324  
/organism="Danio rerio"  
/mol\_type="mRNA"  
/db\_xref="taxon:7955"  
/clone="RK132A1C12"  
/dev\_stage="mature"

/note="Organ: kidney; Vector: pBS-CMV; Site 1: XhoI;  
Site 2: EcoRI; Total RNA was extracted from the kidney  
tissues of mature zebrafish. The poly (A)+ RNA fraction  
was separated from total RNA by oligo (dT) cellulose  
chromatography. Library was initially constructed in the  
lambdaZAP Express vector (Stratagene) and in vivo excised  
into pBS-CMV vector."

## ORIGIN

Query Match 70.8%; Score 17; DB 14; Length 324;  
Best Local Similarity 100.0%; Pred. No. 33;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 AACATGAGCCCTTCAG 21  
|||||  
Db 127 AACATGAGCCCTTCAG 111

## RESULT 13

CD601373/c  
LOCUS  
DEFINITION  
330 bp mRNA linear EST 16-JUN-2003  
clone RK132A2C11 T3 Zebrafish Kidney Marrow cDNA library Danio rerio cDNA  
clone RK132A2C11 5', mRNA sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

CD601373.1 GI:31782249  
EST.  
Danio rerio (zebrafish)  
Danio rerio  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;  
Cypriniformes; Cyprinidae; Danio.

REFERENCE  
AUTHORS  
Song, H.D., Wu, X.Y., Sun, X.J., Zhou, Y., Liu, T.X., Zhang, G.W.,  
Sheng, Y., Chen, Y., Ruan, Z., Jiang, C.L., Fan, H.Y., Look, A.T.,  
Zou, L.I. and Chen, Z.

TITLE  
JOURNAL  
COMMENT  
Gene Expression Profiling in the Zebrafish Kidney Marrow Tissue  
Unpublished (2003)  
Contact: Chen Z.

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Shanghai Institute of Hematology, Ruijin Hospital Affiliated to  
Shanghai Second Medical University

197 Rui Jin Road II, Shanghai 200025, P. R. China  
 Tel: 86-21-64740490  
 Fax: 86-21-64743206  
 Email: zchen@stn.sh.cn  
 Seq primer: T3

FEATURES  
 source  
 Location/Qualifiers  
 1..330

/organism="Danio rerio"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:7955"  
 /clone="RK13A2C11"  
 /dev\_stage="mature"  
 /clone\_lib="Zebrafish Kidney Marrow cDNA library"  
 /note="Organ: Kidney; Vector: pBS-CMV; Site 1: XhoI;  
 Site 2: EcoRI; Total RNA was extracted from the kidney  
 tissues of mature zebrafish. The poly (A) + RNA fraction  
 was separated from total RNA by oligo (dT) cellulose  
 chromatography. Library was initially constructed in the  
 lambdaZAP Express vector (Stratagene) and in vivo excised  
 into pBS-CMV vector."

## ORIGIN

Query Match 70.8%; Score 17; DB 14; Length 330;  
 Best Local Similarity 100.0%; Pred. No. 33;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 AACATGAAGCCCTTCAG 21  
 |||||  
 Db 127 AACATGAAGCCCTTCAG 111

## RESULT 14

CD602150/c  
 LOCUS  
 DEFINITION  
 RK140A2F04\_T3 Zebrafish Kidney Marrow cDNA library Danio rerio cDNA  
 clone RK140A2F04 5', mRNA sequence.

ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 CD602150.1 GI:31783502  
 EST.

ORGANISM  
 Danio rerio (zebrafish)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Actinopterygii; Neopterygii; Teleostei; Ostariophysi;  
 Cypriniformes; Cyprinidae; Danio.

REFERENCE  
 AUTHORS  
 1 (bases 1 to 330)  
 Song,H.D., Wu,X.Y., Sun,X.J., Zhou,Y., Liu,T.X., Zhang,G.W.,  
 Sheng,Y., Chen,Y., Ruan,Z., Jiang,C.L., Fan,H.Y., Look,A.T.,  
 Zou,L.I. and Chen,Z.

TITLE  
 JOURNAL  
 COMMENT  
 Gene Expression Profiling in the Zebrafish Kidney Marrow Tissue  
 Unpublished (2003)  
 Contact: Chen Z.

State Key Lab for Medical Genomics  
 Shanghai Institute of Hematology, Ruijin Hospital Affiliated to  
 Shanghai Second Medical University  
 197 Rui Jin Road II, Shanghai 200025, P. R. China  
 Tel: 86-21-64740490  
 Fax: 86-21-64743206  
 Email: zchen@stn.sh.cn  
 Seq primer: T3

## FEATURES

source  
 Location/Qualifiers  
 1..330  
 /organism="Danio rerio"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:7955"  
 /clone="RK140A2F04"  
 /dev\_stage="mature"

/clone\_lib="Zebrafish Kidney Marrow cDNA library"  
 /note="Organ: Kidney; Vector: pBS-CMV; Site 1: XhoI;  
 Site 2: EcoRI; Total RNA was extracted from the kidney  
 tissues of mature zebrafish. The poly (A) + RNA fraction  
 was separated from total RNA by oligo (dT) cellulose  
 chromatography. Library was initially constructed in the  
 lambdaZAP Express vector (Stratagene) and in vivo excised

ORIGIN  
 into pBS-CMV vector."

Query Match 70.8%; Score 17; DB 14; Length 330;  
 Best Local Similarity 100.0%; Pred. No. 33;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 AACATGAAGCCCTTCAG 21  
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 Db 139 AACATGAAGCCCTTCAG 123

## RESULT 15

CD603852/c  
 LOCUS  
 DEFINITION  
 RZ150A3E05\_T3 Zebrafish Kidney Marrow cDNA library Danio rerio cDNA  
 clone RZ150A3E05 5', mRNA sequence.

ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 CD603852.1 GI:31785204  
 EST.

## ORGANISM

Danio rerio (zebrafish)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Actinopterygii; Neopterygii; Teleostei; Ostariophysi;  
 Cypriniformes; Cyprinidae; Danio.

## REFERENCE

AUTHORS  
 1 (bases 1 to 496)  
 Song,H.D., Wu,X.Y., Sun,X.J., Zhou,Y., Liu,T.X., Zhang,G.W.,  
 Sheng,Y., Chen,Y., Ruan,Z., Jiang,C.L., Fan,H.Y., Look,A.T.,  
 Zou,L.I. and Chen,Z.

TITLE  
 JOURNAL  
 COMMENT  
 Gene Expression Profiling in the Zebrafish Kidney Marrow Tissue  
 Unpublished (2003)  
 Contact: Chen Z.

State Key Lab for Medical Genomics  
 Shanghai Institute of Hematology, Ruijin Hospital Affiliated to  
 Shanghai Second Medical University  
 197 Rui Jin Road II, Shanghai 200025, P. R. China  
 Tel: 86-21-64740490  
 Fax: 86-21-64743206  
 Email: zchen@stn.sh.cn  
 Seq primer: T3.

## FEATURES

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 Location/Qualifiers  
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 /clone="RZ150A3E05"  
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 Site 2: EcoRI; Total RNA was extracted from the kidney  
 tissues of mature zebrafish. The poly (A) + RNA fraction  
 was separated from total RNA by oligo (dT) cellulose  
 chromatography. Library was initially constructed in the  
 lambdaZAP Express vector (Stratagene) and in vivo excised  
 into pBS-CMV vector."

## ORIGIN

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 Best Local Similarity 100.0%; Pred. No. 37;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 196 AACATGAAGCCCTTCAG 180

Search completed: May 26, 2004, 22:44:34  
 Job time : 852.385 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004, Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 26, 2004, 16:00:31 ; Search time 510.783 Seconds  
(without alignments)  
2036.547 Million cell updates/sec

Title: US-09-121-239-17

Perfect score: 24

Sequence: 1 GUGGACACAGAGACCCUACGCGG 24

Scoring table: OLIGO\_NUC

Gapop 60.0 , Gapext 60.0

Searched: 3470272 seqs, 21671516995 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

GenEmbl.\*

1: gb\_ba.\*

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6: gb\_pat.\*

7: gb\_ph.\*

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14: gb\_vl.\*

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16: em\_fun.\*

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18: em\_in.\*

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23: em\_pat.\*

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25: em\_pl.\*

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33: em\_hg\_mus.\*

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36: em\_hg\_mam.\*

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38: em\_sy.\*

39: em\_hgo\_hum.\*

40: em\_hgo\_mus.\*

41: em\_hgo\_other.\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	24	100.0	24	6	BD222538	BD222538 Methods f
2	24	100.0	24	6	BD222539	BD222539 Methods f
C 3	24	100.0	24	6	BD222540	BD222540 Methods f
C 4	24	100.0	24	6	BD222541	BD222541 Methods f
C 5	24	100.0	299	6	BD222547	BD222547 Methods f
C 6	18	75.0	34125	14	AT12CGA	XJ3487 Adenovirus
C 7	18	75.0	238483	2	AC132177	AC132177 Rattus no
C 8	17	70.8	60456	2	AC087634	AC087634 Homo sapi
C 9	17	70.8	104244	10	AL805925	AL805925 Mouse DNA
C 10	17	70.8	138152	10	AL954170	AL954170 Mouse DNA
C 11	17	70.8	152804	2	BX248232	BX248232 Danio rer
C 12	17	70.8	162077	2	AC109200	AC109200 Mus muscu
C 13	17	70.8	184317	10	AL606494	AL606494 Mouse DNA
C 14	17	70.8	215356	10	AC096363	AC096363 Rattus no
C 15	17	70.8	215958	2	AC102091	AC102091 Mus muscu
C 16	17	70.8	256703	2	AC114076	AC114076 Rattus no
C 17	17	70.8	259220	2	AC097694	AC097694 Rattus no
C 18	16	66.7	404	8	AF082605	AF082605 Leavenwor
C 19	16	66.7	415	8	AF082606	AF082606 Leavenwor
C 20	16	66.7	556	11	G85739	G85739 S209P6356RA
C 21	16	66.7	688	11	G97604	G97604 S209P6432FF
C 22	16	66.7	751	6	BD018368	BD018368 Novel gen
C 23	16	66.7	751	6	BD098306	BD098306 Novel gen
C 24	16	66.7	760	8	AF082603	AF082603 Leavenwor
C 25	16	66.7	1050	10	AF039216	AF039216 Mus muscu
C 26	16	66.7	1109	10	BC005636	BC005636 Mus muscu
C 27	16	66.7	1454	8	AY266141	AY266141 Setaria i
C 28	16	66.7	1599	8	ZMA430386	AJ430386 Zea mays
C 29	16	66.7	2233	8	AY166687	AY166687 Cryphonec
C 30	16	66.7	2370	8	ZMA430205	AJ430205 Zea mays
C 31	16	66.7	2577	9	BC028075	BC028075 Homo sapi
C 32	16	66.7	3335	5	AY422997	AY422997 Danio rer
C 33	16	66.7	3337	9	HSA295142	AJ295142 Homo sapi
C 34	16	66.7	3398	5	BC045427	BC045427 Danio rer
C 35	16	66.7	3398	5	BC047178	BC047178 Danio rer
C 36	16	66.7	3460	6	AR079398	AR079398 Sequence
C 37	16	66.7	3460	9	HSU94333	U94333 Human Clq/M
C 38	16	66.7	4194	10	MUSCTNC	J04971 M.musculus
C 39	16	66.7	14652	1	AE004799	AE004799 Pseudomon
C 40	16	66.7	48139	9	AC109827	AC109827 Homo sapi
C 41	16	66.7	50436	9	AL391258	AL391258 Human DNA
C 42	16	66.7	60631	1	AF006628_8	Continuation (9 of
C 43	16	66.7	67542	9	AC026422	AC026422 Homo sapi
C 44	16	66.7	70305	1	YPCD1	AL117189 Yersinia
C 45	16	66.7	70504	1	AF053946	AF053946 Yersinia

ALIGNMENTS

RESULT 1  
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LOCUS BD222538 24 bp DNA linear PAT 17-JUL-2003  
DEFINITION Methods for detecting and measuring spliced nucleic acids.  
ACCESSION BD222538  
VERSION BD222538.1 GI:33032308  
KEYWORDS JP 2002521037-A/16.  
SOURCE synthetic construct  
ORGANISM synthetic construct  
artificial sequences.  
REFERENCE 1 (bases 1 to 24)  
AUTHORS Harvey, R.C. and Eastman, P.S.  
TITLE Methods for detecting and measuring spliced nucleic acids  
JOURNAL Patent: JP 2002521037-A 16 16-JUL-2002;  
GEN PROBE INC

```

COMMENT      OS      Artificial Sequence
              PN      JP 2002521037-A/16
              PD      16-JUL-2002
              PF      23-JUL-1999 JP 2000561364
              PR      23-JUL-1998 US 09/121239
              PI      RICHARD C HARVEY, PAUL S EASTMAN
              PC      C12Q1/68, C12N15/09, C12N15/00
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Matches 20; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

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LOCUS
DEFINITION      Methods for detecting and measuring spliced nucleic acids.
ACCESSION      BD222539
VERSION      BD222539.1 GI:33032309
KEYWORDS      JP 2002521037-A/17.
SOURCE      synthetic construct
ORGANISM      artificial sequences.
REFERENCE      1 (bases 1 to 24)
AUTHORS      Harvey, R.C. and Eastman, P.S.
TITLE      Methods for detecting and measuring spliced nucleic acids
JOURNAL      Patent: JP 2002521037-A 17 16-JUL-2002;
GEN PROBE INC
COMMENT      OS      Artificial Sequence
              PN      JP 2002521037-A/17
              PD      16-JUL-2002
              PF      23-JUL-1999 JP 2000561364
              PR      23-JUL-1998 US 09/121239
              PI      RICHARD C HARVEY, PAUL S EASTMAN
              PC      C12Q1/68, C12N15/09, C12N15/00
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Matches 20; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

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      1 GTGGAACATGAAGCCCTTCAGCGG 24

RESULT 3
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LOCUS
DEFINITION      Methods for detecting and measuring spliced nucleic acids
ACCESSION      BD222540
VERSION      BD222540.1 GI:33032310
KEYWORDS      JP 2002521037-A/18.
SOURCE      synthetic construct
ORGANISM      artificial sequences.
REFERENCE      1 (bases 1 to 24)
AUTHORS      Harvey, R.C. and Eastman, P.S.
TITLE      Methods for detecting and measuring spliced nucleic acids
JOURNAL      Patent: JP 2002521037-A 18 16-JUL-2002;
GEN PROBE INC
COMMENT      OS      Artificial Sequence
              PN      JP 2002521037-A/18
              PD      16-JUL-2002
              PF      23-JUL-1999 JP 2000561364
              PR      23-JUL-1998 US 09/121239
              PI      RICHARD C HARVEY, PAUL S EASTMAN
              PC      C12Q1/68, C12N15/09, C12N15/00
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Matches 20; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

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DEFINITION      Methods for detecting and measuring spliced nucleic acids.
ACCESSION      BD222540
VERSION      BD222540.1 GI:33032310
KEYWORDS      JP 2002521037-A/18.
SOURCE      synthetic construct
ORGANISM      artificial sequences.
REFERENCE      1 (bases 1 to 24)
AUTHORS      Harvey, R.C. and Eastman, P.S.
TITLE      Methods for detecting and measuring spliced nucleic acids
JOURNAL      Patent: JP 2002521037-A 18 16-JUL-2002;
GEN PROBE INC
COMMENT      OS      Artificial Sequence
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              PD      16-JUL-2002
              PF      23-JUL-1999 JP 2000561364
              PR      23-JUL-1998 US 09/121239
              PI      RICHARD C HARVEY, PAUL S EASTMAN
              PC      C12Q1/68, C12N15/09, C12N15/00
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Matches 20; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

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      1 GTGGAACATGAAGCCCTTCAGCGG 24

RESULT 4
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LOCUS
DEFINITION      Methods for detecting and measuring spliced nucleic acids.
ACCESSION      BD222541
VERSION      BD222541.1 GI:33032311
KEYWORDS      JP 2002521037-A/19.
SOURCE      synthetic construct
ORGANISM      artificial sequences.
REFERENCE      1 (bases 1 to 24)
AUTHORS      Harvey, R.C. and Eastman, P.S.
TITLE      Methods for detecting and measuring spliced nucleic acids
JOURNAL      Patent: JP 2002521037-A 19 16-JUL-2002;
GEN PROBE INC
COMMENT      OS      Artificial Sequence
              PN      JP 2002521037-A/19
              PD      16-JUL-2002
              PF      23-JUL-1999 JP 2000561364
              PR      23-JUL-1998 US 09/121239
              PI      RICHARD C HARVEY, PAUL S EASTMAN
              PC      C12Q1/68, C12N15/09, C12N15/00
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              Key source      18      Location/Qualifiers
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FEATURES
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Query Match      100.0%; Score 24; DB 6; Length 24;
Best Local Similarity 83.3%; Pred. No. 0.0025;
Matches 20; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY      1 GUGGAACAUGAACCCUUCAGCGG 24
      1 GTGGAACATGAAGCCCTTCAGCGG 24
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      1 GTGGAACATGAAGCCCTTCAGCGG 24

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Query Match      100.0%; Score 24; DB 6; Length 24;
Best Local Similarity 83.3%; Pred. No. 0.0025;
Matches 20; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 GUGGAACAUGAGCCCUUACGCGG 24
Db 24 GTGGAACATGAAGCCCTTCAGCGG 1

RESULT 5
BD222547
LOCUS BD222547 239 bp DNA linear PAT 17-JUL-2003
DEFINITION Methods for detecting and measuring spliced nucleic acids.
ACCESSION BD222547
VERSION BD222547.1 GI:33032317
KEYWORDS JP 2002521037-A/25.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 299)
AUTHORS Harvey,R.C. and Eastman,P.S.
TITLE Methods for detecting and measuring spliced nucleic acids
JOURNAL Patent: JP 2002521037-A 25 16-JUL-2002;
GEN PROBE INC
OS Homo sapiens (human)
PN JP 2002521037-A/25
PD 16-JUL-2002
PF 23-JUL-1999 JP 2000561364
PR 23-JUL-1998 US 09/121239
PT RICHARD C HARVEY, PAUL S EASTMAN
PC C12Q1/68; C12N15/09; C12N15/00
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Db 142 GTGGAACATGAAGCCCTTCAGCGG 165

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AT12CGA/c
LOCUS AT12CGA 34125 bp DNA linear VRL 17-FEB-1997
DEFINITION Adenovirus type 12 DNA, complete genome.
ACCESSION X73487
VERSION X73487.1 GI:313361
KEYWORDS complete genome; core protein; DNA polymerase; DNA-binding protein;
endoprotease; fiber protein; hexon protein; large T-antigen;
maturation protein; minor core protein; penton protein;
peripentonal hexon-associated protein; promoter; repeat region;
small t-antigen; transcriptional activation.
SOURCE Human adenovirus type 12
ORGANISM Human adenovirus type 12
Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
REFERENCE 1 (bases 1 to 3957)
AUTHORS Tolun,A., Alestrom,P. and Pettersson,U.
TITLE Sequence of inverted terminal repetitions from different
adenoviruses: demonstration of conserved sequences and homology
between SA7 termini and SV40 DNA
JOURNAL Cell 17 (3), 705-713 (1979)

MEDLINE
PUBMED 80001962
REFERENCE 2 (bases 1 to 3957)
AUTHORS Shimojo,H., Sugimoto,K., Takanami,M., Shiroki,K., Saito,I.,
Shimojo,H., Sawada,Y., Uemizu,Y., Uesugi,S. and Fujinaga,K.
TITLE Structure and gene organization in the transformed Hind III-G
fragment of Ad12
JOURNAL Cell 20 (3), 777-786 (1980)
MEDLINE 81022638
PUBMED 6251973
REFERENCE 3 (bases 1 to 3957)
AUTHORS Shinagawa,M. and Padmanabhan,R.
TITLE Comparative sequence analysis of the inverted terminal repetitions
from different adenoviruses
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 77 (7), 3831-3835 (1980)
MEDLINE 81054665
PUBMED 6253991
REFERENCE 4
AUTHORS Kimura,T., Sawada,Y., Shinawawa,M., Shimizu,Y., Shiroki,K.,
Shimojo,H., Sugisaki,H., Takanami,M., Uemizu,Y. and Fujinaga,K.
TITLE Nucleotide sequence of the transforming early region E1b of
adenovirus type 12 DNA: structure and gene organization, and
comparison with those of adenovirus type 5 DNA
JOURNAL Nucleic Acids Res. 9 (23), 6571-6589 (1981)
MEDLINE 82105565
PUBMED 6275367
REMARK (sites)
REFERENCE 5 (bases 24334 to 24703)
AUTHORS Engler,J.A. and van Bree,M.P.
TITLE The nucleotide sequence of the gene encoding protein IVa2 in human
adenovirus type 7
JOURNAL Gene 19 (1), 71-80 (1982)
MEDLINE 83054637
PUBMED 6292051
REFERENCE 6 (bases 1488 to 3861)
AUTHORS Kimura,T.
TITLE Structure and sequence analysis of the transforming region E1b of
human adenovirus type 12
JOURNAL Sapporo Igaku Zasshi 52, 253-267 (1983)
REFERENCE 7 (bases 20966 to 22966)
AUTHORS Kruijer,W., van Schaik,F.M., Speijer,J.G. and Sussenbach,J.S.
TITLE Structure and function of adenovirus DNA binding protein:
comparison of the amino acid sequences of the Ad5 and Ad12 proteins
derived from the nucleotide sequence of the corresponding genes
JOURNAL Virology 128 (1), 140-153 (1983)
MEDLINE 83277521
PUBMED 6308889
REFERENCE 8 (bases 1 to 3957)
AUTHORS van Ormondt,H. and Galibert,F.
TITLE Nucleotide sequences of adenovirus DNAs
JOURNAL Curr. Top. Microbiol. Immunol. 110, 73-142 (1984)
MEDLINE 85002829
PUBMED 6383725
REFERENCE 9 (bases 4831 to 10470)
AUTHORS Shu,L.M., Hong,J.S., Wei,Y.F. and Engler,J.A.
TITLE Nucleotide sequence of the genes encoded in early region 2b of
human adenovirus type 12
JOURNAL Gene 46 (2-3), 187-195 (1986)
MEDLINE 87106854
PUBMED 3803925
REFERENCE 10 (bases 1 to 530)
AUTHORS Shibata,H., Zheng,J.H., Koikeda,S., Masamune,Y. and Nakanishi,Y.
TITLE Cis- and trans-acting factors for transcription of the adenovirus
12 E1A gene
JOURNAL Biochim. Biophys. Acta 1007 (2), 184-191 (1989)
MEDLINE 89150250
PUBMED 2522011
REFERENCE 11
AUTHORS Juttermann,R., Weyer,U. and Doerfler,W.
TITLE Defect of adenovirus type 12 replication in hamster cells: absence
of transcription of viral virus-associated and L1 RNAs
JOURNAL J. Virol. 63 (8), 3535-3540 (1989)
MEDLINE 89311650

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PUBMED 2746738
REMARK (sites)
REFERENCE 12
AUTHORS Zock,C., Iselt,A. and Doerfler,W.
TITLE A unique mitigator sequence determines the species specificity of
the major late promoter in adenovirus type 12 DNA
JOURNAL J. Virol. 67 (2), 682-693 (1993)
MEDLINE 93124560
PUBMED 8419643
REMARK (sites)
REFERENCE 13
AUTHORS Sprengel,J., Schmitz,B., Heuss-Neitzel,D., Zock,C. and Doerfler,W.
TITLE Nucleotide sequence of human adenovirus type 12 DNA: comparative
functional analysis
JOURNAL J. Virol. 68 (1), 379-389 (1994)
MEDLINE 94076430
PUBMED 8254750
REFERENCE 14 (bases 1 to 34125)
AUTHORS Sprengel,J.
TITLE Direct Submission
JOURNAL Submitted (21-JUN-1993) J. Sprengel, Institute of Genetics/Dept.
Virology, Weyertal 121, 50931 Cologne 41, FRG
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/function="E1b promoter region (-499 to +100)"
1542. .2033
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/product="E1B protein, small T-antigen"

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EYREFENILADCPGLLADLCYHLVQEKVRSLSDFSGVTRVASTAFATILDK
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VEK"
variation
1740
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variation
1742
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1847. .3295
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/codon_start=1
/product="E1B protein, large T-antigen"
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/db_xref="SWISS-PROT:P04491"
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/replace="gcg"
2417. .2418
/citation=[6]
Query Match 75.0%; Score 18; DB 14; Length 34125;
Best Local Similarity 83.3%; Pred. No. 4.6;
Matches 15; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 3 GGAAACAUGAAGCCCUCA 20
|||||:|||||:|
Db 4015 GGAACATGAAGCCCTTCA 3998
RESULT 7
AC132177 238483 bp DNA linear HTG 10-OCT-2002
LOCUS Rattus norvegicus clone CH230-165B1, WORKING DRAFT SEQUENCE, 6
DEFINITION unordered pieces.
AC132177
AC132177.4 GI:23683197
VERSION HTG; HTGS PHASE1; HTGS DRAFT; HTGS_FULLTOP.
KEYWORDS Rattus norvegicus (Norway rat)
SOURCE Rattus norvegicus
ORGANISM Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 238483)
AUTHORS Muzny,D,Marie., Metzker,M.Lee., Abramson,S., Adams,C., Alder,J.,
Allen,C., Allen,H., Alsbrooks,S., Amin,A., Anguiano,D.,
Anyalebechi,V., Ayagi,A., Ayodeji,M., Baca,E., Baden,H.,
Baldwin,D., Bandaranaike,D., Barber,M., Barnstead,M., Benahmed,F.,
Biswalo,K., Blair,J., Blankenburg,K., Blyth,P., Brown,M.,
Bryant,N., Buhay,C., Burch,P., Burrell,K., Calderon,E.,
Cardenas,V., Carter,K., Cavazos,I., Ceasar,H., Center,A.,
Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Y., Chen,Z., Chu,J.,
Cleveland,C., Cockrell,R., Cox,C., Coyle,M., Cree,A., D'Souza,L.,
Davila,M.L., Davis,C., Davy-Carroll,L., De Anda,C., Dederich,D.,
Delgado,O., Denson,S., Deramo,C., Ding,Y., Dinh,H., Divya,K.,
Draper,H., Dugan-Rocha,S., Dunn,A., Durbin,K., Duval,B., Eaves,K.,
Egan,A., Escotto,M., Eugene,C., Evans,C.A., Falls,T., Fan,G.,

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Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P., Frazer, C.M., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Garza, M., Gregor, E., Geer, K., Gill, R., Grady, M., Grady, W., Guevara, W., Gunaratne, P., Haaland, W., Hamill, C., Hamilton, C., Hamilton, K., Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J., Hernandez, R., Hines, S., Hladun, S.L., Hodgson, A., Hoques, M., Hollins, B., Howells, S., Hulyk, S., Hume, J., Idlebird, D., Jackson, A., Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Joliviet, A., Karpathy, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C., Kowis, C., Kratt, C.L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J., Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J., Lorensu, L., Louise, H., Lozano, R., Lu, X., Ma, J., Maheshwari, M., Mahindartne, M., Mahmoud, M., Malloy, K., Mangum, A., Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, E., Mawhinney, S., McLeod, M.P., McNeill, T.Z., Meenen, E., Milosavljevic, A., Miner, G.S., Minja, E., Montemayor, J., Moore, S., Morgan, M., Morris, K., Morris, S., Munidasa, M., Murphy, M., Nair, L., Nankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S., Parks, K., Pasceriak, S., Paul, H., Perez, A., Perez, L., Prannkoch, C., Plopper, F., Polindexter, A., Popovic, D., Primus, E., Pu, L., Puzo, M., Quiroz, J., Rachlin, E., Reeves, K., Regier, M.A., Reigh, R., Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F., Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S.J., Sanders, W., Savary, G., Scherer, S., Scott, G., Shatsman, S., Shen, H., Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smajs, D., Snead, A., Sodargren, E., Song, X.-Z., Sorelle, R., Sosa, J., Steimle, M., Strong, R., Sutton, A., Svatek, A., Taber, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Usmani, K., Valas, R., Vera, V., Villasana, D., Waldron, L., Walker, B., Wang, J., Wang, Q., Wang, S., Warren, J., Warren, R., Wei, X., White, F., Williams, G., Willson, R., Wleczek, R., Wooden, H., Worley, K., Wright, D., Wright, J., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von Niederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O., Weinstock, G. and Gibbs, R.A.

Direct Submission  
Unpublished  
2 (bases 1 to 238483)  
Rat Genome Sequencing Consortium.  
Direct Submission  
Submitted (30-AUG-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA  
3 (bases 1 to 238483)  
Rat Genome Sequencing Consortium.  
Direct Submission  
Submitted (10-OCT-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA  
On Oct 10, 2002 this sequence version replaced gi:22725823.  
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome-shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.

----- Genome Center  
Center: Baylor College of Medicine  
Center code: BCM  
Web site: http://www.hgsc.bcm.tmc.edu/  
Contact: hgsc-help@bcm.tmc.edu  
----- Project Information  
Center project name: GOVP  
Center clone name: CH230-165B1  
----- Summary Statistics  
Assembly program: Phrap; version 0.990329

Consensus quality: 22924 bases at least Q40  
Consensus quality: 22513 bases at least Q30  
Consensus quality: 226732 bases at least Q20  
Estimated insert size: 226330; sum-of-contigs estimation  
Quality coverage: 7x in Q20 bases; sum-of-contigs estimation

-----  
\* NOTE: Estimated insert size may differ from sequence length  
\* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank\_draft\_data.html).  
\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 6 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.

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3208 3307: gap of unknown length  
3308 184048: contig of 180741 bp in length  
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197236 197335: gap of unknown length  
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227087 227186: gap of unknown length  
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228537 238483: contig of 9947 bp in length.

Location/Qualifiers  
1. 238483  
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194764. .195895  
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misc\_feature  
ORIGIN

Query Match 75.0%; Score 18; DB 2; Length 238483;  
Best Local Similarity 77.8%; Pred. No. 3.8;  
Matches 14; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 2 UGGAACAUGAGCCCUUC 19  
DB 13348 TGGACATGAGCCCTTC 13365

RESULT 8  
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LOCUS  
DEFINITION  
AC087634 Homo sapiens chromosome 15 clone RP11-302D8 map 15, LOW-PASS  
SEQUENCE SAMPLING.  
AC087634 AC087634.1 GI:12229409  
VERSION  
KEYWORDS  
HTG; HTGS\_PHASE0.  
SOURCE  
Homo sapiens (human)  
ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE  
1 (bases 1 to 60456)  
Birren, B., Linton, L., Nusbaum, C. and Lander, E.  
AUTHORS  
TITLE  
Homo sapiens chromosome 15, clone RP11-302D8  
JOURNAL  
REFERENCE  
2 (bases 1 to 60456)  
Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, S., Barna, N., Bastien, V., Boguslavsky, L., Boukhalter, B., Brown, A., Camarata, J., Campopiano, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Fato, S., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Headford, A., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Karatas, A., LaRocque, K., Lamazares, R., Landers, T.,

Lehoczyk, J., Levine, R., Liu, G., Maclean, C., Macdonald, P.,  
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 Travers, M., Travis, N., Trigglio, J., Vassiliev, H., Viel, R., Vo, A.,  
 Wembek, L., Zimmer, A., Zody, M.,  
 Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G., Zainoun, J.,  
 Direct Submission

Submitted (15-JAN-2001) Whitehead Institute/MIT Center for Genome  
 Research, 320 Charles Street, Cambridge, MA 02141, USA  
 All repeats were identified using RepeatMasker:  
 Smit, A.F.A. & Green, P. (1996-1997)  
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

----- Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIBR

Web site: <http://www-seq.wi.mit.edu>

Contact: [sequence\\_submissions@genome.wi.mit.edu](mailto:sequence_submissions@genome.wi.mit.edu)

----- Project Information

Center project name: L11917

Center clone name: 302\_D\_8

-----  
 \* NOTE: This record contains 72 individual  
 \* sequencing reads that have not been assembled into  
 \* contigs. Runs of N are used to separate the reads  
 \* and the order in which they appear is completely  
 \* arbitrary. Low-pass sequence sampling is useful for  
 \* identifying clones that may be gene-rich and allows  
 \* overlap relationships among clones to be deduced.  
 \* However, it should not be assumed that this clone  
 \* will be sequenced to completion. In the event that  
 \* the record is updated, the accession number will  
 \* be preserved.

1 785: contig of 785 bp in length  
 \* 786 885: gap of 100 bp  
 \* 886 1621: contig of 736 bp in length  
 \* 1622 1721: gap of 100 bp  
 \* 1722 2493: contig of 772 bp in length  
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 \* 2594 3335: contig of 742 bp in length  
 \* 3336 3435: gap of 100 bp  
 \* 3436 4147: contig of 712 bp in length  
 \* 4148 4247: gap of 100 bp  
 \* 4248 4982: contig of 735 bp in length  
 \* 4983 5082: gap of 100 bp  
 \* 5083 5805: contig of 723 bp in length  
 \* 5806 5905: gap of 100 bp  
 \* 5906 6635: contig of 730 bp in length  
 \* 6636 6735: gap of 100 bp  
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 \* 7461 7560: gap of 100 bp  
 \* 7561 8283: contig of 723 bp in length  
 \* 8284 8383: gap of 100 bp  
 \* 8384 9142: contig of 759 bp in length  
 \* 9143 9242: gap of 100 bp  
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 \* 9976 10075: gap of 100 bp  
 \* 10076 10813: contig of 738 bp in length  
 \* 10814 10913: gap of 100 bp  
 \* 10914 11649: contig of 736 bp in length  
 \* 11650 11749: gap of 100 bp  
 \* 11750 12481: contig of 732 bp in length  
 \* 12482 12581: gap of 100 bp  
 \* 12582 13315: contig of 734 bp in length  
 \* 13316 13415: gap of 100 bp  
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14252 14975: contig of 724 bp in length  
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 \* 15815 15914: gap of 100 bp  
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 \* 17633 18362: contig of 730 bp in length  
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 \* 20152 20880: contig of 729 bp in length  
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 \* 25160 25259: gap of 100 bp  
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 \* 28488 28587: gap of 100 bp  
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 \* 29325 29424: gap of 100 bp  
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 \* 36913 37012: gap of 100 bp  
 \* 37013 37770: contig of 758 bp in length  
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 \* 37871 38611: contig of 741 bp in length  
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 \* 42880 42979: gap of 100 bp  
 \* 42980 43712: contig of 733 bp in length  
 \* 43713 43812: gap of 100 bp  
 \* 43813 44509: contig of 697 bp in length  
 \* 44510 44511: gap of 100 bp  
 \* 44512 45341: contig of 732 bp in length

TITLE  
 JOURNAL

COMMENT

```

* 45342 45441: gap of 100 bp
* 45442 contig of 727 bp in length
* 46168 contig of 100 bp
* 46268 contig of 752 bp in length
* 46269 contig of 752 bp in length
* 47021 47120: gap of 100 bp
* 47121 47867: contig of 747 bp in length
* 47868 47967: gap of 100 bp
* 47968 48712: contig of 745 bp in length
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* 48813 49531: contig of 719 bp in length
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* 50375 50474: gap of 100 bp
* 50475 51198: contig of 724 bp in length
* 51199 51298: gap of 100 bp
* 51299 52022: contig of 724 bp in length
* 52023 52122: gap of 100 bp
* 52123 52898: contig of 766 bp in length
* 52899 52988: gap of 100 bp
* 52989 53726: contig of 737 bp in length
* 53726 53826: gap of 100 bp
* 53826 54566: contig of 741 bp in length
* 54567 54666: gap of 100 bp
* 54667 55445: contig of 779 bp in length
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* 55446 56281: contig of 736 bp in length
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* 57127 57226: gap of 100 bp
* 57227 57965: contig of 739 bp in length
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Query Match 70.8%; Score 17; DB 2; Length 60456;
Best Local Similarity 76.5%; Pred. No. 17;
Matches 13; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 2 UGACACUAGAGCCU 18
DB 9941 TGGACATGAGCCCTT 9925

RESULT 9
AL805925
LOCUS AL805925.6 GI:22531408 linear ROD 24-AUG-2002
DEFINITION Mouse DNA sequence from clone RP23-210E20 on chromosome X, complete
sequence.
ACCESSION AL805925
VERSION AL805925.6
KEYWORDS HTG.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 104244)
AUTHORS Johnson, C.
TITLE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
JOURNAL Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REMARK Submitted (24-AUG-2002) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Aug 27, 2002 this sequence version replaced gi:22416054.
----- Genome Center
Center: Wellcome Trust Sanger Institute
Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
-----
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as plasmid subclones or more than one M13 subclone; and the
assembly was confirmed by restriction digest. The following
abbreviations are used to associate primary accession numbers given
in the feature table with their source databases: Em:, EMBL; SW:,
SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP
database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP23-210E20 is
from the RPCI-23 Mouse PAC Library
constructed by the group of Pieter de Jong.
For further details see http://www.chori.org/bacpac/home.htm
VECTOR: pBACE3.6.

FEATURES
Location/Qualifiers
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1..104244
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/mol_type="genomic DNA"
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/chromosome="X"
/clone="RP23-210E20"
/clone_lib="RPCI-23"

ORIGIN
Query Match 70.8%; Score 17; DB 10; Length 104244;
Best Local Similarity 82.4%; Pred. No. 16;
Matches 14; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 5 AACACGAGCCUUCAG 21
DB 2162 AACATGAGCCCTTCAG 2178

RESULT 10
AL954170/c
LOCUS AL954170.4 GI:33636222 linear ROD 13-AUG-2003
DEFINITION Mouse DNA sequence from clone RP23-467H15 on chromosome 2, complete
sequence.
ACCESSION AL954170
VERSION AL954170.4
KEYWORDS HTG.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 138152)
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
North, P., Leaves, N., Greystrom, J., Coppola, M., Manjunath, S.,
Russell, E., Smith, M., Strachan, G., Tofts, C., Boal, E., Cobley, V.,
Hunter, G., Kimberley, C., Thomas, D., Cave-Berry, L., Weston, P. and
Botcherby, M.R.M.
TITLE Direct Submission
JOURNAL Submitted (13-AUG-2003) Mouse Sequencing Group, HGMP-PC, Hinxton,
Cambridge, CB10 1SB, UK. E-mail enquiries:- mrbotche@hgmp.mrc.ac.uk
or pnoth@hgmp.mrc.ac.uk
HGMP-RC part of the UK Mouse Sequencing Consortium
On Aug 13, 2003 this sequence version replaced gi:32567581.
----- Genome Center
Center: UK Medical Research Council
Center code: UK-MRC
Web site: http://mrcseq.har.mrc.ac.uk
Contact: mouseq@har.mrc.ac.uk
-----
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such

```

as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em, EMBL; Sw, SWISSPROT; Tr, TREMBL; Wp, WORMPEP; Information on the WORMPEP database can be found at [http://www.sanger.ac.uk/Projects/C\\_elegans/wormpep](http://www.sanger.ac.uk/Projects/C_elegans/wormpep) RP23-467H15 is from the RPCI-23 Mouse BAC library

constructed by the group of Pieter de Jong.

For further details see <http://www.chori.org/bacpac/home.htm>

VECTOR: pBACE3.6

Sequence from the Mouse Genome Sequencing Consortium whole genome shotgun may have been used to confirm this sequence. Sequence data from the whole genome shotgun alone has only been used where it has a phred quality of at least 30.

## FEATURES

source

```

1. .138152
   Location/Qualifiers
     /organism="Mus musculus"
     /mol_type="genomic DNA"
     /db_xref="taxon:10090"
     /chromosomes="2"
     /clone_lib="RP23-467H15"
     /clone_lib="RPCI-23"

```

## ORIGIN

```

Query Match          70.8%; Score 17; DB 10; Length 138152;
Best Local Similarity 82.4%; Pred. No. 16;
Matches 14; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

```

QY 4 GAACAUGAGCCCUCA 20

```

|||||:|||||:|||||

```

Db 137169 GAACATGAGCCCTTCA 137153

## RESULT 11

BX248232

LOCUS

```

DEFINITION
  BX248232             152804 bp    DNA    linear    HTG 07-NOV-2003
  Danio rerio clone CH211-23215, WORKING DRAFT SEQUENCE, 3 unordered
  pieces.

```

ACCESSION

BX248232.6 GI:38228942

VERSION

HTG; HTGS PHASE1; HTGS ACTIVEFIN; HTGS\_DRAFT; HTGS\_FULLTOP.

KEYWORDS

SOURCE

ORGANISM

```

  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
  Cypriniformes; Cyprinidae; Danio.
  1 (bases 1 to 152804)
  Giselle.H.

```

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

```

  Submitted (06-NOV-2003) Wellcome Trust Sanger Institute, Hinxton,
  Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
  zfish-help@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
  On Nov 7, 2003 this sequence version replaced gi:38141652.
  ----- Genome Center
  Center: Wellcome Trust Sanger Institute
  Center code: SC
  Web site: http://www.sanger.ac.uk
  Contact: zfish-help@sanger.ac.uk
  ----- Project Information
  Center project name: zC23215
  ----- Summary Statistics
  Assembly program: XGAP4; version 4.5
  Chemistry: Dye-terminator; 100% of reads
  Consensus quality: 152578 bases at least Q40
  Consensus quality: 152597 bases at least Q30
  Consensus quality: 152598 bases at least Q20
  Insert size: 152604; sum-of-contigs
  Insert size: 161454; 2.1% error; agarose-fp
  Quality coverage: 10.26x in Q20 bases; sum-of-contigs Quality
  coverage: 9.69x in Q20 bases; agarose-fp

```

```

-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 3 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

```

```

* 1 86810: contig of 86810 bp in length
* 86811 86910: gap of 100 bp
* 86911 138019: contig of 51109 bp in length
* 138020 138119: gap of 100 bp
* 138120 152804: contig of 14685 bp in length.

```

## FEATURES

source

```

1. .152804
   Location/Qualifiers
     /organism="Danio rerio"
     /mol_type="genomic DNA"
     /db_xref="taxon:7955"
     /clone_lib="CH211-23215"
     /clone_lib="CHORI-211"
     /note="assembly_fragment:02232"
     /fragment_chain:1"
     1. .86810
     /note="assembly_fragment:00979"
     /fragment_chain:1"
     138120..152804
     /note="assembly_fragment:01208"
     /fragment_chain:1"

```

## ORIGIN

```

Query Match          70.8%; Score 17; DB 2; Length 152804;
Best Local Similarity 82.4%; Pred. No. 16;
Matches 14; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

```

QY 5 AACAUAGAGCCCUCA 21

```

|||||:|||||:|||||

```

Db 137360 AACATGAGCCCTTCAG 137376

## RESULT 12

AC109200

LOCUS

```

DEFINITION
  AC109200             162077 bp    DNA    linear    HTG 19-NOV-2003
  Mus musculus chromosome 8 clone RP23-26G21 map 8, WORKING DRAFT
  SEQUENCE, 6 ordered pieces.

```

ACCESSION

AC109200.5 GI:38424184

VERSION

HTG; HTGS PHASE2; HTGS\_DRAFT; HTGS\_FULLTOP.

KEYWORDS

SOURCE

ORGANISM

```

  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
  1 (bases 1 to 162077)
  Birren,B., Nusbaum,C. and Lander,E.
  Mus musculus chromosome 8, clone RP23-26G21
  Unpublished

```

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

```

  2 (bases 1 to 162077)
  Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
  Anderson,S., Barna,N., Bastien,V., Boguslavsky,I., Boukhgalter,B.,
  Brown,A., Camarata,J., Campopiano,A., Chang,J., Chazaro,B.,
  Choquel,Y., Collangelo,M., Collins,S., Collymore,A., Cook,A.,
  Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S.,
  Ferreira,P., Fitzhugh,W., Gage,D., Galagan,J., Gardyna,S.,
  Ginde,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N.,
  Hagos,B., Horton,L., Hulme,W., Iliiev,I., Johnson,R., Jones,C.,
  Kamat,A., Karatas,A., Kells,C., Lacroque,K., Lamazares,R.,
  Landers,T., Lehoczy,J., Levine,N., Liu,G., MacLean,C.,
  Macdonald,P., Major,J., Marquis,N., Matthews,C., McCarthy,M.,
  McEwan,P., McKernan,K., Meldrum,J., Meneus,L., Mihova,T.,
  Mlenga,V., Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C.,
  Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D., Oliver,J.,
  Peterson,K., Phunkhang,P., Pierre,N., Pollara,V., Raymond,C.,

```

Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schuback, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Travis, N., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

Direct Submission  
Submitted (03-FEB-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA  
3 (bases 1 to 162077)

Birren, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N., Anderson, M., Arachchi, H. M., Barna, N., Bastien, V., Bloom, T., Boguslavsky, L., Boukagter, B., Camarata, J., Chang, J., Choepel, V., Collymore, A., Cook, A., Cooke, P., Corum, B., DeArellano, K., Diaz, J. S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Faro, S., Ferreira, P., Fitzgerald, M., Gage, D., Galagan, J., Gardyna, S., Graham, L., Grand-pierre, N., Hafez, N., Hagopian, D., Hagos, B., Hall, J., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kellis, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., Lui, X., Mabbitt, R., MacLean, C., MacDonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M., Meldrim, J., Menues, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Rachupka, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schuback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Venkataraman, V. S., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

Direct Submission  
Submitted (19-NOV-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA  
On Nov 19, 2003 this sequence version replaced gi:21313786.  
All repeats were identified using RepeatMasker:  
Smit, A.F.A. & Green, P. (1996-1997)  
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

TITLE  
JOURNAL  
COMMENT

Center: Whitehead Institute/ MIT Center for Genome Research  
Center code: WIBR  
Web site: <http://www-seq.wi.mit.edu>  
Contact: [sequence\\_submissions@genome.wi.mit.edu](mailto:sequence_submissions@genome.wi.mit.edu)

----- Project Information  
Center project name: L20459  
Center clone name: 26 G 21

----- Summary Statistics  
Sequencing vector: Plasmid; n/a; 100% of reads  
Chemistry: Dye-terminator Big Dye; 100% of reads  
Assembly program: Phrap; version 0.960731  
Consensus quality: 160977 bases at least Q40  
Consensus quality: 161390 bases at least Q30  
Consensus quality: 161524 bases at least Q20  
Insert size: 157000; agarose-ep  
Insert size: 161577; sum-of-contigs  
Quality coverage: 13.8 in Q20 bases; agarose-ep  
Quality coverage: 13.4 in Q20 bases; sum-of-contigs

-----  
\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 6 contigs. Gaps between the contigs  
\* are represented as runs of N. The order of the pieces  
\* is believed to be correct as given, however the sizes  
\* of the gaps between them are based on estimates that have  
\* provided by the submitter.  
\* This sequence will be replaced  
\* by the finished sequence as soon as it is available and  
\* the accession number will be preserved.  
\* 1 53642: contig of 53642 bp in length  
\* 53643 53742: gap of 100 bp  
\* 53743 54202: contig of 460 bp in length  
\* 54203 54302: gap of 100 bp  
\* 54303 55174: contig of 872 bp in length  
\* 55175 55274: gap of 100 bp

\* 55275 127105: contig of 71831 bp in length  
\* 127106 127205: gap of 100 bp  
\* 127206 152575: contig of 25370 bp in length  
\* 152576 152675: gap of 100 bp  
\* 152676 162077: contig of 9402 bp in length.

FEATURES  
source  
1..162077  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:10090"  
/chromosome="8"  
/map="8"  
/clone="RP23-26G21"  
/clone\_lib="RPCI-23 Female Mouse BAC"  
1..53642  
/note="assembly\_fragment"  
clone end:SP6  
vector\_side:left  
53743..54202  
/note="assembly\_fragment"  
54303..55174  
/note="assembly\_fragment"  
55275..127105  
/note="assembly\_fragment"  
127206..152575  
/note="assembly\_fragment"  
152676..162077  
/note="assembly\_fragment"  
clone end:T7  
vector\_side:right

ORIGIN

Query Match 70.8%; Score 17; DB 2; Length 162077;  
Best Local Similarity 82.4%; Pred.No. 16;  
Matches 14; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 GUGGAACAUGAAGCCCU 17  
|:|||||:|||||:  
DB 95197 GTGGAACATGAAGCCCT 95213

RESULT 13  
AL606494/c

LOCUS AL606494 184317 bp DNA linear ROD 12-JUL-2003  
DEFINITION Mouse DNA sequence from clone RP23-198B6 on chromosome 2, complete sequence.

ACCESSION AL606494  
VERSION AL606494.3 GI:32567580  
KEYWORDS HTG.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus

REFERENCE  
AUTHORS North, P., Leaves, N., Greystrom, J., Coppola, M., Manjunath, S., Russell, E., Smith, M., Strachan, G., Tofts, C., Boal, E., Cobley, V., Hunter, G., Kimberley, C., Thomas, D., Cave-Berry, L., Weston, P. and Botcherby, M.R.M.  
Direct Submission  
Submitted (12-JUL-2003) Mouse Sequencing Group, HGMPC-RC, Hinxton, Cambridge, CB10 1SB, UK. E-mail enquiries:- [mrbotche@hgmpr.mrc.ac.uk](mailto:mrbotche@hgmpr.mrc.ac.uk) or [pnothhgmpr.mrc.ac.uk](mailto:pnothhgmpr.mrc.ac.uk)  
HGMPC-RC part of the UK Mouse Sequencing Consortium  
On Jul 12, 2003 this sequence version replaced gi:15723837.

TITLE  
JOURNAL  
REMARK  
COMMENT  
----- Genome Center  
Center: UK Medical Research Council  
Center code: UK-MRC  
Web site: <http://mrcseq.har.mrc.ac.uk>  
Contact: [mouseq@har.mrc.ac.uk](mailto:mouseq@har.mrc.ac.uk)  
-----

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the

variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em: EMBL; Sw: SWISSPROT; Tr: TrEMBL; Wp: WORMPEP; Information

on the WORMPEP database can be found at

[http://www.sanger.ac.uk/Projects/C\\_elegans/wormpep](http://www.sanger.ac.uk/Projects/C_elegans/wormpep) RP23-198B6 is

from the RPCI-23 Mouse BAC library

constructed by the group of Pieter de Jong.

For further details see <http://www.chori.org/bacpac/home.htm>

VECTOR: pBACE3.6

Sequence from the Mouse Genome Sequencing Consortium whole genome shotgun may have been used to confirm this sequence. Sequence data from the whole genome shotgun alone has only been used where it has a phred quality of at least 30.

#### FEATURES

source

```
1. .184317
   /organism="Mus musculus"
   /mol_type="genomic DNA"
   /db_xref="taxon:10090"
   /chromosome="2"
   /clone="RP23-198B6"
   /clone_lib="RPCI-23"
```

#### ORIGIN

```
Query Match      70.8%; Score 17; DB 10; Length 184317;
Best Local Similarity 82.4%; Pred. No. 15;
Matches 14; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      4 GAACAGAGCCCUCA 20
        |||||:|||||:|
Db      1748 GAACATGAGCCCTTCA 1732
```

#### RESULT 14

AC096363/c

LOCUS

DEFINITION

AC096363

HTG.

AC096363.8 GI:32362332

Rattus norvegicus (Norway rat)

AC096363

HTG.

AC096363.8 GI:32362332

Rattus norvegicus (Norway rat)

AC096363

HTG.

AC096363.8 GI:32362332

Rattus norvegicus (Norway rat)

AC096363

HTG.

AC096363.8 GI:32362332

Rattus norvegicus (Norway rat)

AC096363

HTG.

AC096363.8 GI:32362332

Rattus norvegicus (Norway rat)

AC096363

HTG.

AC096363.8 GI:32362332

Rattus norvegicus (Norway rat)

AC096363

HTG.

AC096363.8 GI:32362332

Rattus norvegicus (Norway rat)

AC096363

HTG.

AC096363.8 GI:32362332

Rattus norvegicus (Norway rat)

Gunaratne, P., Haaland, W., Hamil, C., Hamilton, C., Hamilton, K., Harvey, Y., Haylak, P., Hawes, A., Henderson, N., Hernandez, J., Hernandez, R., Hines, S., Hladun, S.L., Hodgson, A., Hogues, M., Hollins, B., Howells, S., Hulyk, S., Hume, J., Idlebird, D., Jackson, A., Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jolivet, A., Karpathy, S., Kelly, S., Khan, Z., King, L., Kovar, C., Kowis, C., Kraft, C.L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J., Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J., Lorenshewa, L., Louisedge, H., Lozano, R.J., Lu, X., Ma, J., Maheshwari, M., Mahindartne, M., Mahmoud, M., Malloy, K., Mangum, A., Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, E., Mawhinney, S., McLeod, M., McNeill, T., Meenen, E., Milosavljevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S., Morgan, M., Morris, K., Morris, S., Munidasa, M., Murphy, M., Nair, L., Nankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S., Nwaokeme, O., Okwuonu, G., Olanunsiogun, A., Pal, S., Parks, K., Pasternak, S., Paul, H., Perez, A., Perez, L., Pfannkuch, C., Plopper, F., Poindeexter, A., Popovic, D., Primus, E., Pu, L.-L., Puazo, M., Quiroz, J., Rachlin, E., Reeves, K., Regier, M.A., Reigh, R., Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F., Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S.J., Sanders, W., Savary, G., Scherer, S., Scott, G., Shatsman, S., Shen, H., Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smajls, D., Sneed, A., Sodergren, E., Song, X.-Z., Sorelle, R., Sosa, J., Steimle, M., Strong, R., Sutton, A., Svatek, A., Tabor, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Usmani, K., Valas, R., Vera, V., Villalana, D., Waldron, L., Walker, B., Wang, J., Wang, Q., Wang, S., Warren, J., Warren, R., Wei, X., White, F., Williams, G., Willson, R., Wleczyk, R., Wooden, H., Worley, K., Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von Niederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O., Weinstock, G. and Gibbs, R.A.

Direct Submission

Unpublished

2 (bases 1 to 215356)

Worley, K.C.

Direct Submission

Submitted (17-SEP-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

3 (bases 1 to 215356)

Direct Submission

Submitted (10-MAY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

4 (bases 1 to 215356)

Worley, K.C.

Direct Submission

Submitted (01-JUL-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On Jul 1, 2003 this sequence version replaced gi:30521822.

Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality does not meet this standard, it will be indicated in the annotation.

Location/Qualifiers

1. .215356

/organism="Rattus norvegicus"

/mol\_type="genomic DNA"

/db\_xref="taxon:10116"

/chromosome="1"

/clone="CH230-54P17"

805. .1138

/rpt\_family="LIMC2"

1148. .1232

/rpt\_family="PB1D9"

complement(1386..1506)

/rpt\_family="MTD"

1507. .1734

/rpt\_family="LIMC2"

#### FEATURES

source

repeat\_region

805. .1138

/rpt\_family="LIMC2"

1148. .1232

/rpt\_family="PB1D9"

complement(1386..1506)

/rpt\_family="MTD"

1507. .1734

/rpt\_family="LIMC2"

#### COMMENT

On Jul 1, 2003 this sequence version replaced gi:30521822. Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality does not meet this standard, it will be indicated in the annotation.

#### FEATURES

source

repeat\_region

805. .1138

/rpt\_family="LIMC2"

1148. .1232

/rpt\_family="PB1D9"

complement(1386..1506)

/rpt\_family="MTD"

1507. .1734

/rpt\_family="LIMC2"



```

repeat_region      complement(1795..1839)
repeat_region      /rpt_family="PB1D7"
repeat_region      1897..2013
repeat_region      /rpt_family="PB1D9"
repeat_region      2030..2186
repeat_region      /rpt_family="B3"
repeat_region      2187..2246
repeat_region      /rpt_family="CA)n"
repeat_region      2247..2259
repeat_region      /rpt_family="B3"
repeat_region      2279..2348
repeat_region      /rpt_family="TG)n"
repeat_region      complement(2411..2531)
repeat_region      /rpt_family="B3F"
repeat_region      complement(2485..2539)
repeat_region      /rpt_family="B4A"
repeat_region      2540..2690
repeat_region      /rpt_family="RLTR28B"
repeat_region      2660..2885
repeat_region      /rpt_family="RLTR28"
repeat_region      complement(2904..3118)
repeat_region      /rpt_family="B3"
repeat_region      3120..3148
repeat_region      /rpt_family="(TTT)TG)n"
repeat_region      3164..3238
repeat_region      /rpt_family="PB1D7"
repeat_region      complement(4251..4341)
repeat_region      /rpt_family="RSINE1"
repeat_region      complement(4340..4439)
repeat_region      /rpt_family="B3A"
repeat_region      complement(4459..4662)
repeat_region      /rpt_family="B3A"
repeat_region      5152..5367
repeat_region      /rpt_family="ID_B1"
repeat_region      5385..5596
repeat_region      /rpt_family="B4A"
repeat_region      5591..5937
repeat_region      /rpt_family="MTC"
repeat_region      5938..5989
repeat_region      /rpt_family="B4A"
repeat_region      6078..6129
repeat_region      /rpt_family="ID_B1"
repeat_region      6130..6147
repeat_region      /rpt_family="BC1_Rn"
repeat_region      6155..6291
repeat_region      /rpt_family="RSINE1"
repeat_region      6320..6354
repeat_region      /rpt_family="(A)n"
repeat_region      7540..7750
repeat_region      /rpt_family="ID_B1"
repeat_region      7760..7963
repeat_region      /rpt_family="B3"
repeat_region      7985..8082
repeat_region      /rpt_family="ID_Rn"
repeat_region      8431..8495
repeat_region      /rpt_family="tRNA-Ala-GCY_"
repeat_region      8502..8526
repeat_region      /rpt_family="(TG)n"
repeat_region      8527..8541
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Query Match      70.8%; Score 17; DB 10; Length 215356;
Best Local Similarity 82.4%; Pred. No. 15;
Matches 14; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

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Db      34030 ACATGAAGCCCTTCAGC 34014
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RESULT 15
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LOCUS      215958 bp DNA linear HTG 24-JAN-2003
DEFINITION Mus musculus clone RP23-9K20, WORKING DRAFT SEQUENCE, 5 unordered
pieces.
ACCESSION AC102091
VERSION AC102091.3 GI:27884970
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 215958)
AUTHORS Birren,B., Nusbaum,C. and Lander,E.
TITLE Mus musculus, clone RP23-9K20
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 215958)
AUTHORS Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
Anderson,S., Barna,N., Bastien,V., Boguski,K., Brown,A., Brown,A.,
Brown,A., Camarata,J., Campopiano,A., Chang,J., Chazaro,B.,
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Lamazaras,R., Landers,T., Lehoczy,J., Levine,R., Liu,G.,
MacLean,C., Macdonald,P., Major,J., Marquis,N., Matthews,C.,
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Seaman,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N.,
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Topham,K., Travers,M., Travis,N., Trigilio,J., Vassiliev,H.,

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TITLE  
 JOURNAL  
 Direct Submission  
 Submitted (23-NOV-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA  
 3 (bases 1 to 215958)  
 Birren, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N., Anderson, S., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Boguelavkiy, L., Boukhalter, B., Camarata, J., Chang, J., Choepel, Y., Collymore, A., Cook, A., Cooke, P., Corum, B., DeArellano, K., Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Faro, S., Ferreira, P., Fitzgerald, M., Gage, D., Galagan, J., Gardyna, S., Graham, L., Grand-Pierre, N., Hafez, N., Hagopian, D., Hagos, B., Hall, J., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., Lui, A., Mabbitt, R., Maclean, C., Macdonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M., Melgrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Rachupka, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schuback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.  
 Direct Submission  
 Submitted (24-JAN-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA  
 On Jan 24, 2003 this sequence version replaced gi:22381287.  
 All repeats were identified using RepeatMasker:  
 Smit, A.F.A. & Green, P. (1996-1997)  
 http://ftp.genome.washington.edu/RM/RepeatMasker.html

----- Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIBR

Web site: http://www-seq.wi.mit.edu

Contact: sequence\_submissions@genome.wi.mit.edu

----- Project Information

Center project name: L18028

Center clone name: 9\_K\_20

----- Summary Statistics

Sequencing vector: Plasmid; n/a; 100% of reads

Chemistry: Dye-terminator Big Dye; 100% of reads

Assembly program: Phrap; version 0.960731

Consensus quality: 214869 bases at least Q40

Consensus quality: 215183 bases at least Q30

Consensus quality: 215314 bases at least Q20

Insert size: 220000; agarose-fp

Insert size: 215358; sum-of-contigs

Quality coverage: 11.4 in Q20 bases; agarose-fp

Quality coverage: 11.6 in Q20 bases; sum-of-contigs

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\* NOTE: This is a 'working draft' sequence. It currently  
 \* consists of 5 contigs. The true order of the pieces  
 \* is not known and their order in this sequence record is  
 \* arbitrary. Gaps between the contigs are represented as  
 \* runs of N, but the exact sizes of the gaps are unknown.  
 \* This record will be updated with the finished sequence  
 \* as soon as it is available and the accession number will  
 \* be preserved.

\* 1 16300: contig of 16300 bp in length  
 \* 16301 16400: gap of 100 bp  
 \* 16401 122337: contig of 105937 bp in length  
 \* 122338 122437: gap of 100 bp  
 \* 122438 139749: contig of 17312 bp in length  
 \* 139750 139849: gap of 100 bp  
 \* 139850 211515: contig of 71666 bp in length  
 \* 211516 211615: gap of 100 bp  
 \* 211616 215958: contig of 4343 bp in length.

Location/Qualifiers

1. 215958

/organism="Mus musculus"

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Query Match 70.8%; Score 17; DB 2; Length 215958;  
 Best Local Similarity 82.4%; Pred. No. 15;  
 Matches 14; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 6 ACAUGAAGCCCUUCAGC 22

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Db 106575 ACATGAGCCCTCAGC 106591

Search completed: May 27, 2004, 02:16:50  
 Job time : 511.783 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 26, 2004, 14:55:11 ; Search time 107.037 Seconds  
(without alignments)  
952.539 Million cell updates/sec

Title: US-09-121-239-17

Perfect score: 24

Sequence: 1 GUGGACAGGAGCCCUACGGG 24

Scoring table: OLIGO NUC

Gapop 60.0 , Gapext 60.0

Searched: 3373863 seqs, 2124099041 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : N Geneseq 29Jan04:\*

- 1: geneseqn1980s:\*
- 2: geneseqn1990s:\*
- 3: geneseqn2000s:\*
- 4: geneseqn2001as:\*
- 5: geneseqn2001bs:\*
- 6: geneseqn2002as:\*
- 7: geneseqn2003as:\*
- 8: geneseqn2003bs:\*
- 9: geneseqn2003cs:\*
- 10: geneseqn2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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C 1	24	100.0	24	3 AAZ60857	AAZ60857 Oligonucleotide
C 2	24	100.0	24	3 AAZ60855	AAZ60855 Oligonucleotide
C 3	24	100.0	24	3 AAZ60858	AAZ60858 Oligonucleotide
C 4	24	100.0	24	3 AAZ60856	AAZ60856 Oligonucleotide
5	24	100.0	299	3 AAZ60864	AAZ60864 Region su
6	24	100.0	3380	7 ABZ18520	ABZ18520 Group III
C 7	18	75.0	34125	6 ABS69903	ABS69903 Human ade
8	16	66.7	65	6 ABS54940	ABS54940 Mouse spl
C 9	16	66.7	751	4 AA194531	AA194531 Human neu
10	16	66.7	1044	4 AA54224	AA54224 Pseudomon
11	16	66.7	1044	7 ACA42504	ACA42504 Prokaryot
12	16	66.7	2278	3 AAZ89962	AAZ89962 Corn ADA2
13	16	66.7	2599	3 AAZ56382	AAZ56382 Escherich
C 14	16	66.7	3460	2 AAZ36957	AAZ36957 Nucleotid
C 15	16	66.7	3460	2 AAZ34989	AAZ34989 Human cel
C 16	16	66.7	3460	6 ABX84482	ABX84482 Human cDN
C 17	16	66.7	6699	7 ABX08804	ABX08804 Angiogene
C 18	16	66.7	6699	7 ABX76302	ABX76302 Lung canc
C 19	16	66.7	185035	6 ABT10147	ABT10147 Human bre
C 20	16	66.7	185035	6 ACA64951	ACA64951 Human PPN
C 21	15	62.5	23	2 AAT56765	AAT56765 Human bcr
22	15	62.5	23	2 AAT56766	AAT56766 Human bcr
23	15	62.5	33	2 AAT10497	AAT10497 ABL oncog

24	15	62.5	33	2 AAT10495	AAT10495 BCR-ABL o
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26	15	62.5	47	2 AAQ66785	AAQ66785 Ribozyme
C 27	15	62.5	52	2 AAT12637	AAT12637 T7 promot
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31	15	62.5	80	2 AAQ34631	AAQ34631 Human PHL
32	15	62.5	80	2 AAV20460	AAV20460 Human bcr
C 33	15	62.5	205	6 ABL87455	ABL87455 Human ova
34	15	62.5	257	2 AAQ34625	AAQ34625 Human bcr
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C 37	15	62.5	436	7 ADA40048	ADA40048 Bovine ES
C 38	15	62.5	483	7 ADA71111	ADA71111 Rice gene
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ID AAZ60857 standard; DNA; 24 BP.  
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AC AAZ60857;  
XX  
DT 16-MAY-2000 (first entry)  
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XX  
KW Fusion transcript; translocation; bcr b3 region; abl gene;  
KW amplification assay; detection assay; medical diagnosis;  
KW clinical monitoring; chimeric RNA; fusion RNA; condition marker;  
KW disease marker; cancer; leukemia; ss.  
XX  
OS Synthetic.  
XX  
PN WO200005418-A1.  
XX  
PD 03-FEB-2000.  
XX  
PF 23-JUL-1999; 99WO-US016832.  
XX  
PR 23-JUL-1998; 98US-00121239.  
XX  
PA (GENP-) GEN-PROBE INC.  
XX  
PI Harvey RC, Eastman PS;  
XX  
DR WPI; 2000-182730/16.  
XX  
PT Novel methods for preparing RNA from biological samples, used for the  
XX detection and measurement of nucleic acids and fusion nucleic acids.  
XX  
PS Claim 19; Page 43; 49pp; English.  
XX  
CC Oligonucleotides AAZ60840-62 and AAZ60865-66 are used in the method of  
CC the invention to detect fusion transcripts produced from a translocation  
CC between the bcr b3 region and the abl gene. The specification describes a  
CC method for detecting a fusion nucleic acid (particularly chimeric mRNA  
CC species), in a biological sample. The method comprises contacting a  
CC sample of fusion nucleic acid with primers, amplifying the hybridized  
CC fusion nucleic acid, and detecting the target hybrid. The method is used  
CC for the sample and rapid preparation of RNA from a biological sample,  
CC particularly from the cytoplasm of eukaryotic cells, which is suitable  
CC for use in an amplification and detection assay. The methods are used for

CC the analysis and detection of nucleic acids in biological samples. The  
 CC methods are useful in the human medical and veterinary fields, for  
 CC medical diagnoses and clinical monitoring of a patients response to  
 CC therapy where a disease or medical condition is associated with a  
 CC particular type and/or level of mRNA present in the sample. The methods  
 CC are also useful for detecting or quantifying fusion or chimeric RNA  
 CC species, and for detecting a translocation as a marker for a given  
 CC condition or disease, e.g. translocations associate with cancers,  
 CC particularly forms of leukemia  
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 AC AAZ60855;  
 XX  
 DT 16-MAY-2000 (first entry)  
 XX  
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 KW amplification assay; detection assay; medical diagnosis;  
 KW clinical monitoring; chimeric RNA; fusion RNA; condition marker;  
 KW disease marker; cancer; leukemia; ss.  
 XX Synthetic.  
 OS  
 XX WO200005418-A1.  
 PN  
 XX 03-FEB-2000.  
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 PR 23-JUL-1998; 98US-00121239.  
 XX  
 PA (GENP-) GEN-PROBE INC.  
 PI Harvey RC, Eastman PS;  
 XX WPI; 2000-182730/16.  
 DR  
 XX Novel methods for preparing RNA from biological samples, used for the  
 PT detection and measurement of nucleic acids and fusion nucleic acids.  
 PT  
 PS Claim 19; Page 42; 49pp; English.  
 XX  
 CC Oligonucleotides AAZ60840-62 and AAZ60865-66 are used in the method of  
 CC the invention to detect fusion transcripts produced from a translocation  
 CC between the bcr b3 region and the abl gene. The specification describes a  
 CC method for detecting a fusion nucleic acid (particularly chimeric mRNA  
 CC species), in a biological sample. The method comprises contacting a  
 CC sample of fusion nucleic acid with primers, amplifying the hybridized  
 CC fusion nucleic acid, and detecting the target hybrid. The method is used  
 CC for the simple and rapid preparation of RNA from a biological sample,  
 CC particularly from the cytoplasm of eukaryotic cells, which is suitable  
 CC for use in an amplification and detection assay. The methods are used for  
 CC the analysis and detection of nucleic acids in biological samples. The  
 CC methods are useful in the human medical and veterinary fields, for  
 CC medical diagnoses and clinical monitoring of a patients response to  
 CC therapy where a disease or medical condition is associated with a  
 CC particular type and/or level of mRNA present in the sample. The methods  
 CC are also useful for detecting or quantifying fusion or chimeric RNA  
 CC species, and for detecting a translocation as a marker for a given  
 CC condition or disease, e.g. translocations associate with cancers,  
 CC particularly forms of leukemia  
 CC are also useful for detecting or quantifying fusion or chimeric RNA

CC species, and for detecting a translocation as a marker for a given  
 CC condition or disease, e.g. translocations associate with cancers,  
 CC particularly forms of leukemia  
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 AC AAZ60858;  
 XX  
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 XX  
 DE Oligonucleotide used to detect bcr b3-abl fusion transcripts.  
 XX Fusion transcript; translocation; bcr b3 region; abl gene;  
 KW amplification assay; detection assay; medical diagnosis;  
 KW clinical monitoring; chimeric RNA; fusion RNA; condition marker;  
 KW disease marker; cancer; leukemia; ss.  
 XX Synthetic.  
 OS  
 XX WO200005418-A1.  
 PN  
 XX 03-FEB-2000.  
 PD  
 PF 23-JUL-1999; 99WO-US016832.  
 XX  
 PR 23-JUL-1998; 98US-00121239.  
 XX  
 PA (GENP-) GEN-PROBE INC.  
 PI Harvey RC, Eastman PS;  
 XX WPI; 2000-182730/16.  
 DR  
 XX Novel methods for preparing RNA from biological samples, used for the  
 PT detection and measurement of nucleic acids and fusion nucleic acids.  
 PT  
 PS Claim 19; Page 43; 49pp; English.  
 XX  
 CC Oligonucleotides AAZ60840-62 and AAZ60865-66 are used in the method of  
 CC the invention to detect fusion transcripts produced from a translocation  
 CC between the bcr b3 region and the abl gene. The specification describes a  
 CC method for detecting a fusion nucleic acid (particularly chimeric mRNA  
 CC species), in a biological sample. The method comprises contacting a  
 CC sample of fusion nucleic acid with primers, amplifying the hybridized  
 CC fusion nucleic acid, and detecting the target hybrid. The method is used  
 CC for the simple and rapid preparation of RNA from a biological sample,  
 CC particularly from the cytoplasm of eukaryotic cells, which is suitable  
 CC for use in an amplification and detection assay. The methods are used for  
 CC the analysis and detection of nucleic acids in biological samples. The  
 CC methods are useful in the human medical and veterinary fields, for  
 CC medical diagnoses and clinical monitoring of a patients response to  
 CC therapy where a disease or medical condition is associated with a  
 CC particular type and/or level of mRNA present in the sample. The methods  
 CC are also useful for detecting or quantifying fusion or chimeric RNA  
 CC species, and for detecting a translocation as a marker for a given  
 CC condition or disease, e.g. translocations associate with cancers,  
 CC particularly forms of leukemia  
 XX Sequence 24 BP; 4 A; 8 C; 6 G; 0 T; 6 U; 0 Other;

Query Match 100.0%; Score 24; DB 3; Length 24;  
 Best Local Similarity 83.3%; Pred. No. 0.00026;  
 Matches 20; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 GUGGAACAUGAAGCCCUUCAGCGG 24  
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 AC AAZ60856;  
 XX  
 DT 16-MAY-2000 (first entry)  
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 XX  
 KW Fusion transcript; translocation; bcr b3 region; abl gene;  
 KW amplification assay; detection assay; medical diagnosis;  
 KW clinical monitoring; chimeric RNA; fusion RNA; condition marker;  
 KW disease marker; cancer; leukemia; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200005418-A1.  
 XX  
 PD 03-FEB-2000.  
 XX  
 PF 23-JUL-1999; 99WO-US016832.  
 XX  
 PR 23-JUL-1998; 98US-00121239.  
 XX  
 PA (GENP-) GEN-PROBE INC.  
 XX  
 PI Harvey RC, Eastman PS;  
 XX  
 WPI; 2000-182730/16.  
 XX  
 Novel methods for preparing RNA from biological samples, used for the  
 detection and measurement of nucleic acids and fusion nucleic acids.  
 Claim 19; Page 42; 49pp; English.  
 XX  
 Oligonucleotides AAZ60840-62 and AAZ60865-66 are used in the method of  
 the invention to detect fusion transcripts produced from a translocation  
 between the bcr b3 region and the abl gene. The specification describes a  
 method for detecting a fusion nucleic acid (particularly chimeric mRNA  
 species), in a biological sample. The method comprises contacting a  
 sample of fusion nucleic acid with primers, amplifying the hybridized  
 fusion nucleic acid, and detecting the target hybrid. The method is used  
 for the simple and rapid preparation of RNA from a biological sample,  
 particularly from the cytoplasm of eukaryotic cells, which is suitable  
 for use in an amplification and detection assay. The methods are used for  
 the analysis and detection of nucleic acids in biological samples. The  
 methods are useful in the human medical and veterinary fields, for  
 medical diagnoses and clinical monitoring of a patient's response to  
 therapy where a disease or medical condition is associated with a  
 particular type and/or level of mRNA present in the sample. The methods  
 are also useful for detecting or quantifying fusion or chimeric RNA  
 species, and for detecting a translocation as a marker for a given  
 condition or disease, e.g. translocations associate with cancers,  
 particularly forms of leukemia

XX Sequence 24 BP; 6 A; 6 C; 8 G; 0 T; 4 U; 0 Other;

Query Match 100.0%; Score 24; DB 3; Length 24;  
 Best Local Similarity 100.0%; Pred. No. 0.00026;  
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GUGGAACAUGAAGCCCUUCAGCGG 24  
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Db 1 GUGGAACAUGAAGCCCUUCAGCGG 24

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 XX  
 AC AAZ60864;  
 XX  
 DT 16-MAY-2000 (first entry)  
 XX  
 DE Region surrounding a splice junction in a normal abl transcript.  
 XX  
 KW Fusion transcript; translocation; bcr b3 region; abl gene;  
 KW amplification assay; detection assay; medical diagnosis;  
 KW clinical monitoring; chimeric RNA; fusion RNA; condition marker;  
 KW disease marker; cancer; leukemia; ss.  
 XX  
 OS Unidentified.  
 XX  
 PN WO200005418-A1.  
 XX  
 PD 03-FEB-2000.  
 XX  
 PF 23-JUL-1999; 99WO-US016832.  
 XX  
 PR 23-JUL-1998; 98US-00121239.  
 XX  
 PA (GENP-) GEN-PROBE INC.  
 XX  
 PI Harvey RC, Eastman PS;  
 XX  
 WPI; 2000-182730/16.  
 XX  
 Novel methods for preparing RNA from biological samples, used for the  
 detection and measurement of nucleic acids and fusion nucleic acids.  
 Disclosure; Fig 3; 49pp; English.  
 XX  
 The present sequence represents a region surrounding a potential splice  
 junction in a normal abl transcript. The specification describes  
 oligonucleotides which are used to detect fusion transcripts produced  
 from a translocation between the bcr b3 region and the abl gene. The  
 specification also describes a method for detecting a fusion nucleic acid  
 (particularly chimeric mRNA species), in a biological sample. The method  
 comprises contacting a sample of fusion nucleic acid with primers,  
 amplifying the hybridized fusion nucleic acid, and detecting the target  
 hybrid. The method is used for the simple and rapid preparation of RNA  
 from a biological sample, particularly from the cytoplasm of eukaryotic  
 cells, which is suitable for use in an amplification and detection assay.  
 The methods are used for the analysis and detection of nucleic acids in  
 biological samples. The methods are useful in the human medical and  
 veterinary fields, for medical diagnoses and clinical monitoring of a  
 patient's response to therapy where a disease or medical condition is  
 associated with a particular type and/or level of mRNA present in the  
 sample. The methods are also useful for detecting or quantifying fusion  
 or chimeric RNA species, and for detecting a translocation as a marker  
 for a given condition or disease, e.g. translocations associate with  
 cancers, particularly forms of leukemia

XX Sequence 299 BP; 77 A; 70 C; 81 G; 71 T; 0 U; 0 Other;

Query Match 100.0%; Score 24; DB 3; Length 299;  
 Best Local Similarity 83.3%; Pred. No. 0.00028;  
 Matches 20; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 GUGGAACAUGAAGCCCUUCAGCGG 24  
 |||

Db 142 GTGGAACATGAAGCCCTTCAGCGG 165

RESULT 6  
 AB218520

```

ID ABZ18520 standard; cDNA; 3380 BP.
XX
AC ABZ18520;
XX
XX 23-JAN-2003 (first entry)
DT
DE Group III CDNA cancer related clone SEQ ID NO:946.
DE
XX Human; cancer; tumour; therapy; diagnosis; CT antigen; CP antigen;
KW immune response; virology; immunology; microbiology; molecular biology;
KW recombinant DNA technology; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200278516-A2.
XX
XX 10-OCT-2002.
PD
XX 28-MAR-2002; 2002WO-US010421.
PF
XX 30-MAR-2001; 2001US-0280255P.
PR
XX 28-AUG-2001; 2001US-0315563P.
PR
XX 09-JAN-2002; 2002US-0347313P.
PR
XX (CORI-) CORIXA CORP.
PA
XX Wang T, Wang S, Bangur CS, Gaiger A;
XX
XX WPI; 2003-058387/05.
DR
XX
XX New immunogenic polynucleotides or polypeptides useful for diagnosing,
PT preventing and treating cancer expressing CT or CP mRNA antigens, and in
PT virology, immunology, microbiology, molecular biology and recombinant DNA
PT techniques.
XX
PS Claim 1; SEQ ID NO 946; 207pp; English.
XX
CC ABQ17575 to ABQ20506 represent isolated polynucleotide (I) sequences, and
CC ABP54446 to ABP54472 represent protein (II) sequences, from the present
CC invention. (I) and (II) have cytostatic activity and can be used in gene
CC therapy and vaccines. (I), (II), antibodies and compositions from the
CC present invention are useful for diagnosing, preventing and treating
CC cancer, which expresses CT or CP mRNA antigens. They are useful for
CC stimulating immune response. They can also be useful in virology,
CC immunology, microbiology, molecular biology and recombinant DNA
CC techniques. N.B. The sequence data for this patent did not form part of
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 3380 BP; 819 A; 1005 C; 989 G; 567 T; 0 U; 0 Other;
Query Match 100.0%; Score 24; DB 7; Length 3380;
Best Local Similarity 83.3%; Pred. No. 0.00029;
Matches 20; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

OY 1 GUGAACCAUGAACCCUUCACGG 24
Db 57 GTGACATGACGCCCTTCACGG 80

RESULT 7
ID ABS69903/c
XX ABS69903 standard; DNA; 34125 BP.
XX
AC ABS69903;
XX
XX 21-NOV-2002 (first entry)
DT
XX Human adenovirus type 12 genome sequence.
DE
XX Vector; adenovirus; adeno-associated; adenosine deaminase gene; receptor;
KW adenosine deaminase deficiency; severe combined immune deficiency; PAH;
KW beta-chain; haemoglobin gene; beta-thalassaemia; sickle cell disease;

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```

KW low density lipoprotein gene; familial hypercholesterolaemia;
KW hypoxanthine-guanine phosphoribosyltransferase; Lesch-Nyhan syndrome;
KW phenylalanine hydroxylase gene; gene therapy; phenylketonuria;
KW dystrophin gene; muscular dystrophy; cystic fibrosis; immunostimulant;
KW human cystic fibrosis transmembrane conductance regulator gene;
KW antianaemic; antilipaeamic; nootropic; cytostatic; dermatological;
KW human adenovirus genome; ds.
XX
OS Human adenovirus type 12.
XX
XX US2002102731-A1.
PN
XX 01-AUG-2002.
PD
XX 12-FEB-2001; 2001US-00782378.
PF
XX 02-OCT-2000; 2000US-0237747P.
PR
XX (UYN ) UNIV NEW YORK STATE RES FOUND.
PA
XX Hearing P, Bahou WF, Sandalon Z, Gnatenko DV;
XX
XX WPI; 2002-690619/74.
DR
XX
XX Producing vector, by introducing vector having nucleotide sequence,
PT adenovirus inverted terminal repeats and packaging sequence, and adeno-
PT associated virus terminal repeat, into cell, and culturing cell.
XX
XX Disclosure; Page 135-150; 191pp; English.
XX
CC The present invention relates to a new method of producing a vector. The
CC method involves introducing recombinant vector having nucleotide sequence
CC (NS) having 5' and 3' end, left and right inverted terminal repeats of
CC adenovirus flanking NS, adenovirus packaging sequence linked to inverted
CC terminal repeat, and adeno-associated virus terminal repeat linked to 3'
CC end of NS, into cell expressing adenovirus early gene lacking from vector
CC ; and culturing cell to produce another vector. The method is useful for
CC generating vectors, especially mAd vectors. The method is useful in
CC transferring nucleotide sequences of interest into a cell, for gene
CC transfer applications (e.g. gene therapy) in vitro, ex vivo and in vivo.
CC The nucleotide sequences are useful for treating diseases associated with
CC it, i.e. adenosine deaminase gene associated with adenosine deaminase
CC deficiency with severe combined immune deficiency, beta-chain of
CC haemoglobin gene associated with beta-thalassaemia and sickle cell
CC disease, receptor for low density lipoprotein gene associated with
CC familial hypercholesterolaemia, hypoxanthine-guanine
CC phosphoribosyltransferase associated with Lesch-Nyhan syndrome,
CC phenylalanine hydroxylase (PAH) gene associated with phenylketonuria,
CC dystrophin gene associated with muscular dystrophy, and human cystic
CC fibrosis transmembrane conductance regulator gene associated with cystic
CC fibrosis. The present nucleic acid sequence represents a human adenovirus
CC genome sequence that was used in the methods of the invention
XX
SQ Sequence 34125 BP; 9330 A; 8012 C; 7864 G; 8919 T; 0 U; 0 Other;
Query Match 75.0%; Score 18; DB 6; Length 34125;
Best Local Similarity 83.3%; Pred. No. 0.95;
Matches 15; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 3 GGAACAUGAACCCUUCUA 20
Db 4015 GGAACATGAAGCCCTTCA 3998

RESULT 8
ABN54940
ID ABN54940 standard; DNA; 65 BP.
XX
XX ABN54940;
XX
XX 15-JUL-2002 (first entry)
DT
XX Mouse spliced transcript detection oligonucleotide SEQ ID NO:27688.
DE

```

XX Human; mouse; rat; splice transcript; detection; RNA transcript;  
KW splice variant; transcriptome; oligonucleotide library; ss.  
XX  
XX Mus musculus.  
OS  
XX WO200210449-A2.  
PN  
XX 07-FEB-2002.  
PD  
XX  
XX 20-JUL-2001; 2001WO-IB001903.  
PF  
XX 28-JUL-2000; 2000US-0221607P.  
PR  
XX 02-MAY-2001; 2001US-0287724P.  
PA  
XX (COMP-) COMPUGEN INC.  
PI  
XX Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;  
DR WPI; 2002-257383/30.  
XX  
XX New oligonucleotide libraries comprising oligonucleotides which  
PT selectively hybridize to mRNAs transcribed from a transcription unit of a  
PT genome, useful for detecting tissue-, pathology-, and developmental-  
PT specific genes.  
XX  
XX Example 1; SEQ ID NO 27688; 47pp; English.  
PS  
XX The present invention describes oligonucleotide libraries for detecting  
CC messenger RNAs that populate a (sub-)transcriptome, where the (sub-  
CC )transcriptome comprises messenger RNAs transcribed from multiple  
CC transcription units that populate a genome. The library comprises several  
CC oligonucleotides, each capable of hybridising selectively to a set of  
CC messenger RNAs transcribed from a given transcription unit of the genome,  
CC which encodes one or more messenger RNA splice variants. The  
CC oligonucleotide libraries are useful for detecting mRNAs from a  
CC biological sample, in expression profiling studies, in qualitatively or  
CC quantitatively characterising the corresponding transcriptome, and in  
CC detecting RNA transcripts and splice variants of human or animal  
CC transcriptomes. The libraries may also be used as specialised mini  
CC libraries to detect transcripts of a sub-transcriptome under a particular  
CC biological or pathological state, and so allowing the detection of tissue  
CC - and pathology-specific genes such as those genes only expressed in  
CC specific tissue under a specific pathological condition; to detect  
CC developmental specific genes; and to detect RNA transcripts and splice  
CC variants of a transcriptome of a patient suffering from a particular  
CC disorder. ABN27253 to ABN59589 represent oligonucleotide sequences from  
CC rats, humans and mice, which are used in the exemplification of the  
CC present invention. N.B. The sequence data for this patent did not form  
CC part of the printed specification, but was obtained in electronic format  
CC directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
XX  
XX Sequence 65 BP; 18 A; 16 C; 19 G; 12 T; 0 U; 0 Other;  
SQ  
Query Match 66.7%; Score 16; DB 6; Length 65;  
Best Local Similarity 87.5%; Pred. No. 12;  
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GUGGAACAUAGAAGCCC 16  
DB 7 GTGGACATGAAGCCC 22  
RESULT 9  
AAI94531/c  
ID AAI94531 standard; cDNA; 751 BP.  
XX  
XX AAI94531;  
AC  
XX  
XX 13-NOV-2001 (first entry)  
DT  
XX Human neuroblastoma expressed polynucleotide SEQ ID NO 606.  
DE  
XX

KW Human; neuroblastoma; malignancy; cancer; tumour marker; N-myc; TrkA; ss.  
XX  
XX Homo sapiens.  
XX  
XX WO200166719-A1.  
PN  
XX 13-SEP-2001.  
PD  
XX  
XX 02-MAR-2001; 2001WO-JP001629.  
PF  
XX 07-MAR-2000; 2000JP-00159195.  
PR  
XX (CHIB-) CHIBA PREFECTURE.  
PA (HISM ) HISAMITSU PHARM CO LTD.  
XX  
XX Nakagawara A;  
PI  
XX WPI; 2001-565584/53.  
DR  
XX Nucleic acids originating in gene expressed in human neuroblastoma,  
PT useful as probe or primer in diagnosing prognosis of human neuroblastoma,  
PT malignancy and susceptibility indicator or tumor marker for anti-cancer  
PT agents.  
XX  
XX Claim 1; Page 485; 2979pp; Japanese.  
PS  
XX The invention relates to novel genes (AAI93926-AAI97963) expressed in  
CC human neuroblastoma. The nucleic acids are applicable as a probe or  
CC primer in diagnosing the prognosis of human neuroblastoma, malignancy and  
CC susceptibility indicators or tumour markers for anti-cancer agents. The  
CC gene information for diagnosing prognosis is related to factors similar  
CC to that for N-myc and TrkA genes  
XX  
XX Sequence 751 BP; 176 A; 176 C; 215 G; 157 T; 0 U; 27 Other;  
SQ  
Query Match 66.7%; Score 16; DB 4; Length 751;  
Best Local Similarity 81.2%; Pred. No. 12;  
Matches 13; Conservative 3; Mismatches 0; Indels 0; Gaps 0;  
QY 7 CAUGAAGCCCUUACGC 22  
DB 563 CATGAAGCCCTTCAGC 548  
RESULT 10  
AAS54224  
ID AAS54224 standard; DNA; 1044 BP.  
XX  
XX AAS54224;  
AC  
XX  
XX 13-FEB-2002 (first entry)  
DT  
XX Pseudomonas aeruginosa DNA for cellular proliferation protein #355.  
DE  
XX Antisense; ds; prokaryotic cellular proliferation gene; antibiotic;  
KW antibacterial; drug design.  
XX  
XX Pseudomonas aeruginosa.  
OS  
XX WO200170955-A2.  
PN  
XX 27-SEP-2001.  
PD  
XX  
XX 21-MAR-2001; 2001WO-US009180.  
PF  
XX 21-MAR-2000; 2000US-0191078P.  
PR 23-MAY-2000; 2000US-0206848P.  
PR 26-MAY-2000; 2000US-020727P.  
PR 23-OCT-2000; 2000US-0242578P.  
PR 27-NOV-2000; 2000US-0253625P.  
PR 22-DEC-2000; 2000US-0257931P.  
PR 16-FEB-2001; 2001US-0269308P.  
XX

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PA (ELIT-) ELITRA PHARM INC.
XX
XX Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;
PI Yamamoto RT, Xu HH;
XX
XX WPI; 2001-611495/70.
DR P-PSDB; AAU36365.
XX
XX New polynucleotides for the identification and development of
PT antibiotics, comprise sequences of antisense nucleic acids.
XX
XX Claim 27; SEQ ID NO 7861; 51lpp; English.
XX
XX The invention relates to antisense inhibitors of genes essential to
CC prokaryotic cellular proliferation, their use in identifying the genes,
CC their use in the discovery of novel antibiotics, the essential genes
CC themselves and the encoded proteins. The prokaryotes used are Escherichia
CC coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae,
CC Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also
CC useful for the identification of potential new targets for antibiotic
CC development. The antisense nucleic acids can also be used to identify
CC proteins used in proliferation, to express these proteins, and to obtain
CC antibodies capable of binding to the expressed proteins. The proteins can
CC be used to screen compounds in rational drug discovery programmes. The
CC antisense nucleic acid sequence is also useful to screen for homologous
CC nucleic acids which are required for cell proliferation in a wide variety
CC of organisms. The present sequence encodes an essential prokaryotic
CC cellular proliferation protein. Note: The sequence data for this patent
CC did not form part of the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 1044 BP; 159 A; 373 C; 334 G; 178 T; 0 U; 0 Other;

Query Match 66.7%; Score 16; DB 4; Length 1044;
Best Local Similarity 81.2%; Pred. No. 13;
Matches 13; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 9 UGAAGCCCUUCACGG 24
Db :|||||:|||||
797 TGAAGCCCTTCACGG 812

RESULT 11
ACA42504
ID ACA42504 standard; DNA; 1044 BP.
XX
XX ACA42504;
XX
XX 19-JUN-2003 (first entry)
XX
XX Prokaryotic essential gene #24161.
XX
XX Antisense; ds; prokaryotic essential gene; cell proliferation;
XX drug design; gene.
XX
XX Pseudomonas aeruginosa.
XX
XX WO20027183-A2.
XX
XX 03-OCT-2002.
XX
XX 21-MAR-2002; 2002WO-US009107.
XX
XX 21-MAR-2001; 2001US-00815242.
XX 06-SEP-2001; 2001US-00948993.
XX 25-OCT-2001; 2001US-0342923P.
XX 08-FEB-2002; 2002US-00072851.
XX 06-MAR-2002; 2002US-0362659P.
XX
XX (ELIT-) ELITRA PHARM INC.
XX
XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
PI

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PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
XX
XX WPI; 2003-029926/02.
DR P-PSDB; ABU38634.
XX
XX New antisense nucleic acids, useful for identifying proteins or screening
PT for homologous nucleic acids required for cellular proliferation to
PT isolate candidate molecules for rational drug discovery programs.
XX
XX Claim 14; SEQ ID NO 30374; 1766pp; English.
XX
XX The invention relates to an isolated nucleic acid comprising any one of
CC the 6213 antisense sequences given in the specification where expression
CC of the nucleic acid inhibits proliferation of a cell. Also included are:
CC (1) a vector comprising a promoter operably linked to the nucleic acid
CC encoding a polypeptide whose expression is inhibited by the antisense
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC polypeptide or its fragment whose expression is inhibited by the
CC antisense nucleic acid; (4) an antibody capable of specifically binding
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
CC proliferation or the activity of a gene in an operon required for
CC proliferation; (7) identifying a compound that influences the activity of
CC the gene product or that has an activity against a biological pathway
CC required for proliferation, or that inhibits cellular proliferation; (8)
CC identifying a gene required for cellular proliferation or the biological
CC pathway in which a proliferation-required gene or its gene product lies
CC or a gene on which the test compound that inhibits proliferation of an
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC compound's activity; (11) a culture comprising strains in which the gene
CC product is overexpressed or underexpressed; (12) determining the extent
CC to which each of the strains is present in a culture or collection of
CC strains; or (13) identifying the target of a compound that inhibits the
CC proliferation of an organism. The antisense nucleic acids are useful for
CC identifying proteins or screening for homologous nucleic acids required
CC for cellular proliferation to isolate candidate molecules for rational
CC drug discovery programs, or for screening homologous nucleic acids
CC required for proliferation in cells other than S. aureus, S. typhimurium,
CC K. pneumoniae or P. aeruginosa. The present sequence is one of the target
CC prokaryotic essential genes. Note: The sequence data for this patent did
CC not form part of the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 1044 BP; 159 A; 373 C; 334 G; 178 T; 0 U; 0 Other;

Query Match 66.7%; Score 16; DB 7; Length 1044;
Best Local Similarity 81.2%; Pred. No. 13;
Matches 13; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 9 UGAAGCCCUUCACGG 24
Db :|||||:|||||
797 TGAAGCCCTTCACGG 812

RESULT 12
AAZ89962
ID AAZ89962 standard; cDNA; 2278 BP.
XX
XX AAZ89962;
XX
XX 05-MAY-2000 (first entry)
XX
XX Corn ADA2 transcription co-activator nucleotide sequence.
XX
XX ADA2; transcription co-activator; adaptor; plant breeding; corn; ss;
XX transgenic plant.
XX
XX Zea mays.
XX
XX WO200003026-A2.
XX
XX 20-JAN-2000.
XX
XX

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PF 12-JUL-1999; 99WO-US015664.
XX
PR 13-JUL-1998; 98US-0092659P.
XX
PA (DUPO ) DU PONT DE NEMOURS & CO E I.
XX
PI Cahoon RE, Liu Z, Odell JT, Sakai H;
XX
DR WPI; 2000-160931/14.
DR P-PSDB; AAY78518.
XX
XX New isolated nucleic acid fragment encoding a transcription coactivator
PT in plants and seeds useful as a probe to isolate genes encoding
PT homologous proteins from other plant species, and as a primer.
XX
XX Claim 3; Page 29-30; 42pp; English.
PS
XX This sequence represents an ADA2 transcription adaptor/co-activator. In
CC yeast ADA2 functionally interacts with the acidic activation domain of
CC transcriptional activators. The invention relates to ADA2 nucleotide and
CC protein sequences, and also to a chimeric gene comprising of the ADA2
CC nucleotide sequence operably linked to a suitable regulatory sequence.
CC The ADA2 nucleotide sequence can be used as a DNA hybridization probe to
CC screen libraries from any desired plant and to isolate cDNAs and genes
CC encoding other ADA2 transcription adaptors, either as cDNAs or genomic
CC DNAs from the same or other plant species. The ADA2 nucleotide sequence
CC is also used as a primer to amplify longer nucleic acid fragments
CC encoding homologous genes from DNA or RNA. The ADA2 nucleotide and
CC peptide sequences are used in the immunological screening of cDNA
CC expression libraries. The nucleotide sequence is used to create
CC transgenic plants in which the protein is present at higher or lower
CC levels than normal or in cell types or developmental stages in which they
CC are not normally found. This would have the effect of altering the level
CC of transcription initiation in those cells. The ADA2 protein is used to
CC prepare antibodies which are useful for detecting them in situ in cells
CC or in vitro in cell extracts. All or a substantial portion of the ADA2
CC nucleotide sequence is used as probes for genetically and physically
CC mapping the genes that they are a part of, and as markers of traits
CC linked to those genes. Such information may be useful in plant breeding
CC in order to develop lines with desired phenotypes. In addition, they are
CC used to probe southern blots containing restriction endonuclease-treated
CC genomic DNAs of a set of individuals representing parent and progeny of a
CC defined genetic cross. Loss of function mutant phenotypes for the cDNA
CC clones identified by target gene disruption or by identifying specific
CC mutants for the genes contained in maize population carrying mutations in
CC all possible genes, are used for producing a plant containing a mutation
CC in the endogenous gene encoding ADA2. This mutant plant can then be used
CC to determine or confirm the natural function of ADA2
XX
SQ Sequence 2278 BP; 669 A; 451 C; 590 G; 561 T; 0 U; 7 Other;
Query Match 66.7%; Score 16; DB 3; Length 2278;
Best Local Similarity 81.2%; Pred. No. 13;
Matches 13; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 GGACCAUGAGCCCUU 18
Db 1274 GGAACATGAAGCCCT 1289
|||||:|||||:|

RESULT 13
AAZ56382
ID AAZ56382 standard; DNA; 2599 BP.
XX
AC AAZ56382;
XX
XX Escherichia coli flagellin protein nucleotide sequence SEQ ID NO:52.
DT 17-MAR-2000 (first entry)
XX
DE Escherichia coli flagellin protein nucleotide sequence SEQ ID NO:52.
XX
XX Flagellin; fliC; antigen; detection; ds.
KW
XX Escherichia coli.
OS

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XX WO9961458-A1.
XX
XX 02-DEC-1999.
XX
XX 21-MAY-1999; 99WO-AU000385.
XX
XX 21-MAY-1998; 98AU-00003634.
XX
XX (UNSY ) UNIV SYDNEY.
XX
XX Reeves PR, Wang L;
XX
XX WPI; 2000-072598/06.
XX
XX Novel nucleic acid molecule useful for the detection of flagellated
PT bacterial strains in food, feces, etc.
XX
XX Claim 3; Page 226-227; 245pp; English.
XX
XX AAZ56331 to AAZ56398 represent nucleic acid molecules (I) encoding all or
CC part of an Escherichia coli flagellin protein except a protein expressed
CC by E. coli H1, H7, H12 or H48 type strains. The present invention also
CC describes a method of detecting the presence of E. coli of a particular H
CC serotype in a sample, comprising specifically hybridising a nucleic acid,
CC preferably at least a pair, derived from a flagellating gene, specific
CC for a particular flagellin gene associated with the H serotype, to any
CC E. coli in the sample which contain the gene, and detecting any hybridised
CC molecules, identifying the presence of that serotype in the sample. (I)
CC are useful for: (1) detecting the presence of E. coli of H serotype in a
CC sample by hybridising at least one or a pair of (I) to any E. coli in the
CC sample and detecting the hybridised nucleic acid molecules; and (2) for
CC detecting the presence of both O and H-serotypes of E. coli by
CC hybridising at least one or a pair of (I) to any E. coli present in the
CC sample and detecting the hybridised nucleic acid molecules. (I) is
CC particularly useful for detecting the combination of O and H antigen.
CC Hybridised (I) when using at least one (I) is detected by southern blot
CC analysis and, when using a pair of (I), is detected by polymerase chain
CC reaction (PCR). AAZ56399 to AAZ56420 represent primers used in the
CC exemplification of the present invention
XX
SQ Sequence 2599 BP; 708 A; 651 C; 615 G; 625 T; 0 U; 0 Other;
Query Match 66.7%; Score 16; DB 3; Length 2599;
Best Local Similarity 81.2%; Pred. No. 13;
Matches 13; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 5 AACAGAGAGCCCUUCA 20
Db 1057 AACATGAAGCCCTTCA 1072
|||||:|||||:|

RESULT 14
AAV36957/c
ID AAV36957 standard; cDNA; 3460 BP.
XX
AC AAV36957;
XX
XX 26-OCT-1998 (first entry)
XX
XX Nucleotide sequence of human ClqR gene.
XX
XX Human; Clq receptor protein; ClqR; phagocytosis; complement;
KW immune system; inflammation; prophylactic; genetic immune deficiency;
KW HIV; cancer; chemotherapy; inhibition; vasculitis; sepsis; Fragment;
KW primer; probe; antibody; ss.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
XX 149..2107
XX /*tag= a
XX /product= "ClqR gene product"

```

XX WO9822584-A1.  
 XX PD 28-MAY-1998.  
 XX PF 12-NOV-1997; 97WO-US021205.  
 XX PR 18-NOV-1996; 96US-00751305.  
 XX PA (REGC ) UNIV CALIFORNIA.  
 XX PI Tenner AJ, Nepomuceno RR;  
 XX DR WPI; 1998-312470/27.  
 XX DR P-PSDB; AAW49879.  
 XX PT New complement Clq receptor - and methods for identifying modulators,  
 PT useful for controlling phagocytosis, e.g. to prevent infection or to  
 PT treat sepsis.  
 XX PS Claim 3; Fig 3A-3C; 99pp; English.  
 CC This is the nucleotide sequence of the novel human Clq receptor (ClqRp)  
 CC gene, used in the method of the invention to identify modulators useful  
 CC for the control of phagocytosis. Delivering the ClqRp nucleic acid to a  
 CC cell (in vivo, in vitro or ex vivo) alters the level of ClqRp mRNA. ClqRp  
 CC stimulates the complement component of the immune system, particularly  
 CC phagocytosis, without simultaneous increase in inflammation. ClqRp  
 CC regulation is used for prophylactic treatment of subjects at risk of  
 CC infection (e.g. those with genetic immune deficiency, human immune  
 CC deficiency virus infection, undergoing cancer chemotherapy or high risk  
 CC surgery), also for treating cancer. Antisense or similar sequences are  
 CC used to inhibit phagocytosis or the complement component of immunity,  
 CC e.g. in cases of vasculitis or sepsis. Fragments of ClqRp are useful as  
 CC primers and probes for detecting ClqRp and related nucleic acids. ClqRp  
 CC polypeptides and antibodies are all useful for treating disorders  
 CC involving the complement component or immune deficiencies  
 XX SQ Sequence 3460 BP; 764 A; 943 C; 996 G; 757 T; 0 U; 0 Other;  
 Query Match 66.7%; Score 16; DB 2; Length 3460;  
 Best Local Similarity 81.2%; Pred. No. 13;  
 Matches 13; Conservative 3; Mismatches 0; Indels 0; Gaps 0;  
 QY 9 UGAAGCCCUUCAGCGG 24  
 Db :|||||:|||||  
 491 TGAAGCCCTTCAGCGG 476  
 RESULT 15  
 AA234989/c  
 ID AA234989 standard; cDNA; 3460 BP.  
 XX AC AA234989;  
 XX DT 28-FEB-2000 (first entry)  
 XX DE Human cell surface receptor ClqRp cDNA.  
 XX KW ClqRp; receptor; cell surface; transmembrane; glycoprotein; human;  
 KW host defence; infection; HIV; therapy; immunodeficiency; immunostimulant;  
 KW phagocytosis; signal transduction; ss.  
 XX OS Homo sapiens.  
 XX FH Key Location/Qualifiers  
 FT CDS 149..2107  
 FT /tag= a  
 FT sig\_peptide 149..211  
 FT /tag= b  
 FT mat\_peptide 212..2104  
 FT /tag= b  
 XX

PN WO9955839-A1.  
 XX PD 04-NOV-1999.  
 XX PF 29-APR-1999; 99WO-US009335.  
 XX PR 30-APR-1998; 98US-00071386.  
 XX PA (REGC ) UNIV CALIFORNIA.  
 XX PI Tenner AJ, Nepomuceno RR;  
 XX DR WPI; 2000-062021/05.  
 XX DR P-PSDB; AAV32345.  
 XX PT A new cell surface receptor protein used as a prophylactic for  
 PT individuals at risk from infection, e.g. HIV.  
 XX PS Claim 5; Fig 3; 49pp; English.  
 CC This is the nucleotide sequence of isolated cDNA coding for a novel human  
 CC cell surface transmembrane glycoprotein receptor designated ClqRp (see  
 CC AAY32345). The cDNA was obtained from a 937 library by PCR using primers  
 CC based on tryptic peptides of ClqRp. The receptor plays a role in  
 CC stimulating the classic complement component of the immune system,  
 CC specifically in stimulating phagocytosis in cells without a concomitant  
 CC increase in inflammation. A method of hybridisation based on the ClqRp  
 CC nucleic acid sequence is provided, as well as methods for detecting novel  
 CC ligands for ClqRp, including those which function as agonists or  
 CC antagonists. ClqRp nucleic acid or recombinant protein can be used to  
 CC effect the role of the classical complement component of the immune  
 CC system. Transgenic animals may be created to aid in the study of the role  
 CC of ClqRp during growth and metabolism and as a model for disease states  
 CC in which the normal level of ClqRp is effected. The ability to regulate  
 CC the phagocytic capacity of myeloid cells via the regulation of cell  
 CC surface expression and function of ClqRp will be valuable as a  
 CC prophylactic treatment of individuals at risk from infection,  
 CC particularly those with genetic immunodeficiencies, HIV infection, or  
 CC undergoing cancer chemotherapy or high risk surgery  
 XX SQ Sequence 3460 BP; 764 A; 943 C; 996 G; 757 T; 0 U; 0 Other;  
 Query Match 66.7%; Score 16; DB 3; Length 3460;  
 Best Local Similarity 81.2%; Pred. No. 13;  
 Matches 13; Conservative 3; Mismatches 0; Indels 0; Gaps 0;  
 QY 9 UGAAGCCCUUCAGCGG 24  
 Db :|||||:|||||  
 491 TGAAGCCCTTCAGCGG 476  
 Search completed: May 26, 2004, 16:52:24  
 Job time : 107.037 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 26, 2004, 16:02:51 ; Search time 20.2274 Seconds  
(without alignments)  
658.454 Million cell updates/sec

Title: US-09-121-239-17

Perfect score: 24

Sequence: 1 GUGGACACUAGAGCCCUUACGCG 24

Scoring table: OLIGO\_NUC

Gapop 60.0 , Gapext 60.0

Searched: 682709 seqs, 277475446 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents NA.\*

- 1: /cgn2\_6/ptodata/2/ina/5A\_COMB.seq.\*
- 2: /cgn2\_6/ptodata/2/ina/5B\_COMB.seq.\*
- 3: /cgn2\_6/ptodata/2/ina/6A\_COMB.seq.\*
- 4: /cgn2\_6/ptodata/2/ina/6B\_COMB.seq.\*
- 5: /cgn2\_6/ptodata/2/ina/PCTUS\_COMB.seq.\*
- 6: /cgn2\_6/ptodata/2/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	16	66.7	306	4	US-09-252-991A-6328
C 2	16	66.7	897	4	US-09-252-991A-6056
C 3	16	66.7	1536	4	US-09-252-991A-6218
C 4	16	66.7	3460	2	US-08-751-305-1
5	15	62.5	23	1	US-08-363-233B-21
6	15	62.5	23	1	US-08-363-233B-22
7	15	62.5	33	3	US-08-793-408-9
8	15	62.5	33	3	US-08-793-408-11
9	15	62.5	33	3	US-09-139-762A-9
10	15	62.5	33	3	US-09-139-762A-11
11	15	62.5	47	3	US-08-448-446B-12
12	15	62.5	62	3	US-08-448-446B-1
13	15	62.5	80	1	US-08-152-621-7
14	15	62.5	80	1	US-08-306-691B-38
15	15	62.5	80	5	PCT-US92-05035-7
16	15	62.5	204	5	PCT-US93-06251-5
17	15	62.5	257	1	US-08-152-621-1
18	15	62.5	257	5	US-08-306-691B-36
19	15	62.5	257	5	PCT-US92-05035-1
C 20	15	62.5	1818	4	US-09-252-991A-3290
21	15	62.5	2115	4	US-09-252-991A-3388
22	15	62.5	3623	1	US-08-306-691B-35
C 23	15	62.5	30001	1	US-08-125-468-1
C 24	15	62.5	30001	2	US-08-474-933-1
25	14	58.3	23	1	US-08-152-621-34
26	14	58.3	23	1	US-08-363-233B-24
27	14	58.3	23	1	US-08-363-233B-25

ALIGNMENTS

RESULT 1

US-09-252-991A-6328  
; Sequence 6328, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18

; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 6328  
; LENGTH: 306  
; TYPE: DNA  
; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-6328

Query Match 66.7%; Score 16; DB 4; Length 306;  
Best Local Similarity 81.2%; Pred. No. 2.4;  
Matches 13; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 9 UGAAGCCCUUACGCG 24  
Db 59 TGAAGCCCTCAGCG 74

RESULT 2

US-09-252-991A-6056/c  
; Sequence 6056, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A

; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 6056  
; LENGTH: 897  
; TYPE: DNA

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; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-6056

Query Match
Best Local Similarity 66.7%; Score 16; DB 4; Length 897;
Matches 13; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 9 UGAAGCCCUUCACGG 24
Db 34 TGAAGCCCTTCACGG 19

RESULT 3
US-09-252-991A-6218/c
; Sequence 6218, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 6218
; LENGTH: 1536
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-6218

Query Match
Best Local Similarity 66.7%; Score 16; DB 4; Length 1536;
Matches 13; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 9 UGAAGCCCUUCACGG 24
Db 1334 TGAAGCCCTTCACGG 1319

RESULT 4
US-08-751-305-1/c
; Sequence 1, Application US/08751305
; Patent No. 5965439
; GENERAL INFORMATION:
; APPLICANT: Tenner et al., Andrea J.
; TITLE OF INVENTION: HOST DEFENSE ENHANCEMENT
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/751,305
; FILING DATE: 18-NOV-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Wetherell, Jr., John R.
; REGISTRATION NUMBER: 31,678
; REFERENCE/DOCKET NUMBER: 07306/012001
; TELEPHONE: 619/678-5070
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; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3460 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 149..2105
; US-08-751-305-1

Query Match
Best Local Similarity 66.7%; Score 16; DB 2; Length 3460;
Matches 13; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 9 UGAAGCCCUUCACGG 24
Db 491 TGAAGCCCTTCACGG 476

RESULT 5
US-08-363-233B-21
; Sequence 21, Application US/08363233B
; Patent No. 5714383
; GENERAL INFORMATION:
; APPLICANT: Thompson, James D.
; TITLE OF INVENTION: METHOD AND REAGENT FOR TREATING CHRONIC
; MYELOGENOUS LEUKEMIA
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/363,233B
; FILING DATE: December 23, 1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION DATA: including application
; PRIOR APPLICATION DATA: described below: 2
; APPLICATION NUMBER: 07/882,822
; FILING DATE: May 14, 1992
; APPLICATION NUMBER: 08/193,922
; FILING DATE: February 7, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 209/165
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 23 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-363-233B-21

Query Match
Best Local Similarity 62.5%; Score 15; DB 1; Length 23;
; TELEPHONE: 100.0%; Pred. No. 9.1;
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Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GAAGCCCUUCAGCGG 24  
|||||  
Db 4 GAAGCCCUUCAGCGG 18

## RESULT 6

US-08-363-233B-22  
; Sequence 22, Application US/08363233B  
; Patent No. 5714383

## GENERAL INFORMATION:

APPLICANT: Thompson, James D.  
TITLE OF INVENTION: METHOD AND REAGENT FOR TREATING CHRONIC  
MYELOGENOUS LEUKEMIA

NUMBER OF SEQUENCES: 39

CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon

STREET: 633 West Fifth Street

SUITE: Suite 4700

CITY: Los Angeles

STATE: California

COUNTRY: U.S.A.

ZIP: 90071-2066

## COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

MEDIUM TYPE: storage

COMPUTER: IBM Compatible

OPERATING SYSTEM: IBM P.C. DOS 5.0

SOFTWARE: FastSeq for Windows 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/363,233B

FILING DATE: December 23, 1994

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA: including application

PRIOR APPLICATION DATA: described below: 2

APPLICATION NUMBER: 07/882,822

FILING DATE: May 14, 1992

APPLICATION NUMBER: 08/193,922

FILING DATE: February 7, 1994

ATTORNEY/AGENT INFORMATION:

NAME: Warburg, Richard J.

REGISTRATION NUMBER: 32,327

REFERENCE/DOCKET NUMBER: 209/165

TELEPHONE: (213) 489-1600

TELEFAX: (213) 955-0440

TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 22:

SEQUENCE CHARACTERISTICS:

LENGTH: 23 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-363-233B-22

Query Match 62.5%; Score 15; DB 1; Length 23;

Best Local Similarity 100.0%; Pred. No. 9.1;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GAAGCCCUUCAGCGG 24

|||||

Db 3 GAAGCCCUUCAGCGG 17

## RESULT 7

US-08-793-408-9

; Sequence 9, Application US/08793408

; Patent No. 6007988

## GENERAL INFORMATION:

APPLICANT: Choo, Yen

APPLICANT: Klug, Aaron

APPLICANT: Sanchez Garcia, Isidro  
TITLE OF INVENTION: Improvements in or Relating to  
Binding Proteins for Recognition of DNA

NUMBER OF SEQUENCES: 18

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pillsbury Madison & Sutro, L.L.P.

STREET: 1100 New York Avenue, N.W.

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20005-3918

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Word Perfect

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/793,408

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/GB95/01949

FILING DATE: 17-AUG-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: GB 9514698.1

FILING DATE: 18-JUL-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: GB 9422534.9

FILING DATE: 08-NOV-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: GB 9416880.4

FILING DATE: 20-AUG-1994

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 33 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-793-408-9

Query Match 62.5%; Score 15; DB 3; Length 33;

Best Local Similarity 86.7%; Pred. No. 9.1;

Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 10 GAAGCCCUUCAGCGG 24

|||||

Db 16 GAAGCCCTTCAGCGG 30

## RESULT 8

US-08-793-408-11

; Sequence 11, Application US/08793408

; Patent No. 6007988

## GENERAL INFORMATION:

APPLICANT: Choo, Yen

APPLICANT: Klug, Aaron

APPLICANT: Sanchez Garcia, Isidro

TITLE OF INVENTION: Improvements in or Relating to

Binding Proteins for Recognition of DNA

NUMBER OF SEQUENCES: 18

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pillsbury Madison & Sutro, L.L.P.

STREET: 1100 New York Avenue, N.W.

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20005-3918

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Word Perfect

CURRENT APPLICATION DATA:

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; APPLICATION NUMBER: US/08/793,408
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA: PCT/GB95/01949
; FILING DATE: 17-AUG-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9514698.1
; FILING DATE: 18-JUL-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9422534.9
; FILING DATE: 08-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9416880.4
; FILING DATE: 20-AUG-1994
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 33 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-793-408-11

Query Match      62.5%; Score 15; DB 3; Length 33;
Best Local Similarity 86.7%; Pred. No. 9.1;
Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      10 GAAGCCCUUCAGCGG 24
DB      16 GAAGCCCTTCAGCGG 30

RESULT 9
US-09-139-762A-9
; Sequence 9, Application US/09139762A
; Patent No. 6013453
; GENERAL INFORMATION:
; APPLICANT: Choo, Yen
; APPLICANT: Klug, Aaron
; APPLICANT: Sanchez Garcia, Isidro
; TITLE OF INVENTION: Improvements in or Relating to
; TITLE OF INVENTION: Binding Proteins for Recognition of DNA
; NUMBER OF SEQUENCES: 125
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pillsbury Madison & Sutro, L.L.P.
; STREET: 1100 New York Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3918
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/139,762A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/793,408
; FILING DATE: 02-JUN-1997
; APPLICATION NUMBER: PCT/GB95/01949
; FILING DATE: 17-AUG-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9514698.1
; FILING DATE: 18-JUL-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9422534.9
; FILING DATE: 08-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9416880.4
; FILING DATE: 20-AUG-1994
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 33 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-139-762A-11

Query Match      62.5%; Score 15; DB 3; Length 33;
Best Local Similarity 86.7%; Pred. No. 9.1;
Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      10 GAAGCCCUUCAGCGG 24
DB      16 GAAGCCCTTCAGCGG 30

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; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 33 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-139-762A-9

Query Match      62.5%; Score 15; DB 3; Length 33;
Best Local Similarity 86.7%; Pred. No. 9.1;
Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      10 GAAGCCCUUCAGCGG 24
DB      16 GAAGCCCTTCAGCGG 30

RESULT 10
US-09-139-762A-11
; Sequence 11, Application US/09139762A
; Patent No. 6013453
; GENERAL INFORMATION:
; APPLICANT: Choo, Yen
; APPLICANT: Klug, Aaron
; APPLICANT: Sanchez Garcia, Isidro
; TITLE OF INVENTION: Improvements in or Relating to
; TITLE OF INVENTION: Binding Proteins for Recognition of DNA
; NUMBER OF SEQUENCES: 125
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pillsbury Madison & Sutro, L.L.P.
; STREET: 1100 New York Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3918
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/139,762A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/793,408
; FILING DATE: 02-JUN-1997
; APPLICATION NUMBER: PCT/GB95/01949
; FILING DATE: 17-AUG-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9514698.1
; FILING DATE: 18-JUL-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9422534.9
; FILING DATE: 08-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9416880.4
; FILING DATE: 20-AUG-1994
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 33 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-139-762A-11

Query Match      62.5%; Score 15; DB 3; Length 33;
Best Local Similarity 86.7%; Pred. No. 9.1;
Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      10 GAAGCCCUUCAGCGG 24
DB      16 GAAGCCCTTCAGCGG 30

```

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RESULT 11
US-08-448-446B-12
; Sequence 12, Application US/08448446B
; Patent No. 6080851
; GENERAL INFORMATION:
; APPLICANT: Pachuk et al.
; TITLE OF INVENTION: Compounds and Methods for the Treatment
; OF LEUKEMIA
; TITLE OF INVENTION: of Leukemias
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn
; ADDRESSEE: Kurtz Mackiewicz & No. 6080851iris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/448,446B
; FILING DATE: July 10, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/989,852
; FILING DATE: December 4, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Doreen Yanko Trujillo
; REGISTRATION NUMBER: 35,719
; REFERENCE/DOCKET NUMBER: APOL-0020
; TELECOMMUNICATION INFORMATION: C
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 47
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; ANTI-SENSE:
; US-08-448-446B-12

Query Match 62.5%; Score 15; DB 3; Length 47;
Best Local Similarity 100.0%; Pred. No. 9.1;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 GAAGCCCUUCAGCGG 24
Db 16 GAAGCCCUUCAGCGG 30

RESULT 12
US-08-448-446B-1
; Sequence 1, Application US/08448446B
; Patent No. 6080851
; GENERAL INFORMATION:
; APPLICANT: Pachuk et al.
; TITLE OF INVENTION: Compounds and Methods for the Treatment
; OF LEUKEMIA
; TITLE OF INVENTION: of Leukemias
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn
; ADDRESSEE: Kurtz Mackiewicz & No. 6080851iris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103

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; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/448,446B
; FILING DATE: July 10, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/989,852
; FILING DATE: December 4, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Doreen Yanko Trujillo
; REGISTRATION NUMBER: 35,719
; REFERENCE/DOCKET NUMBER: APOL-0020
; TELECOMMUNICATION INFORMATION: C
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 62
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; ANTI-SENSE: No
; US-08-448-446B-1

Query Match 62.5%; Score 15; DB 3; Length 62;
Best Local Similarity 100.0%; Pred. No. 9;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 GAAGCCCUUCAGCGG 24
Db 31 GAAGCCCUUCAGCGG 45

RESULT 13
US-08-152-621-7
; Sequence 7, Application US/08152621
; Patent No. 5652222
; GENERAL INFORMATION:
; APPLICANT: Calabretta, Bruno
; APPLICANT: Gwirtz, Alan M.
; TITLE OF INVENTION: Selective Inhibition of
; OF LEUKEMIA CELL PROLIFERATION
; TITLE OF INVENTION: Leukemic Cell Proliferation by bcr-abl
; TITLE OF INVENTION: Antisense Oligonucleotides
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEIDEL, GONDA, LAVORGNA
; ADDRESSEE: & MONACO, P.C.
; STREET: 1800 Two Penn Center
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: U.S.A.
; ZIP: 19102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/152,621
; FILING DATE: No. 5652222ember 15, 1993
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/718,302
; FILING DATE: June 18, 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Monaco, Daniel A.
; REGISTRATION NUMBER: 30,480
; REFERENCE/DOCKET NUMBER: 6056-120 (CT.) 1
; TELECOMMUNICATION INFORMATION:

```

TELEPHONE: (215) 568-8383  
TELEFAX: (215) 568-5549  
TELEX: No. 565222ze  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 80 Nucleotides  
TYPE: nucleic acid  
STRANDEDNESS: single stranded  
TOPOLOGY: linear  
US-08-152-621-7

Query Match 62.5%; Score 15; DB 1; Length 80;  
Best Local Similarity 86.7%; Pred. No. 9;  
Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 10 GAAGCCCUUCAGCGG 24  
DB 31 GAAGCCCTTCAGCGG 45

RESULT 14  
US-08-306-691B-38  
Sequence 38, Application US/08306691B  
Patent No. 5734039  
GENERAL INFORMATION:  
APPLICANT: Calabretta, Bruno  
APPLICANT: Skorski, Tomasz  
TITLE OF INVENTION: ANTISENSE  
TITLE OF INVENTION: OLIGONUCLEOTIDES TARGETING COOPERATING ONCOGENES  
NUMBER OF SEQUENCES: 55  
CORRESPONDENCE ADDRESS:  
ADDRESSES: Seidel, Gonda, Lavorigna & Monaco, P.C.  
STREET: Two Penn Center, Suite 1800  
CITY: Philadelphia  
STATE: Pennsylvania  
COUNTRY: U.S.A.  
ZIP: 19102

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb  
COMPUTER: IBM PS/2  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: WordPerfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/306,691B  
FILING DATE: September 15, 1994  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Monaco, Daniel A.  
REGISTRATION NUMBER: 30,480  
REFERENCE/DOCKET NUMBER: 8321-8  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (215) 568-8383  
TELEFAX: (215) 568-5549  
TELEX: No. 5734039e  
INFORMATION FOR SEQ ID NO: 38:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 80 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-306-691B-38

Query Match 62.5%; Score 15; DB 1; Length 80;  
Best Local Similarity 86.7%; Pred. No. 9;  
Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 10 GAAGCCCUUCAGCGG 24  
DB 31 GAAGCCCTTCAGCGG 45

RESULT 15  
PCT-US92-05035-7  
Sequence 7, Application PC/TUS9205035  
GENERAL INFORMATION:  
APPLICANT: Calabretta, Bruno  
APPLICANT: Gewirtz, Alan M.  
TITLE OF INVENTION: Selective Inhibition of  
TITLE OF INVENTION: Leukemic Cell Proliferation by bcr-abl  
TITLE OF INVENTION: Antisense Oligonucleotides  
NUMBER OF SEQUENCES: 34  
CORRESPONDENCE ADDRESS:  
ADDRESSES: Temple University - Of The Common-  
ADDRESS: wealth System of Higher Education  
STREET: 406 University Services Building  
CITY: Philadelphia  
STATE: Pennsylvania  
COUNTRY: U.S.A.  
ZIP: 19122  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb  
COMPUTER: IBM PS/2  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: WordPerfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US92/05035  
FILING DATE: 19920615  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/718,302  
FILING DATE: June 18, 1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/869,911  
FILING DATE: April 14, 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Monaco, Daniel A.  
REGISTRATION NUMBER: 30,480  
REFERENCE/DOCKET NUMBER: 6056-120 (CIP) 1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (215) 568-8383  
TELEFAX: (215) 568-5549  
TELEX: None  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 80 Nucleotides  
TYPE: NUCLEIC ACID  
STRANDEDNESS: single stranded  
TOPOLOGY: linear  
PCT-US92-05035-7

Query Match 62.5%; Score 15; DB 5; Length 80;  
Best Local Similarity 86.7%; Pred. No. 9;  
Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 10 GAAGCCCUUCAGCGG 24  
DB 31 GAAGCCCTTCAGCGG 45

Search completed: May 27, 2004, 02:25:15  
Job time : 20.2274 secs



GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: May 27, 2004, 11:30:47 ; Search time 126.301 Seconds  
(without alignments)  
864.392 Million cell updates/sec

Title: US-09-121-239-17

Perfect score: 24

Sequence: 1 GUGAACAUAGAGCCUUCACGG 24

Scoring table: OLIGO NUC

Gapop 60.0 , Gapext 60.0

Searched: 2960401 seqs, 2274450654 residues

Word size : 0

Total number of hits satisfying chosen parameters: 5920802

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published Applications NA:\*

- 1: /cgn2\_6/ptodata/2/pubpna/US07\_PUBCOMB.seq:\*
- 2: /cgn2\_6/ptodata/2/pubpna/PCT\_NEW\_PUB.seq:\*
- 3: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq:\*
- 4: /cgn2\_6/ptodata/2/pubpna/US06\_PUBCOMB.seq:\*
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- 8: /cgn2\_6/ptodata/2/pubpna/US08\_PUBCOMB.seq:\*
- 9: /cgn2\_6/ptodata/2/pubpna/US09A\_PUBCOMB.seq:\*
- 10: /cgn2\_6/ptodata/2/pubpna/US09B\_PUBCOMB.seq:\*
- 11: /cgn2\_6/ptodata/2/pubpna/US09C\_PUBCOMB.seq:\*
- 12: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq:\*
- 13: /cgn2\_6/ptodata/2/pubpna/US10A\_PUBCOMB.seq:\*
- 14: /cgn2\_6/ptodata/2/pubpna/US10B\_PUBCOMB.seq:\*
- 15: /cgn2\_6/ptodata/2/pubpna/US10C\_PUBCOMB.seq:\*
- 16: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq:\*
- 17: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq:\*
- 18: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq:\*
- 19: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Match	Length	DB	ID	Description
1	24	100.0	3450	16	US-10-457-954-5	Sequence 5, Appli
2	18	75.0	34125	9	US-09-782-378A-25	Sequence 25, Appli
3	16	66.7	65	10	US-09-908-975-27688	Sequence 27688, A
4	16	66.7	310	15	US-10-029-386-26614	Sequence 26614, A
5	16	66.7	555	15	US-10-029-386-12914	Sequence 12914, A
6	16	66.7	1044	9	US-09-815-242-7861	Sequence 7861, Ap
7	16	66.7	1044	13	US-10-282-122A-30374	Sequence 30374, A
8	16	66.7	1424	13	US-10-425-114-523	Sequence 523, App
9	16	66.7	1951	15	US-10-029-386-22997	Sequence 22997, A
10	16	66.7	6699	13	US-10-211-462-130	Sequence 130, App
11	16	66.7	6699	15	US-10-021-660-15	Sequence 15, Appli
12	16	66.7	85076	16	US-10-085-117-97	Sequence 97, Appli
13	16	66.7	126413	13	US-10-087-192-1831	Sequence 1831, Ap
14	15	62.5	24	13	US-10-382-634-21	Sequence 21, Appli

15	15	62.5	24	15	US-10-349-320-20	Sequence 20, Appli
16	15	62.5	205	9	US-09-867-701-10433	Sequence 10433, A
17	15	62.5	436	9	US-09-960-352-5213	Sequence 5213, Ap
18	15	62.5	489	13	US-10-424-599-43483	Sequence 43483, A
19	15	62.5	491	13	US-10-424-599-7082	Sequence 7082, Ap
20	15	62.5	499	13	US-10-027-632-85551	Sequence 85551, A
21	15	62.5	499	16	US-10-027-632-85551	Sequence 85551, A
22	15	62.5	729	13	US-10-107-431-100	Sequence 100, App
23	15	62.5	773	13	US-10-027-632-133705	Sequence 133705, A
24	15	62.5	773	16	US-10-027-632-133705	Sequence 133705, A
25	15	62.5	1133	13	US-10-425-114-4855	Sequence 4855, Ap
26	15	62.5	1163	13	US-10-027-632-118039	Sequence 118039, A
27	15	62.5	1163	13	US-10-027-632-118040	Sequence 118040, A
28	15	62.5	1163	16	US-10-027-632-118039	Sequence 118039, A
29	15	62.5	1163	16	US-10-027-632-118040	Sequence 118040, A
30	15	62.5	1590	16	US-10-369-493-27261	Sequence 27261, A
31	15	62.5	1749	13	US-10-282-122A-25460	Sequence 25460, A
32	15	62.5	1765	13	US-10-424-599-103532	Sequence 103532, A
33	15	62.5	1806	9	US-09-815-242-4015	Sequence 4015, Ap
34	15	62.5	1806	13	US-10-282-122A-7373	Sequence 7373, Ap
35	15	62.5	2482	13	US-10-363-616-49	Sequence 49, Appli
36	15	62.5	3393	13	US-10-263-480-1	Sequence 1, Appli
37	15	62.5	3606	16	US-10-214-529-6	Sequence 6, Appli
38	15	62.5	3840	15	US-10-204-041-3	Sequence 3, Appli
39	15	62.5	5527	9	US-09-880-107-3710	Sequence 3710, Ap
40	15	62.5	5744	16	US-10-439-703-5	Sequence 5, Appli
41	15	62.5	38734	10	US-09-373-658-30	Sequence 30, Appli
42	15	62.5	38734	11	US-09-989-687-30	Sequence 30, Appli
43	15	62.5	45055	13	US-10-107-431-277	Sequence 277, App
44	15	62.5	84539	9	US-09-962-436-35	Sequence 36, Appli
45	15	62.5	212231	13	US-10-087-192-1126	Sequence 1126, Ap

ALIGNMENTS

RESULT 1  
US-10-457-954-5  
; Sequence 5, Application US/10457954  
; Publication No. US20040005623A1  
; GENERAL INFORMATION:  
; APPLICANT: Longley, B. Jack  
; TITLE OF INVENTION: Method of determining tumor sensitivities to therapeutic drugs  
; FILE REFERENCE: 960296.98890  
; CURRENT APPLICATION NUMBER: US/10/457,954  
; CURRENT FILING DATE: 2003-06-10  
; PRIOR APPLICATION NUMBER: 60/387,370  
; PRIOR FILING DATE: 2002-06-10  
; PRIOR APPLICATION NUMBER: 60/387,406  
; PRIOR FILING DATE: 2002-06-10  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 5  
; LENGTH: 3450  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(3447)  
; FEATURE:  
; NAME/KEY: misc\_structure  
; LOCATION: (730)..(765)  
; OTHER INFORMATION: encode amino acids 244-255 for forming the sides of the enzymatic  
; OTHER INFORMATION: pocket  
; FEATURE:  
; NAME/KEY: misc\_structure  
; LOCATION: (931)..(1077)  
; OTHER INFORMATION: encode amino acids 311-359 for forming the sides of the enzymatic  
; OTHER INFORMATION: pocket  
; FEATURE:  
; NAME/KEY: misc\_structure  
; LOCATION: (1141)..(1206)  
; OTHER INFORMATION: encode amino acids 381-402 for forming the enzymatic pocket's

; OTHER INFORMATION: activation loop  
US-10-457-954-5

Query Match 100.0%; Score 24; DB 16; Length 3450;  
Best Local Similarity 83.3%; Pred. No. 0.00011;  
Matches 20; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 GUGAACAUAGAGCCCUACGCG 24  
|:|||||:|||||:|||||:|||||  
Db 127 GTGGAACATGAAGCCCTTCAGCG 150

## RESULT 2

US-09-782-378A-25/c  
; Sequence 25, Application US/09782378A  
; Patent No. US20020102731A1  
; GENERAL INFORMATION:  
; APPLICANT: Hearing, Patrick  
; APPLICANT: Bahou, Wadie  
; APPLICANT: Sandalon, Ziv  
; APPLICANT: Gnatenko, Dmitri  
; TITLE OF INVENTION: Adenoviral Vectors  
; FILE REFERENCE: STONYB-04970  
; CURRENT APPLICATION NUMBER: US/09/782,378A  
; CURRENT FILING DATE: 2001-02-12  
; PRIOR APPLICATION NUMBER: 60/237,747  
; PRIOR FILING DATE: 2000-10-02  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: Patent in version 3.0  
; SEQ ID NO 25  
; LENGTH: 34125  
; TYPE: DNA  
; ORGANISM: Human adenovirus type 12  
US-09-782-378A-25

Query Match 75.0%; Score 18; DB 9; Length 34125;  
Best Local Similarity 83.3%; Pred. No. 0.41;  
Matches 15; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 GGAACAUGAGCCCUUCA 20  
|||||:|||||:|||||:|||||  
Db 4015 GGAACATGAAGCCCTTCA 3998

## RESULT 3

US-09-908-975-27688  
; Sequence 27688, Application US/09908975  
; Publication No. US20030165843A1  
; GENERAL INFORMATION:  
; APPLICANT: SHOSHAN, Avi  
; APPLICANT: WASSERMAN, Alon  
; APPLICANT: MINTZ, Eli  
; APPLICANT: MINTZ, Liat  
; APPLICANT: FAIGLER, Simchon  
; TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICING  
; FILE REFERENCE: 36688-0005  
; CURRENT APPLICATION NUMBER: US/09/908,975  
; CURRENT FILING DATE: 2001-07-20  
; PRIOR APPLICATION NUMBER: US 60/287,724  
; PRIOR FILING DATE: 2001-05-02  
; PRIOR APPLICATION NUMBER: US 60/221,607  
; PRIOR FILING DATE: 2000-07-28  
; NUMBER OF SEQ ID NOS: 32337  
; SOFTWARE: Patent in version 3.0  
; SEQ ID NO 27688  
; LENGTH: 65  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-09-908-975-27688

Query Match 66.7%; Score 16; DB 10; Length 65;  
Best Local Similarity 87.5%; Pred. No. 7.9;

Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GUGAACAUAGAGCC 16  
|:|||||:|||||:|||||  
Db 7 GTGGAACATGAAGCC 22

## RESULT 4

US-10-029-386-26614  
; Sequence 26614, Application US/10029386  
; Publication No. US20030194704A1  
; GENERAL INFORMATION:  
; APPLICANT: Penn, Sharron G.  
; APPLICANT: Rank, David R.  
; APPLICANT: Hanzel, David K.  
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR GENOTYPING  
; FILE REFERENCE: AEOMICA-X-2  
; CURRENT APPLICATION NUMBER: US/10/029,386  
; CURRENT FILING DATE: 2001-12-20  
; NUMBER OF SEQ ID NOS: 34288  
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1  
; SEQ ID NO 26614  
; LENGTH: 310  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: MAP TO CHR20.3  
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.2  
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 3.5  
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.5  
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.9  
; OTHER INFORMATION: SWISSPROT HIT: P07204, EVALUE 2.00e-08  
; OTHER INFORMATION: NT HIT: g112742414, EVALUE 0.00e+00  
; OTHER INFORMATION: EST\_HUMAN HIT: B1907890.1, EVALUE 0.00e+00  
US-10-029-386-26614

Query Match 66.7%; Score 16; DB 15; Length 310;  
Best Local Similarity 81.2%; Pred. No. 7.5;  
Matches 13; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 9 UGAAGCCCUACGCG 24  
|:|||||:|||||:|||||  
Db 47 TGAAGCCCTTCAGCG 62

## RESULT 5

US-10-029-386-12914  
; Sequence 12914, Application US/10029386  
; Publication No. US20030194704A1  
; GENERAL INFORMATION:  
; APPLICANT: Penn, Sharron G.  
; APPLICANT: Rank, David R.  
; APPLICANT: Hanzel, David K.  
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR GENOTYPING  
; FILE REFERENCE: AEOMICA-X-2  
; CURRENT APPLICATION NUMBER: US/10/029,386  
; CURRENT FILING DATE: 2001-12-20  
; NUMBER OF SEQ ID NOS: 34288  
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1  
; SEQ ID NO 12914  
; LENGTH: 555  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: MAP TO CHR20.3  
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.2  
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 3.5  
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.5  
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.9  
; OTHER INFORMATION: SWISSPROT HIT: P07204, EVALUE 4.00e-08  
; OTHER INFORMATION: NT HIT: g112742414, EVALUE 0.00e+00

; OTHER INFORMATION: EST\_HUMAN HIT: BI907890.1, EVALUATE 0.00e+00  
US-10-029-386-12914

Query Match 66.7%; Score 16; DB 15; Length 555;  
Best Local Similarity 81.2%; Pred. No. 7.3;  
Matches 13; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 9 UGAAGCCCUUACGCG 24  
DB 75 TGAAGCCCTTCAGCG 90

## RESULT 6

US-09-815-242-7861  
; Sequence 7861, Application US/09815242  
; Patent No. US20020061569A1

; GENERAL INFORMATION:

; APPLICANT: Haselbeck, Robert  
; APPLICANT: Ohlsen, Kari L.  
; APPLICANT: Zyskind, Judith W.  
; APPLICANT: Wall, Daniel  
; APPLICANT: Trawick, John D.  
; APPLICANT: Carr, Grant J.  
; APPLICANT: Yamamoto, Robert T.  
; APPLICANT: Xu, H. Howard

; TITLE OF INVENTION: Identification of Essential Genes in

; FILE REFERENCE: ELITRA.011A

; CURRENT APPLICATION NUMBER: US/09/815,242  
; CURRENT FILING DATE: 2001-03-21

; PRIOR APPLICATION NUMBER: 60/191,078

; PRIOR FILING DATE: 2000-03-21

; PRIOR APPLICATION NUMBER: 60/206,848

; PRIOR FILING DATE: 2000-05-23

; PRIOR APPLICATION NUMBER: 60/207,727

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: 60/242,578

; PRIOR FILING DATE: 2000-10-23

; PRIOR APPLICATION NUMBER: 60/253,625

; PRIOR FILING DATE: 2000-11-27

; PRIOR APPLICATION NUMBER: 60/257,931

; PRIOR FILING DATE: 2000-12-22

; PRIOR APPLICATION NUMBER: 60/269,308

; PRIOR FILING DATE: 2001-02-16

; NUMBER OF SEQ ID NOS: 14110

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 7861

; LENGTH: 1044

; TYPE: DNA

; ORGANISM: Pseudomonas aeruginosa

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (1)...(1044)

US-09-815-242-7861

Query Match 66.7%; Score 16; DB 9; Length 1044;  
Best Local Similarity 81.2%; Pred. No. 7.2;  
Matches 13; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 9 UGAAGCCCUUACGCG 24  
DB 797 TGAAGCCCTTCAGCG 812

## RESULT 7

US-10-282-122A-30374

; Sequence 30374, Application US/10282122A

; Publication No. US20040029129A1

; GENERAL INFORMATION:

; APPLICANT: Wang, Liangsu

; APPLICANT: Zamudio, Carlos

; APPLICANT: Malone, Cheryl

; APPLICANT: Haselbeck, Robert

; APPLICANT: Ohlsen, Kari  
; APPLICANT: Zyskind, Judith  
; APPLICANT: Wall, Daniel  
; APPLICANT: Trawick, John  
; APPLICANT: Carr, Grant  
; APPLICANT: Yamamoto, Robert  
; APPLICANT: Forsyth, R.  
; APPLICANT: Xu, H.  
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms  
; FILE REFERENCE: ELITRA.034A  
; CURRENT APPLICATION NUMBER: US/10/282,122A  
; CURRENT FILING DATE: 2003-02-20  
; PRIOR APPLICATION NUMBER: 60/191,078  
; PRIOR FILING DATE: 2000-03-21  
; PRIOR APPLICATION NUMBER: 60/206,848  
; PRIOR FILING DATE: 2000-05-23  
; PRIOR APPLICATION NUMBER: 60/207,727  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: 60/230,335  
; PRIOR FILING DATE: 2000-09-06  
; PRIOR APPLICATION NUMBER: 60/230,347  
; PRIOR FILING DATE: 2000-09-09  
; PRIOR APPLICATION NUMBER: 60/242,578  
; PRIOR FILING DATE: 2000-10-23  
; PRIOR APPLICATION NUMBER: 60/253,625  
; PRIOR FILING DATE: 2000-11-27  
; PRIOR APPLICATION NUMBER: 60/257,931  
; PRIOR FILING DATE: 2000-12-22  
; PRIOR APPLICATION NUMBER: 60/267,636  
; PRIOR FILING DATE: 2001-02-09  
; PRIOR APPLICATION NUMBER: 60/269,308  
; PRIOR FILING DATE: 2001-02-16  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 78614

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 30374

; LENGTH: 1044

; TYPE: DNA

; ORGANISM: Pseudomonas aeruginosa

US-10-282-122A-30374

Query Match 66.7%; Score 16; DB 13; Length 1044;  
Best Local Similarity 81.2%; Pred. No. 7.2;  
Matches 13; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 9 UGAAGCCCUUACGCG 24  
DB 797 TGAAGCCCTTCAGCG 812

## RESULT 8

US-10-425-114-523

; Sequence 523, Application US/10425114

; Publication No. US20040034888A1

; GENERAL INFORMATION:

; APPLICANT: Liu, Jingdong

; APPLICANT: Zhou, Yihua

; APPLICANT: Kovalic, David K.

; APPLICANT: Screen, Steven E

; APPLICANT: Tabaska, Jack E

; APPLICANT: Cao, Yongwei

; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; FILE REFERENCE: 38-21(53313)B  
; CURRENT APPLICATION NUMBER: US/10/425,114  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 73128  
; SEQ ID NO 523  
; LENGTH: 1424  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: 700076886\_FLI

US-10-425-114-523

Query Match 66.7%; Score 16; DB 13; Length 1424;  
 Best Local Similarity 81.2%; Pred. No. 7.1;  
 Matches 13; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 GGAACAUGAGCCCUU 18  
 |||||:|||||:  
 Db 466 GGAACATGAGCCCTT 481

RESULT 9  
 US-10-029-386-22997/c  
 ; Sequence 22997, Application US/10029386  
 ; Publication No. US20030194704A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Penn, Sharon G.  
 ; APPLICANT: Rank, David R.  
 ; APPLICANT: Hanzel, David K.  
 ; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G  
 ; TITLE OF INVENTION: EXPRESSION ANALYSIS TWO  
 ; FILE REFERENCE: AEOMICA-X-2  
 ; CURRENT APPLICATION NUMBER: US/10/029,386  
 ; CURRENT FILING DATE: 2001-12-20  
 ; NUMBER OF SEQ ID NOS: 34288  
 ; SOFTWARE: Annonmax Sequence Listing Engine vers. 1.1  
 ; SEQ ID NO 22997  
 ; LENGTH: 1951  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; OTHER INFORMATION: MAP TO AL118508.6  
 ; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.4  
 ; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.83  
 ; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.3  
 ; OTHER INFORMATION: SWISSPROT HIT: O73775, EVALUATE 1.00e-39  
 ; OTHER INFORMATION: NT HIT: G112742414, EVALUATE 0.00e+00  
 ; OTHER INFORMATION: EST\_HUMAN HIT: B1907890.1, EVALUATE 0.00e+00  
 US-10-029-386-22997

Query Match 66.7%; Score 16; DB 15; Length 1951;  
 Best Local Similarity 81.2%; Pred. No. 7;  
 Matches 13; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 9 UGAAGCCCUUACGCGG 24  
 :|||||:|||||  
 Db 343 TGAAGCCCTTCAGCGG 328

RESULT 10  
 US-10-211-462-130/c  
 ; Sequence 130, Application US/10211462  
 ; Publication No. US20040033495A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Murray, Richard  
 ; APPLICANT: Glynnne, Richard  
 ; APPLICANT: Watson, Susan R.  
 ; APPLICANT: Aziz, Natasha  
 ; APPLICANT: Eos Biotechnology, Inc.  
 ; TITLE OF INVENTION: Methods of Diagnosis of Angiogenesis, Compositions and  
 ; TITLE OF INVENTION: Methods of Screening for Angiogenesis Modulators  
 ; FILE REFERENCE: 018501-006200US  
 ; CURRENT APPLICATION NUMBER: US/10/211,462  
 ; CURRENT FILING DATE: 2003-02-13  
 ; PRIOR APPLICATION NUMBER: US 09/784,356  
 ; PRIOR FILING DATE: 2001-02-14  
 ; PRIOR APPLICATION NUMBER: US 09/791,390  
 ; PRIOR FILING DATE: 2001-02-22  
 ; PRIOR APPLICATION NUMBER: US 60/310,025  
 ; PRIOR FILING DATE: 2001-08-03  
 ; PRIOR APPLICATION NUMBER: US 60/334,244  
 ; PRIOR FILING DATE: 2001-11-29  
 ; NUMBER OF SEQ ID NOS: 230

US-10-425-114-523

SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 130  
 ; LENGTH: 6699  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-10-211-462-130

Query Match 66.7%; Score 16; DB 13; Length 6699;  
 Best Local Similarity 81.2%; Pred. No. 6.7;  
 Matches 13; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 9 UGAAGCCCUUACGCGG 24  
 :|||||:|||||  
 Db 491 TGAAGCCCTTCAGCGG 476

RESULT 11  
 US-10-021-660-15/c  
 ; Sequence 15, Application US/10021660  
 ; Publication No. US20030152926A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Murray, Richard  
 ; APPLICANT: Glynnne, Richard  
 ; APPLICANT: Watson, Susan R.  
 ; APPLICANT: Eos Biotechnology, Inc.  
 ; TITLE OF INVENTION: No. US20030152926A1 Methods of Diagnosis of Angiogenesis,  
 ; TITLE OF INVENTION: Compositions and Methods of Screening for Angiogenesis  
 ; TITLE OF INVENTION: Modulators  
 ; FILE REFERENCE: 018501-000710US  
 ; CURRENT APPLICATION NUMBER: US/10/021,660  
 ; CURRENT FILING DATE: 2001-12-06  
 ; PRIOR APPLICATION NUMBER: US/09/784,356  
 ; PRIOR FILING DATE: 2001-02-14  
 ; PRIOR APPLICATION NUMBER: US 09/637,977  
 ; PRIOR FILING DATE: 2000-08-11  
 ; NUMBER OF SEQ ID NOS: 135  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 15  
 ; LENGTH: 6699  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-10-021-660-15

Query Match 66.7%; Score 16; DB 15; Length 6699;  
 Best Local Similarity 81.2%; Pred. No. 6.7;  
 Matches 13; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 9 UGAAGCCCUUACGCGG 24  
 :|||||:|||||  
 Db 491 TGAAGCCCTTCAGCGG 476

RESULT 12  
 US-10-085-117-97  
 ; Sequence 97, Application US/10085117  
 ; Publication No. US20030232334A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Morris, David W.  
 ; APPLICANT: Engelhard, Eric K.  
 ; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER  
 ; FILE REFERENCE: 529452000121  
 ; CURRENT APPLICATION NUMBER: US/10/085,117  
 ; CURRENT FILING DATE: 2002-02-27  
 ; PRIOR APPLICATION NUMBER: US 09/798,586  
 ; PRIOR FILING DATE: 2001-03-02  
 ; NUMBER OF SEQ ID NOS: 361  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 97  
 ; LENGTH: 85076  
 ; TYPE: DNA  
 ; ORGANISM: Mus musculus  
 ; FEATURE:  
 ; NAME/KEY: variation

```
; LOCATION: (1)....(85076)
; OTHER INFORMATION: n = any nucleotide
US-10-085-117-97

Query Match      66.7%; Score 16; DB 16; Length 85076;
Best Local Similarity 81.2%; Pred. No. 6.2;
Matches 13; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 7 CAUGAAGCCUUCAGC 22
Db 30782 CATGAAGCCCTTCAGC 30797

RESULT 13
US-10-087-192-1831/c
; Sequence 1831, Application US/10087192
; Publication No. US20020182586A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Engelhard, Eric K.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
; FILE REFERENCE: 529452000122
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US/10/087,192
; PRIOR FILING DATE: 2000-12-22
; PRIOR FILING DATE: 2001-03-02
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 2059
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1831
; LENGTH: 126413
; TYPE: DNA
; ORGANISM: Mus musculus
; NAME/KEY: misc_feature
; LOCATION: (1)....(126413)
; OTHER INFORMATION: n = A,T,C or G
US-10-087-192-1831

Query Match      66.7%; Score 16; DB 13; Length 126413;
Best Local Similarity 87.5%; Pred. No. 6.1;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GUGGAACAUAGAAGCCC 16
Db 101496 GTGGAACATGAAGCCC 101481

RESULT 14
US-10-382-634-21
; Sequence 21, Application US/10382634
; Publication No. US2004003821A1
; GENERAL INFORMATION:
; APPLICANT: Kreutzer, Roalnd
; TITLE OF INVENTION: Composition and Method for Inhibiting Expression of a Target Gene
; FILE REFERENCE: 20200/2062
; CURRENT FILING DATE: 2003-03-07
; PRIOR APPLICATION NUMBER: US/10/382,634
; PRIOR FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: DE 101 55 280.7
; PRIOR FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: DE 101 58 411.3
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: DE 101 60 151.4
; PRIOR FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: DE 102 30 996.5
; PRIOR FILING DATE: 2002-07-09
; PRIOR APPLICATION NUMBER: PCT/EP02/00152
; PRIOR FILING DATE: 2002-01-09
; PRIOR APPLICATION NUMBER: PCT/EP02/00151
; PRIOR FILING DATE: 2002-01-09
; PRIOR APPLICATION NUMBER: PCT/EP02/11971
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; PRIOR FILING DATE: 2002-10-25
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 21
; LENGTH: 24
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: PRIMER
US-10-382-634-21

Query Match      62.5%; Score 15; DB 13; Length 24;
Best Local Similarity 86.7%; Pred. No. 32;
Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 10 GAAGCCUUCAGCGG 24
Db 9 GAAGCCCTTCAGCGG 23

RESULT 15
US-10-349-320-20
; Sequence 20, Application US/10349320
; Publication No. US20030190654A1
; GENERAL INFORMATION:
; APPLICANT: Heidenreich, Olaf
; TITLE OF INVENTION: DOUBLE-STRANDED RNA (dsRNA) AND METHOD OF USE
; FILE REFERENCE: 20200/2112
; CURRENT APPLICATION NUMBER: US/10/349,320
; CURRENT FILING DATE: 2003-01-22
; PRIOR APPLICATION NUMBER: DE 102 02 419.7
; PRIOR FILING DATE: 2002-01-22
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Tagman probe
US-10-349-320-20

Query Match      62.5%; Score 15; DB 15; Length 24;
Best Local Similarity 86.7%; Pred. No. 32;
Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 10 GAAGCCUUCAGCGG 24
Db 9 GAAGCCCTTCAGCGG 23

Search completed: May 27, 2004, 14:58:31
Job time : 127.301 secs
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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 26, 2004, 15:22:41 ; Search time 847.385 Seconds  
(without alignments)  
845.770 Million cell updates/sec

Title: US-09-121-239-17

Perfect score: 24  
Sequence: 1 GUGGAACAUGAGCCUUCAGCGG 24

Scoring table: OLIGO NUC  
Gapop 60.0 , Gapext 60.0

Searched: 27513289 seqs, 14931090276 residues

Word size : 0

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

EST:\*

1: em\_estba:\*

2: em\_esthum:\*

3: em\_estin:\*

4: em\_estmu:\*

5: em\_estov:\*

6: em\_estpl:\*

7: em\_estro:\*

8: em\_estro:\*

9: gb\_est1:\*

10: gb\_est2:\*

11: gb\_est3:\*

12: gb\_est4:\*

13: gb\_est5:\*

14: gb\_est5:\*

15: em\_estfun:\*

16: em\_estom:\*

17: em\_gss\_hum:\*

18: em\_gss\_inv:\*

19: em\_gss\_pin:\*

20: em\_gss\_vrt:\*

21: em\_gss\_fun:\*

22: em\_gss\_mam:\*

23: em\_gss\_mus:\*

24: em\_gss\_pro:\*

25: em\_gss\_rod:\*

26: em\_gss\_phg:\*

27: em\_gss\_vrl:\*

28: gb\_gss1:\*

29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
c 1	24	100.0	404	14	H81820	H81820 Ys68e09.r1
2	24	100.0	421	12	BM832613	BM832613 K-EST0107
3	24	100.0	544	9	AL707819	AL707819 DKFp686L
c 4	24	100.0	781	13	BX097261	BX097261 BX097261

c 5	18	75.0	525	14	CD848190	CD848190 DH0AC002Z
6	18	75.0	546	13	B0019091	B0019091 QHE20D24.
c 7	18	75.0	573	13	BY243155	BY243155 BY243155
8	18	75.0	1110	12	BM917206	BM917206 AGENCOURT
c 9	17	70.8	303	14	CD588643	CD588643 RK047A3H0
10	17	70.8	317	14	CD585274	CD585274 RK030A2C0
c 11	17	70.8	323	14	CD591703	CD591703 RK065A4G0
c 12	17	70.8	324	14	CD601328	CD601328 RK132A1C1
c 13	17	70.8	330	14	CD601373	CD601373 RK132A2C1
c 14	17	70.8	330	14	CD602150	CD602150 RK140A2F0
c 15	17	70.8	496	14	CD603852	CD603852 RZ150A3E0
c 16	17	70.8	500	14	CD585675	CD585675 RK032A1E0
c 17	17	70.8	514	12	BJ063595	BJ063595 BJ063595
c 18	17	70.8	705	13	BQ617441	BQ617441 fab04C07.
19	17	70.8	925	10	BF120890	BF120890 601757493
20	16	66.7	157	10	AW386252	AW386252 CM4-PT001
21	16	66.7	191	10	AW420212	AW420212 fj88g07.Y
22	16	66.7	235	9	AI035445	AI035445 ub47a08.r
23	16	66.7	256	9	AA881130	AA881130 v205g05.r
24	16	66.7	281	12	BG985652	BG985652 ba02a03.u
c 25	16	66.7	288	10	BB009502	BB009502 BB009502
c 26	16	66.7	322	14	CD166258	CD166258 BM1-0002P
27	16	66.7	324	10	BB838010	BB838010 BB838010
c 28	16	66.7	325	10	BF148232	BF148232 ux49f03.x
c 29	16	66.7	335	10	BF318395	BF318395 ux1le01.x
c 30	16	66.7	339	12	BM211354	BM211354 C0804F12-
31	16	66.7	342	13	BY139003	BY139003 BY139003
32	16	66.7	344	10	BB869806	BB869806 BB869806
c 33	16	66.7	347	12	BM211586	BM211586 C0808G06-
34	16	66.7	348	13	BY175856	BY175856 BY175856
35	16	66.7	354	13	BY310701	BY310701 BY310701
36	16	66.7	356	9	AA268399	AA268399 va41n09.r
37	16	66.7	359	13	BY020770	BY020770 BY020770
38	16	66.7	361	28	AQ037986	AQ037986 CIT-HSP-2
39	16	66.7	362	28	AQ040284	AQ040284 CIT-HSP-2
c 40	16	66.7	363	12	BM195340	BM195340 C0308E04-
41	16	66.7	363	13	BY304103	BY304103 BY304103
42	16	66.7	364	9	AA119050	AA119050 mp62h06.r
43	16	66.7	373	13	BY319051	BY319051 BY319051
c 44	16	66.7	377	13	BX636769	BX636769 BX636769
c 45	16	66.7	378	14	CD538683	CD538683 B0205E11-

## ALIGNMENTS

RESULT 1	H81820	404 bp	linear	EST 09-NOV-1995
H81820/c	Ys68e09.r1	Soares retina N2b4HR	Homo sapiens	cDNA clone
LOCUS	IMAGE:219976 5'	similar to gb:M14752	PROTO-ONCOGENE	
DEFINITION	TYROSINE-PROTEIN KINASE ABL (HUMAN)			mRNA sequence.
ACCESSION	H81820			
VERSION	H81820.1	GI:1059909		
KEYWORDS	EST.			
SOURCE	Homo sapiens (human)			
ORGANISM	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
REFERENCE	1 (bases 1 to 404)			
AUTHORS	Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfs, T., Soares, M., Tan, F., Trivasakis, E., Waterston, R., Williamson, A., Wohldmann, P. and Wilson, R.			
TITLE	The WashU-Merck EST Project			
JOURNAL	Unpublished (1995)			
COMMENT	Contact: Wilson RK Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: est@watson.wustl.edu			

High quality sequence stops: 382  
 Source: IMAGE Consortium, LLNL  
 This clone is available royalty-free through LLNL; contact the  
 IMAGE Consortium (info@image.llnl.gov) for further information.  
 Insert Length: 1427 Std Error: 0.00  
 Seq primer: M13RP1  
 High quality sequence stops: 382.

#### FEATURES

Location/Qualifiers  
 1..404

/organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="GDB:3847969"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:219976"  
 /sex="male"  
 /tissue\_type="retina"  
 /dev\_stage="55 year old"  
 /lab\_host="PH10B (ampicillin resistant)"  
 /clone\_lib="Soares retina N2b4HR"  
 /note="Organ: eye; Vector: p7T3D (Pharmacia) with a  
 modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st  
 strand cDNA was primed with a Not I - oligo(dT) primer [5'  
 TTTTACCAATCTGAAGTGGAGCGCGCTTTTCTTTTCTTTT 3'],  
 double-stranded cDNA was size selected, ligated to Eco RI  
 adapters (Pharmacia), digested with Not I and cloned into  
 the Not I and Eco RI sites of a modified pT73 vector  
 (Pharmacia). The retinas were obtained from a 55 year old  
 Caucasian and total cellular poly(A)<sup>+</sup> RNA was extracted 6  
 hrs after their removal. The retina RNA was kindly  
 provided by Roderick R. McInnes M.D. Ph.D. from the  
 University of Toronto. Library constructed by Bento  
 Soares and M. Fatima Bonaldo."

#### ORIGIN

Query Match 100.0%; Score 24; DB 14; Length 404;  
 Best Local Similarity 83.3%; Pred. No. 0.0037;  
 Matches 20; Conservative 4; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GUGGAACAUGAAGCCCUACGCGG 24  
 Db 134 GTGGACATGAGCCCTTCAGCGG 111

RESULT 2  
 BM832613 421 bp mRNA linear EST 06-MAR-2002  
 LOCUS K-EST0107122 S11SNUI Homo sapiens cDNA clone S11SNUI-47-E02 5',  
 mRNA sequence.

ACCESSION BM832613  
 VERSION BM832613.1 GI:19189022

KEYWORDS EST.

SOURCE Homo sapiens (human)

#### ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 421)

AUTHORS Kim N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R.,  
 Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and  
 Kim, Y.S.

TITLE 21C Frontier Korean EST Project 2001

JOURNAL Unpublished (2002)

COMMENT Contact: Kim YS

Genome Research Center

Korea Research Institute of Bioscience & Biotechnology

52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea

Tel: +82-42-860-4470

Fax: +82-42-860-4409

Email: yongsung@mail.kribb.re.kr

Plate: 47 row: E column: 02

High quality sequence stop: 421.

Location/Qualifiers

1..421

/organism="Homo sapiens"

#### FEATURES

source

/mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="S11SNUI-47-E02"  
 /sex="M"  
 /tissue\_type="Stomach"  
 /cell\_type="Lymphoblast-like"  
 /cell\_line="SNU-1"  
 /lab\_host="Top10F"  
 /clone\_lib="S11SNUI"

/note="Organ: Stomach; Vector: pME18-FL3; Site 1: XhoI;  
 Site 2: XhoI; The poly (A)<sup>+</sup> RNA was dephosphorylated with  
 bacterial alkaline phosphatase (BAP) and then decapped  
 with tobacco acid pyrophosphatase (TAP). The decapped  
 intact mRNA was ligated with DNA-RNA linker including SfiI  
 site by treatment of T4 RNA ligase and the first strand  
 cDNA was synthesized with Superscript II using SfiI  
 oligo-dT primer. After first strand synthesis, RNA was  
 degraded by NaOH treatment and cDNA was amplified by PCR  
 reaction. The PCR products were digested with SfiI and  
 cloned into DraIII- digested pME18S-FL3 vector. The  
 obtained cDNA vectors were used for transformation of  
 competent cells E. coli Top10F by electroporation method.  
 The cDNA libraries constructed by this method are  
 full-length enriched cDNA library."

#### ORIGIN

Query Match 100.0%; Score 24; DB 12; Length 421;  
 Best Local Similarity 83.3%; Pred. No. 0.0037;  
 Matches 20; Conservative 4; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GUGGAACAUGAAGCCCUACGCGG 24  
 Db 247 GTGGACATGAGCCCTTCAGCGG 270

#### RESULT 3

AL707819

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Contact: MIPS

Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany

This is the 5' sequence of the clone insert

Clone from S. Wiemann, Molecular Genome Analysis, German Cancer

Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;

sequenced by AGOWA (Berlin/Germany) within the cDNA sequencing

consortium of the German Genome Project.

No sl sequence available.

This clone (DKFZp686L0149) is available at the RZPD in Berlin.

Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059

Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

Location/Qualifiers

1..544

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="DKFZp686L0149"

/dev\_stage="adult"

/lab\_host="DH10B"

/clone\_lib="686 (synonym: hlccc3)"

/note="Vector: pTriplex2; Site\_1: SfiI; Site\_2: SfiI;B;



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ORIGIN
Query Match      100.0%; Score 24; DB 9; Length 544;
Best Local Similarity 83.3%; Pred. No. 0.004;
Matches 20; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 GUGGAACAUGAAGCCUUCAGCGG 24
    |:|||||:|||||:|||||
Db 501 GTGGAACATGAAGCCCTTCAGCGG 524

RESULT 4
BX097261/c
LOCUS
DEFINITION BX097261 Soares retina N2b4HR Homo sapiens cDNA clone
ACCESSION BX097261
VERSION
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Euthera; Primates; Catarrhini; Homiidae; Homo.
TITLE 1 (bases 1 to 781)
JOURNAL Ebert, L., Heil, O., Hennig, S., Neubert, P., Partsch, E., Peters, M.,
COMMENT Radelof, U., Schneider, D. and Korn, B.
Human Unigeneset - RZPD3
Unpublished (2003)
Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
RZPD; IMAGp998C17436.
RZPDLIB; I.M.A.G.E. cDNA Clone Collection;
http://www.rzpd.de/CloneCards/cgi-bin/showLib.pl.cgi/responder?libno=972 Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 101
Fax: +49 30 32639 111
www.rzpd.de
This clone is available royalty-free from RZPD;
contact RZPD (clone@rzpd.de) for further information. Seq primer:
M13r, Primer sequence: TTTCACAGGAACAGTATGAC.
FEATURES
source
1..781
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGp998C17436 ; IMAGE:219976"
/sex="male"
/tissue_type="retina"
/dev_stage="55 year old"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares retina N2b4HR"
/note="Organ: eye; Vector: pT7T3D (Pharmacia) with a
modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st
strand cDNA was primed with a Not I.- oligo(GT) primer [5',
TGTTCACATCTGAGTGGAGCGCGCGCTTTTCTTTTCTTTT 3'],
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT7T3 vector
(Pharmacia). The retinas were obtained from a 55 year old
Caucasian and total cellular poly(A)+ RNA was extracted 6
hrs after their removal. The retina RNA was kindly
provided by Roderick R. McInnes M.D. Ph.D. from the
University of Toronto. Library constructed by Bento
Soares and M.Fatima Bernaldo."

ORIGIN
Query Match      100.0%; Score 24; DB 13; Length 781;
Best Local Similarity 83.3%; Pred. No. 0.0045;

ORIGIN
Query Match      75.0%; Score 18; DB 14; Length 525;
Best Local Similarity 77.8%; Pred. No. 10;
Matches 14; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 GUGGAACAUGAAGCCUUC 18
    |:|||||:|||||:
Db 228 GTGGAACATGAAGCCCTT 211

RESULT 6
BU019091
LOCUS
DEFINITION QHE20D24.Yg.ab1 QH EFGHJ sunflower RHA280 Helianthus annuus cDNA
ACCESSION BU019091
VERSION
KEYWORDS
SOURCE
ORGANISM Helianthus annuus (common sunflower)
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Lai, Z., Church, S., Jackson, L. and Bradford, K.
Lettuce and Sunflower ESTs from the Compositae Genome Project

ORIGIN
Query Match      546 bp mRNA linear EST 23-AUG-2002
Best Local Similarity 77.8%; Pred. No. 10;
Matches 14; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 GUGGAACAUGAAGCCUUC 18
    |:|||||:|||||:
Db 228 GTGGAACATGAAGCCCTT 211

RESULT 5
CD848190/c
LOCUS
DEFINITION CD848190 525 bp mRNA linear EST 11-JUL-2003
ACCESSION CD848190.1 GI:32532012
VERSION
KEYWORDS
SOURCE
ORGANISM Helianthus annuus (common sunflower)
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
TITLE 1 (bases 1 to 525)
JOURNAL Heliantheae; Helianthus.
COMMENT Genoplante, a major partnership french program in plant genomics
Unpublished (2003)
Contact: Genoplante
Genoplante
93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplante' (http://www.genoplante.com
and http://genoplante-info.infobiogen.fr).
FEATURES
source
1..525
/organism="Helianthus annuus"
/mol_type="mRNA"
/cultivar="psc8"
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/clone="HaDevR2002H02"
/tissue_type="terminal bud"
/clone_lib="HaDevR2"

```

http://compgenomics.ucdavis.edu/  
 Unpublished (2002)  
 Contact: Alexander Kozik [R.W.Michelmore]  
 Department of Vegetable Crops, R.W.Michelmore Lab  
 University of California at Davis (UCD)  
 Asmudson Hall, UCD, Davis, CA 95616, USA  
 Tel: 1-(530)-742-1742  
 Fax: 1-(530)-752-9659  
 Email: akorikeatgc.org [michelmore@veggmail.ucdavis.edu]  
 singleton, see http://cgpdb.ucdavis.edu/ for details.  
 Plate: QHE20 row: D column: 24.

Location/Qualifiers  
 1. .546  
 /organism="Helianthus annuus"  
 /mol\_type="mRNA"  
 /cultivar="RHA280"  
 /db\_xref="taxon:4232"  
 /clone="QHE20D24"  
 /lab\_host="E.coli"  
 /note="Vector: pBRCNDASFIAB; The library was constructed from 11 different sources of RNA from a single genotype. Separate cDNAs were generated using primers that incorporated unique 5' and 3' tags to distinguish each source of RNA. cDNAs were then pooled, size-fractionated, directionally cloned into a custom medium-copy vector and transfections made with four size classes to minimize size bias. Details of each source of RNA and library construction can be obtained at http://cgpdb.ucdavis.edu/  
 TAG LIB=QH EFGHJ sunflower RHA280  
 TAG TISSUE=roots environmental stress  
 TAG\_SEQ=ATCTCGCGGG"

ORIGIN  
 Query Match 75.0%; Score 18; DB 13; Length 546;  
 Best Local Similarity 77.8%; Pred. No. 10;  
 Matches 14; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 GUGGACACGAGCCCUU 18  
 Db 292 GTGGAACATGAGCCCTT 309  
 |:|||||:|||||:|

RESULT 7  
 BY243155/c  
 LOCUS  
 DEFINITION  
 BY243155 RIKEN full-length enriched, visual cortex Mus musculus  
 cDNA clone K230039L14 5', mRNA sequence.  
 BY243155  
 ACCESSION  
 VERSION  
 BY243155.1 GI:26424667  
 KEYWORDS  
 EST.  
 SOURCE  
 Mus musculus (house mouse)  
 ORGANISM  
 Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 573)  
 Okazaki.Y., Furuno.M., Kasukawa.T., Adachi.J., Bono.H., Kondo.S.,  
 Nikaido.I., Osato.N., Saito.R., Suzuki.H., Yamanaka.I.,  
 Kiyosawa.H., Yagi.K., Tomaru.Y., Hasegawa.Y., Nogami.A.,  
 Schenbach.C., Gojobori.T., Baldarelli.R., Hill.D.P., Bult.C.,  
 Hume.D.A., Quackenbush.J., Schriml.L.M., Kanapin.A., Matsuda.H.,  
 Batalov.S., Beisel.K.W., Blake.J.A., Bradt.D., Brusic.V.,  
 Chothia.C., Corbani.L.E., Cousins.S., Dalla.E., Dragani.T.A.,  
 Fletcher.C.P., Forrest.A., Fraser.K.S., Gaasterland.T.,  
 Gariboldi.M., Gissi.K., Godzik.A., Gough.J., Grimmond.S.,  
 Gustincich.S., Hirokawa.N., Jackson.I.J., Jarvis.E.D., Kanai.A.,  
 Kawaji.H., Kawasawa.Y., Kedzierski.R.M., King.B.L., Konagaya.A.,  
 Kurochkin.I.V., Lee.Y., Lenhard.B., Lyons.P.A., Maglott.D.R.,  
 Maltais.L., Marchionni.L., McKenzie.L., Miki.H., Nagaehima.T.,  
 Numata.K., Okido.T., Pavan.W.J., Pertea.G., Pesole.G.,  
 Petrovsky.N., Pillai.R., Pontius.J.U., Qi.D., Ramachandran.S.,  
 Ravasi.T., Reed.J.C., Reed.D.J., Reid.J., Ring.B.Z., Ringwald.M.,  
 Sandelin.A., Schneider.C., Sempile.C.A., Setou.M., Shimada.K.,

Sultana.R., Takenaka.Y., Taylor.M.S., Teasdale.R.D., Tomita.M.,  
 Verardo.R., Wagner.L., Wahlestedt.C., Wang.Y., Watanabe.Y.,  
 Wells.C., Wilming.L.G., Wynshaw-Boris.A., Yanagisawa.M., Yang.I.,  
 Yang.L., Yuan.Z., Zavolan.M., Zhu.Y., Zimmer.A., Carninci.P.,  
 Hayatsu.N., Hirozane-Kishikawa.T., Konno.H., Nakamura.M.,  
 Sakazume.N., Sato.K., Shiraki.T., Waki.K., Kawai.J., Aizawa.K.,  
 Arakawa.T., Fukuda.S., Hara.A., Hashizume.W., Imotani.K., Ishii.Y.,  
 Itoh.M., Kagawa.I., Miyazaki.A., Sakai.K., Sasaki.D., Shibata.K.,  
 Shinagawa.A., Yasunishi.A., Yoshino.M., Waterston.R., Lander.E.S.,  
 Rogers.J., Birney.E. and Hayashizaki.Y.  
 Analysis of the mouse transcriptome based on functional annotation  
 of 60,770 full-length cDNAs  
 Nature 420, 563-573 (2002)  
 22354683  
 12466851  
 COMMENT  
 Contact: Yoshihide Hayashizaki  
 Laboratory for Genome Exploration Research Group, RIKEN Genomic  
 Sciences Center (GSC), Yokohama Institute  
 The Institute of Physical and Chemical Research (RIKEN)  
 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan  
 Tel: 81-45-503-9222  
 Fax: 81-45-503-9216  
 Email: genome-resgsc.riken.go.jp/  
 URL: http://genome.gsc.riken.go.jp/  
 Aizawa.K., Akimura.T., Arakawa.T., Carninci.P., Fukuda.S.,  
 Hirozane.T., Imotani.K., Ishii.Y., Itoh.M., Kawai.J., Konno.H.,  
 Miyazaki.A., Murata.M., Nakamura.M., Nomura.K., Numazaki.R.,  
 Ohno.M., Sakai.K., Sakazume.N., Sasaki.D., Sato.K., Shibata.K.,  
 Shiraki.T., Tagami.M., Waki.K., Watanishi.A., Muramatsu.M. and  
 Hayashizaki.Y. Direct Submission  
 Computational Analysis of Full-Length Mouse cDNAs Compared with  
 Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)  
 Normalization and subtraction of cap-trapper-selected cDNAs to  
 prepare full-length cDNA libraries for rapid discovery of new  
 genes. Genome Res. 10 (10), 1617-1630 (2000)  
 RIKEN integrated sequence analysis (RISA) system-384-format  
 sequencing pipeline with 384 multicapillary sequencer. Genome Res.  
 10 (11), 1757-1771 (2000)  
 Computer-based methods for the mouse full-length cDNA  
 encyclopedia: real-time sequence clustering for construction of a  
 non-redundant cDNA library. Genome Res. 11 (2), 281-289 (2001)  
 cDNA library was prepared and sequenced in Mouse Genome  
 Encyclopedia Project of Genome Exploration Research Group in Riken  
 Genomic Sciences Center and Genome Science Laboratory in RIKEN.  
 Division of Experimental Animal Research in Riken contributed to  
 prepare mouse tissues.  
 Tissues were provided by Michela Pagiolini and Takao K. Hensch (  
 Laboratory for Neuronal Circuit Development Brain Science Institute  
 RIKEN 2-1 Hiroosawa,Wako-shi,Saitama 351-0198 Japan ) whose  
 assistance we gratefully acknowledge. Please visit our web site  
 (http://genome.gsc.riken.go.jp) for further details.

FEATURES  
 Location/Qualifiers  
 1. .573  
 /organism="Mus musculus"  
 /mol\_type="mRNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="K230039L14"  
 /tissue\_type="visual cortex"  
 /clone\_lib="RIKEN full-length enriched, visual cortex"

ORIGIN  
 Query Match 75.0%; Score 18; DB 13; Length 573;  
 Best Local Similarity 83.3%; Pred. No. 11;  
 Matches 15; Conservative 3; Mismatches 0; Indels 0; Gaps 0;  
 QY 7 CAUGAGCCUUCAGCGG 24  
 Db 479 CATGAAGCCCTTCAGCGG 462  
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RESULT 8  
 BM917206

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LOCUS      BM917206                1110 bp    mRNA    linear    EST 12-MAR-2002
DEFINITION AGENCOURT_6702147 NIH_MGC_106 Homo sapiens cDNA clone IMAGE:5483703
VERSION     BM917206
ACCESSION   BM917206
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
REFERENCE   1 (bases 1 to 1110)
AUTHORS     NIH-MGC http://mcc.ncl.nih.gov/
TITLE       National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL     Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgabbs@mail.nih.gov
            Tissue Procurement: Dr. Daniel McVicar, DBS/NCI
            cDNA Library Preparation: Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2011 row: m column: 16
            High quality sequence stop: 651.

FEATURES             source
     source
     1..1110
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             /organism="Homo sapiens"
             /mol_type="mRNA"
             /db_xref="taxon:9606"
             /clone="IMAGE:5483703"
             /tissue_type="natural killer cells, cell line"
             /lab_host="DH10B (phage-resistant)"
             /clone_lib="NIH MGC 106"
             /note="Organ: blood; Vector: pOTB7; Site 1: XhoI; Site 2:
             EcoRI; cDNA made by oligo-dT priming. Directionally cloned
             into EcoRI/XhoI sites using the following 5' adaptor:
             GGACAGAG(G). Library constructed by Ling Hong in the
             laboratory of Gerald M. Rubin (University of California,
             Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
             Superscript II RT (Life Technologies). Note: this is a
             NIH_MGC Library."

ORIGIN
Query Match      75.0%; Score 18; DB 12; Length 1110;
Best Local Similarity 83.3%; Pred. No. 13;
Matches 15; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      5  AACATGAGCCCTTCAGC 22
        |||:|||||:|||||
DB      806 AACATGAGCCCTTCAGC 823

RESULT 9
CD588643/c
LOCUS      CD588643                303 bp    mRNA    linear    EST 16-JUN-2003
DEFINITION RK047A3H04.T3 Zebrafish Kidney Marrow cDNA library Danio rerio cDNA
clone RK047A3H04 5', mRNA sequence.
ACCESSION   CD588643
VERSION     CD588643
KEYWORDS    EST.
SOURCE      Danio rerio (zebrafish)
ORGANISM    Danio rerio
REFERENCE   1 (bases 1 to 303)
AUTHORS     Song,H.D., Wu,X.Y., Sun,X.J., Zhou,Y., Liu,T.X., Zhang,G.W.,
            Sheng,Y., Chen,Y., Ruan,Z., Jiang,C.L., Fan,H.Y., Look,A.T.,
            Zou,L.I. and Chen,Z.
TITLE       Gene Expression Profiling in the Zebrafish Kidney Marrow Tissue
JOURNAL     Unpublished (2003)
COMMENT     Contact: Chen Z.

FEATURES             source
     source
     1..317
         Location/Qualifiers
             /organism="Danio rerio"
             /mol_type="mRNA"
             /db_xref="taxon:7955"
             /clone="RK030A2C01"
             /dev_stage="mature"
             /note="Organ: kidney; Vector: pBS-CMV; Site 1: XhoI;
             Site 2: EcoRI; Total RNA was extracted from the kidney
             tissues of mature zebrafish. The poly (A)+ RNA fraction
             lambdaDazAP Express vector (Stratagene) and in vivo excised
             into pBS-CMV vector."

ORIGIN
Query Match      70.8%; Score 17; DB 14; Length 303;
Best Local Similarity 82.4%; Pred. No. 32;
Matches 14; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      5  AACATGAGCCCTTCAGC 21
        |||:|||||:|||||
DB      127 AACATGAGCCCTTCAGC 111

RESULT 10
CD585274/c
LOCUS      CD585274                317 bp    mRNA    linear    EST 16-JUN-2003
DEFINITION RK030A2C01.T3 Zebrafish Kidney Marrow cDNA library Danio rerio cDNA
clone RK030A2C01 5', mRNA sequence.
ACCESSION   CD585274
VERSION     CD585274
KEYWORDS    EST.
SOURCE      Danio rerio (zebrafish)
ORGANISM    Danio rerio
REFERENCE   1 (bases 1 to 317)
AUTHORS     Song,H.D., Wu,X.Y., Sun,X.J., Zhou,Y., Liu,T.X., Zhang,G.W.,
            Sheng,Y., Chen,Y., Ruan,Z., Jiang,C.L., Fan,H.Y., Look,A.T.,
            Zou,L.I. and Chen,Z.
TITLE       Gene Expression Profiling in the Zebrafish Kidney Marrow Tissue
JOURNAL     Unpublished (2003)
COMMENT     Contact: Chen Z.

FEATURES             source
     source
     1..317
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             /organism="Danio rerio"
             /mol_type="mRNA"
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             /clone="RK030A2C01"
             /dev_stage="mature"
             /note="Organ: kidney; Vector: pBS-CMV; Site 1: XhoI;
             Site 2: EcoRI; Total RNA was extracted from the kidney
             tissues of mature zebrafish. The poly (A)+ RNA fraction
             lambdaDazAP Express vector (Stratagene) and in vivo excised
             into pBS-CMV vector."

```

```

State Key Lab for Medical Genomics
Shanghai Institute of Hematology, Ruijin Hospital Affiliated to
Shanghai Second Medical University
197 Rui Jin Road II, Shanghai 200025, P. R. China
Tel: 86-21-64740490
Fax: 86-21-64743206
Email: zchen@stn.sh.cn
Seq primer: T3.

FEATURES             source
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             /clone="RK047A3H04"
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             /note="Organ: kidney; Vector: pBS-CMV; Site 1: XhoI;
             Site 2: EcoRI; Total RNA was extracted from the kidney
             tissues of mature zebrafish. The poly (A)+ RNA fraction
             was separated from total RNA by oligo (dT) cellulose
             chromatography. Library was initially constructed in the
             lambdaDazAP Express vector (Stratagene) and in vivo excised
             into pBS-CMV vector."

ORIGIN
Query Match      70.8%; Score 17; DB 14; Length 303;
Best Local Similarity 82.4%; Pred. No. 32;
Matches 14; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      5  AACATGAGCCCTTCAGC 21
        |||:|||||:|||||
DB      127 AACATGAGCCCTTCAGC 111

RESULT 10
CD585274/c
LOCUS      CD585274                317 bp    mRNA    linear    EST 16-JUN-2003
DEFINITION RK030A2C01.T3 Zebrafish Kidney Marrow cDNA library Danio rerio cDNA
clone RK030A2C01 5', mRNA sequence.
ACCESSION   CD585274
VERSION     CD585274
KEYWORDS    EST.
SOURCE      Danio rerio (zebrafish)
ORGANISM    Danio rerio
REFERENCE   1 (bases 1 to 317)
AUTHORS     Song,H.D., Wu,X.Y., Sun,X.J., Zhou,Y., Liu,T.X., Zhang,G.W.,
            Sheng,Y., Chen,Y., Ruan,Z., Jiang,C.L., Fan,H.Y., Look,A.T.,
            Zou,L.I. and Chen,Z.
TITLE       Gene Expression Profiling in the Zebrafish Kidney Marrow Tissue
JOURNAL     Unpublished (2003)
COMMENT     Contact: Chen Z.

FEATURES             source
     source
     1..317
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             /organism="Danio rerio"
             /mol_type="mRNA"
             /db_xref="taxon:7955"
             /clone="RK030A2C01"
             /dev_stage="mature"
             /note="Organ: kidney; Vector: pBS-CMV; Site 1: XhoI;
             Site 2: EcoRI; Total RNA was extracted from the kidney
             tissues of mature zebrafish. The poly (A)+ RNA fraction
             lambdaDazAP Express vector (Stratagene) and in vivo excised
             into pBS-CMV vector."

```

was separated from total RNA by oligo (dT) cellulose chromatography. Library was initially constructed in the lambdaZAP Express vector (Stratagene) and in vivo excised into pBS-CMV vector."

## ORIGIN

Query Match 70.8%; Score 17; DB 14; Length 317;  
Best Local Similarity 82.4%; Pred. No. 32;  
Matches 14; Conservative 3; Mismatches 0; Indels 0; Gaps 0;  
  
QY 5 AACAUAGGCCUUCAG 21  
||||:|||||:|||||  
Db 139 AACATGAGCCCTTCAG 123

## RESULT 11

CD591703/c  
LOCUS  
DEFINITION  
323 bp mRNA linear EST 16-JUN-2003  
clone RK065A4G05.T3 Zebrafish Kidney Marrow cDNA library Danio rerio cDNA  
clone RK065A4G05 5', mRNA sequence.

CD591703

CD591703.1 GI:31773055

EST.

Source: Danio rerio (zebrafish)

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;  
Cypriniformes; Cyprinidae; Danio.

## REFERENCE

1 (bases 1 to 323)  
Song,H.D., Wu,X.Y., Sun,X.J., Zhou,Y., Liu,T.X., Zhang,G.W.,  
Sheng,Y., Chen,Y., Ruan,Z., Jiang,C.L., Fan,H.Y., Look,A.T.,  
Zou,L.I. and Chen,Z.

## TITLE

Gene Expression Profiling in the Zebrafish Kidney Marrow Tissue

## JOURNAL

Unpublished (2003)

## COMMENT

Contact: Chen Z.  
State Key Lab for Medical Genomics  
Shanghai Institute of Hematology, Ruijin Hospital Affiliated to  
Shanghai Second Medical University  
197 Rui Jin Road II, Shanghai 200025, P. R. China  
Tel: 86-21-64740490  
Fax: 86-21-64743206  
Email: zchen@stn.sh.cn  
Seq primer: T3.

## FEATURES

## source

1..323  
Location/Qualifiers  
/organism="Danio rerio"  
/mol\_type="mRNA"  
/db\_xref="taxon:7955"  
/clone="RK065A4G05"  
/dev\_stage="mature"

/note="Organ: kidney; Vector: pBS-CMV; Site 1: XhoI;  
Site 2: EcoRI; Total RNA was extracted from the kidney  
tissues of mature zebrafish. The poly (A)+ RNA fraction  
was separated from total RNA by oligo (dT) cellulose  
chromatography. Library was initially constructed in the  
lambdaZAP Express vector (Stratagene) and in vivo excised  
into pBS-CMV vector."

## ORIGIN

Query Match 70.8%; Score 17; DB 14; Length 323;  
Best Local Similarity 82.4%; Pred. No. 32;  
Matches 14; Conservative 3; Mismatches 0; Indels 0; Gaps 0;  
  
QY 5 AACAUAGGCCUUCAG 21  
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Db 136 AACATGAGCCCTTCAG 120

## RESULT 12

CD591328/c  
LOCUS  
DEFINITION  
324 bp mRNA linear EST 16-JUN-2003  
clone RK132A1C12.T3 Zebrafish Kidney Marrow cDNA library Danio rerio cDNA  
clone RK132A1C12 5', mRNA sequence.

## ACCESSION

## VERSION

## KEYWORDS

## SOURCE

## ORGANISM

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## COMMENT

clone RK132A1C12 5', mRNA sequence.

CD601328

CD601328.1 GI:31782204

EST.

Source: Danio rerio (zebrafish)

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;  
Cypriniformes; Cyprinidae; Danio.

1 (bases 1 to 324)

Song,H.D., Wu,X.Y., Sun,X.J., Zhou,Y., Liu,T.X., Zhang,G.W.,  
Sheng,Y., Chen,Y., Ruan,Z., Jiang,C.L., Fan,H.Y., Look,A.T.,  
Zou,L.I. and Chen,Z.

Gene Expression Profiling in the Zebrafish Kidney Marrow Tissue

Unpublished (2003)

Contact: Chen Z.

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Tel: 86-21-64740490

Fax: 86-21-64743206

Email: zchen@stn.sh.cn

Seq primer: T3.

Location/Qualifiers

1..324

/organism="Danio rerio"

/mol\_type="mRNA"

/db\_xref="taxon:7955"

/clone="RK132A1C12"

/dev\_stage="mature"

/note="Organ: kidney; Vector: pBS-CMV; Site 1: XhoI;  
Site 2: EcoRI; Total RNA was extracted from the kidney  
tissues of mature zebrafish. The poly (A)+ RNA fraction  
was separated from total RNA by oligo (dT) cellulose  
chromatography. Library was initially constructed in the  
lambdaZAP Express vector (Stratagene) and in vivo excised  
into pBS-CMV vector."

## ORIGIN

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Matches 14; Conservative 3; Mismatches 0; Indels 0; Gaps 0;  
  
QY 5 AACAUAGGCCUUCAG 21  
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Db 127 AACATGAGCCCTTCAG 111

## RESULT 13

## LOCUS

## DEFINITION

## ACCESSION

## VERSION

## KEYWORDS

## SOURCE

## ORGANISM

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## COMMENT

CD601373  
330 bp mRNA linear EST 16-JUN-2003  
clone RK132A2C11.T3 Zebrafish Kidney Marrow cDNA library Danio rerio cDNA  
clone RK132A2C11 5', mRNA sequence.

CD601373

CD601373.1 GI:31782249

EST.

Source: Danio rerio (zebrafish)

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;  
Cypriniformes; Cyprinidae; Danio.

1 (bases 1 to 330)

Song,H.D., Wu,X.Y., Sun,X.J., Zhou,Y., Liu,T.X., Zhang,G.W.,  
Sheng,Y., Chen,Y., Ruan,Z., Jiang,C.L., Fan,H.Y., Look,A.T.,  
Zou,L.I. and Chen,Z.

Gene Expression Profiling in the Zebrafish Kidney Marrow Tissue

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Contact: Chen Z.

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197 Rui Jin Road II, Shanghai 200025, P. R. China  
 Tel: 86-21-64740490  
 Fax: 86-21-64743206  
 Email: zchen@stn.sh.cn  
 Seq primer: T3.

# FEATURES

Location/Qualifiers  
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 /organism="Danio rerio"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:7955"  
 /clone="RK132A2C11"  
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 /clone\_lib="Zebrafish Kidney Marrow cDNA library"  
 /note="Organ: kidney; Vector: pBS-CMV; Site: 1: XhoI;  
 Site 2: EcoRI; Total RNA was extracted from the kidney  
 tissues of mature zebrafish. The poly (A)+ RNA fraction  
 was separated from total RNA by oligo (dT) cellulose  
 chromatography. Library was initially constructed in the  
 lambdaZAP Express vector (Stratagene) and in vivo excised  
 into pBS-CMV vector."

## ORIGIN

Query Match 70.8%; Score 17; DB 14; Length 330;  
 Best Local Similarity 82.4%; Pred. No. 33;  
 Matches 14; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 5 AACAUAGAAGCCCUUCAG 21  
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 Db 127 AACATGAAGCCCTTCAG 111

## RESULT 14

CD602150/c  
 LOCUS  
 DEFINITION  
 CD602150 330 bp mRNA linear EST 16-JUN-2003  
 clone RK140A2F04 5', mRNA sequence.

ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM

Danio rerio (zebrafish)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Actinopterygii; Neopterygii; Teleostei; Ostariophysi;  
 Cypriniformes; Cyprinidae; Danio.  
 1 (bases 1 to 330)  
 Song,H.D., Wu,X.Y., Sun,X.J., Zhou,Y., Liu,T.X., Zhang,G.W.,  
 Sheng,Y., Chen,Y., Ruan,Z., Jiang,C.L., Fan,H.Y., Look,A.T.,  
 Zou,L.I. and Chen,Z.  
 Gene Expression Profiling in the Zebrafish Kidney Marrow Tissue  
 Unpublished (2003)  
 Contact: Chen Z.

## REFERENCE

AUTHORS  
 TITLE  
 JOURNAL  
 COMMENT

State Key Lab for Medical Genomics  
 Shanghai Institute of Hematology, Ruijin Hospital Affiliated to  
 Shanghai Second Medical University  
 197 Rui Jin Road II, Shanghai 200025, P. R. China  
 Tel: 86-21-64740490  
 Fax: 86-21-64743206  
 Email: zchen@stn.sh.cn  
 Seq primer: T3.

# FEATURES

Location/Qualifiers  
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 /db\_xref="taxon:7955"  
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 /clone\_lib="Zebrafish Kidney Marrow cDNA library"  
 /note="Organ: kidney; Vector: pBS-CMV; Site 1: XhoI;  
 Site 2: EcoRI; Total RNA was extracted from the kidney  
 tissues of mature zebrafish. The poly (A)+ RNA fraction  
 was separated from total RNA by oligo (dT) cellulose  
 chromatography. Library was initially constructed in the  
 lambdaZAP Express vector (Stratagene) and in vivo excised

into pBS-CMV vector."

## ORIGIN

Query Match 70.8%; Score 17; DB 14; Length 330;  
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 Matches 14; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 5 AACAUAGAAGCCCUUCAG 21  
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 Db 139 AACATGAAGCCCTTCAG 123

## RESULT 15

CD603852/c  
 LOCUS  
 DEFINITION  
 CD603852 496 bp mRNA linear EST 16-JUN-2003  
 clone RZ150A3E05 5', mRNA sequence.

ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM

Danio rerio (zebrafish)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Actinopterygii; Neopterygii; Teleostei; Ostariophysi;  
 Cypriniformes; Cyprinidae; Danio.  
 1 (bases 1 to 496)  
 Song,H.D., Wu,X.Y., Sun,X.J., Zhou,Y., Liu,T.X., Zhang,G.W.,  
 Sheng,Y., Chen,Y., Ruan,Z., Jiang,C.L., Fan,H.Y., Look,A.T.,  
 Zou,L.I. and Chen,Z.  
 Gene Expression Profiling in the Zebrafish Kidney Marrow Tissue  
 Unpublished (2003)  
 Contact: Chen Z.

## REFERENCE

AUTHORS  
 TITLE  
 JOURNAL  
 COMMENT

State Key Lab for Medical Genomics  
 Shanghai Institute of Hematology, Ruijin Hospital Affiliated to  
 Shanghai Second Medical University  
 197 Rui Jin Road II, Shanghai 200025, P. R. China  
 Tel: 86-21-64740490  
 Fax: 86-21-64743206  
 Email: zchen@stn.sh.cn  
 Seq primer: T3.

## FEATURES

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 /db\_xref="taxon:7955"  
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 /clone\_lib="Zebrafish Kidney Marrow cDNA library"  
 /note="Organ: kidney; Vector: pBS-CMV; Site: 1: XhoI;  
 Site 2: EcoRI; Total RNA was extracted from the kidney  
 tissues of mature zebrafish. The poly (A)+ RNA fraction  
 was separated from total RNA by oligo (dT) cellulose  
 chromatography. Library was initially constructed in the  
 lambdaZAP Express vector (Stratagene) and in vivo excised  
 into pBS-CMV vector."

## ORIGIN

Query Match 70.8%; Score 17; DB 14; Length 496;  
 Best Local Similarity 82.4%; Pred. No. 37;  
 Matches 14; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

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 Db 196 AACATGAAGCCCTTCAG 180

Search completed: May 26, 2004, 22:44:34  
 Job time : 847.385 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 26, 2004, 16:00:31 ; Search time 510.783 Seconds  
(without alignments)  
2036.547 Million cell updates/sec

Title: US-09-121-239-18

Perfect score: 24

Sequence: 1 CGCTGAGGCTTCATGTTCCAC 24

Scoring table: OLIGO NUC

Gapop 60.0 , Gapext 60.0

Searched: 3470272 seqs, 21671516995 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

GenEmbl.\*

1: gb\_ba.\*

2: gb\_hgt.\*

3: gb\_in.\*

4: gb\_om.\*

5: gb\_ov.\*

6: gb\_pat.\*

7: gb\_ph.\*

8: gb\_pl.\*

9: gb\_pr.\*

10: gb\_ro.\*

11: gb\_sts.\*

12: gb\_sy.\*

13: gb\_un.\*

14: gb\_vl.\*

15: em\_ba.\*

16: em\_fun.\*

17: em\_hum.\*

18: em\_in.\*

19: em\_mu.\*

20: em\_om.\*

21: em\_or.\*

22: em\_ov.\*

23: em\_pat.\*

24: em\_ph.\*

25: em\_pl.\*

26: em\_ro.\*

27: em\_sts.\*

28: em\_un.\*

29: em\_vl.\*

30: em\_hgt\_hum.\*

31: em\_hgt\_inv.\*

32: em\_hgt\_other.\*

33: em\_hgt\_mus.\*

34: em\_hgt\_pln.\*

35: em\_hgt\_rtd.\*

36: em\_hgt\_nam.\*

37: em\_hgt\_vrt.\*

38: em\_sy.\*

39: em\_hgtgo\_hum.\*

40: em\_hgtgo\_mus.\*

41: em\_hgtgo\_other.\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
C 1	24	100.0	24	6	BD222538	BD222538 Methods f
C 2	24	100.0	24	6	BD222539	BD222539 Methods f
C 3	24	100.0	24	6	BD222540	BD222540 Methods f
C 4	24	100.0	24	6	BD222541	BD222541 Methods f
C 5	24	100.0	299	6	BD222547	BD222547 Methods f
C 6	18	75.0	34125	14	AT12CGA	XJ3487 Adenovirus
C 7	18	75.0	238483	2	AC132177	AC132177 Rattus no
C 8	17	70.8	60456	2	AC087634	AC087634 Homo sapi
C 9	17	70.8	104244	10	AL805925	AL805925 Mouse DNA
C 10	17	70.8	138152	10	AL954170	AL954170 Mouse DNA
C 11	17	70.8	152804	2	BX248232	BX248232 Danio rer
C 12	17	70.8	162077	2	AC109200	AC109200 Mus muscu
C 13	17	70.8	184317	10	AL606494	AL606494 Mouse DNA
C 14	17	70.8	215356	10	AC096363	AC096363 Rattus no
C 15	17	70.8	215958	2	AC102091	AC102091 Mus muscu
C 16	17	70.8	256703	2	AC114076	AC114076 Rattus no
C 17	17	70.8	259220	2	AC097694	AC097694 Rattus no
C 18	16	66.7	404	8	AF082605	AF082605 Leavenwor
C 19	16	66.7	415	8	AF082606	AF082606 Leavenwor
C 20	16	66.7	556	11	G85739	G85739 S209P6356RA
C 21	16	66.7	688	11	G97604	G97604 S209P6432FF
C 22	16	66.7	751	6	BD018368	BD018368 Novel gen
C 23	16	66.7	751	6	BD098306	BD098306 Novel gen
C 24	16	66.7	760	8	AF082603	AF082603 Leavenwor
C 25	16	66.7	1050	10	AF039216	AF039216 Mus muscu
C 26	16	66.7	1109	10	BC005636	BC005636 Mus muscu
C 27	16	66.7	1454	8	AY266141	AY266141 Setaria i
C 28	16	66.7	1599	8	ZMA430386	AJ340386 Zea mays
C 29	16	66.7	2233	8	AY166687	AY166687 Cryphonoc
C 30	16	66.7	2370	8	ZMA430205	AJ340205 Zea mays
C 31	16	66.7	2577	9	BC028075	BC028075 Homo sapi
C 32	16	66.7	3335	5	AY422997	AY422997 Danio rer
C 33	16	66.7	3337	9	HSA295142	AJ295142 Homo sapi
C 34	16	66.7	3398	5	BC045427	BC045427 Danio rer
C 35	16	66.7	3398	5	BC047178	BC047178 Danio rer
C 36	16	66.7	3460	6	AR079398	AR079398 Sequence
C 37	16	66.7	3460	9	HSU94333	U94333 Human Clq/M
C 38	16	66.7	4194	10	MUSCTNC	J04971 M.musculus
C 39	16	66.7	14652	1	AE004799	AE004799 Pseudomon
C 40	16	66.7	48139	9	AC109827	AC109827 Homo sapi
C 41	16	66.7	50436	9	AL391258	AL391258 Human DNA
C 42	16	66.7	60631	1	AF006628	Continuation (9 of
C 43	16	66.7	67542	9	AC026422	AC026422 Homo sapi
C 44	16	66.7	70305	1	YPCD1	AL117189 Yersinia
C 45	16	66.7	70504	1	AF053946	AF053946 Yersinia

ALIGNMENTS

RESULT 1  
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LOCUS BD222538 24 bp DNA linear PAT 17-JUL-2003  
DEFINITION Methods for detecting and measuring spliced nucleic acids.  
ACCESSION BD222538  
VERSION BD222538.1 GI:33032308  
KEYWORDS JP 2002521037-A/16  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1 (bases 1 to 24)  
AUTHORS Harvey, R.C. and Eastman, P.S.  
TITLE Methods for detecting and measuring spliced nucleic acids  
JOURNAL Patent: JP 2002521037-A 16 16-JUL-2002;  
GEN PROBE INC

```

COMMENT      OS      Artificial Sequence
              PN      JP 2002521037-A/16
              PD      16-JUL-2002
              PF      23-JUL-1999 JP 2000561364
              PR      23-JUL-1998 US 09/121239
              PI      RICHARD C HARVEY, PAUL S EASTMAN
              PC      C12Q1/68, C12N15/09, C12N15/00
              CC      Description of Artificial Sequence: Probe for abl sequence FH
              Key source      1. .24      Location/Qualifiers
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ORIGIN
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Best Local Similarity 100.0%; Pred. No. 0.0025;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1      CCGCTGAAGGGCTTCATGTTCCAC 24
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Db      24      CCGCTGAAGGGCTTCATGTTCCAC 1

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LOCUS      BD222539
DEFINITION      Methods for detecting and measuring spliced nucleic acids.
ACCESSION      BD222539
VERSION      1 GI:33032309
KEYWORDS      JP 2002521037-A/17.
SOURCE      synthetic construct
              ORGANISM      artificial sequences.
REFERENCE      1 (bases 1 to 24)
AUTHORS      Harvey,R.C. and Eastman,P.S.
TITLE      Methods for detecting and measuring spliced nucleic acids
JOURNAL      Patent: JP 2002521037-A 17 16-JUL-2002;
              GEN PROBE INC

COMMENT      OS      Artificial Sequence
              PN      JP 2002521037-A/17
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              PR      23-JUL-1998 US 09/121239
              PI      RICHARD C HARVEY, PAUL S EASTMAN
              PC      C12Q1/68, C12N15/09, C12N15/00
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Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1      CCGCTGAAGGGCTTCATGTTCCAC 24
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RESULT 3
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DEFINITION      Methods for detecting and measuring spliced nucleic acids.
ACCESSION      BD222540
VERSION      1 GI:33032310
KEYWORDS      JP 2002521037-A/18.
SOURCE      synthetic construct
              ORGANISM      artificial sequences.
REFERENCE      1 (bases 1 to 24)
AUTHORS      Harvey,R.C. and Eastman,P.S.
TITLE      Methods for detecting and measuring spliced nucleic acids
JOURNAL      Patent: JP 2002521037-A 18 16-JUL-2002;
              GEN PROBE INC

COMMENT      OS      Artificial Sequence
              PN      JP 2002521037-A/18
              PD      16-JUL-2002
              PF      23-JUL-1999 JP 2000561364
              PR      23-JUL-1998 US 09/121239
              PI      RICHARD C HARVEY, PAUL S EASTMAN
              PC      C12Q1/68, C12N15/09, C12N15/00
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source
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DEFINITION      Methods for detecting and measuring spliced nucleic acids.
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VERSION      1 GI:33032310
KEYWORDS      JP 2002521037-A/18.
SOURCE      synthetic construct
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REFERENCE      1 (bases 1 to 24)
AUTHORS      Harvey,R.C. and Eastman,P.S.
TITLE      Methods for detecting and measuring spliced nucleic acids
JOURNAL      Patent: JP 2002521037-A 18 16-JUL-2002;
              GEN PROBE INC

COMMENT      OS      Artificial Sequence
              PN      JP 2002521037-A/18
              PD      16-JUL-2002
              PF      23-JUL-1999 JP 2000561364
              PR      23-JUL-1998 US 09/121239
              PI      RICHARD C HARVEY, PAUL S EASTMAN
              PC      C12Q1/68, C12N15/09, C12N15/00
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FEATURES
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ORIGIN
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Best Local Similarity 100.0%; Pred. No. 0.0025;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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ACCESSION      BD222541
VERSION      1 GI:33032311
KEYWORDS      JP 2002521037-A/19.
SOURCE      synthetic construct
              ORGANISM      artificial sequences.
REFERENCE      1 (bases 1 to 24)
AUTHORS      Harvey,R.C. and Eastman,P.S.
TITLE      Methods for detecting and measuring spliced nucleic acids
JOURNAL      Patent: JP 2002521037-A 19 16-JUL-2002;
              GEN PROBE INC

COMMENT      OS      Artificial Sequence
              PN      JP 2002521037-A/19
              PD      16-JUL-2002
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              PR      23-JUL-1998 US 09/121239
              PI      RICHARD C HARVEY, PAUL S EASTMAN
              PC      C12Q1/68, C12N15/09, C12N15/00
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FEATURES
source
ORIGIN

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PUBMED 2746738
REMARK (sites)
REFERENCE 12
AUTHORS Zock,C., Iselt,A. and Doerfler,W.
TITLE A unique mitigator sequence determines the species specificity of
the major late promoter in adenovirus type 12 DNA
J. Virol. 67 (2), 682-693 (1993)
JOURNAL
MEDLINE 93124560
PUBMED 8419643
REMARK (sites)
REFERENCE 13
AUTHORS Sprengel,J., Schmitz,B., Heuss-Neitzel,D., Zock,C. and Doerfler,W.
TITLE Nucleotide sequence of human adenovirus type 12 DNA: comparative
functional analysis
J. Virol. 68 (1), 379-389 (1994)
JOURNAL
MEDLINE 94076430
PUBMED 8254750
REFERENCE 14 (bases 1 to 34125)
AUTHORS Sprengel,J.
TITLE Direct Submission
JOURNAL Submitted (21-JUN-1993) J. Sprengel, Institute of Genetics/Dept.
Virology, Weyertal 121, 50931 Cologne 41, FRG
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AKLALRPDCSVRIKTITVITSCAYIIGNGAIVEVDTSRVAFRCMQMGPGVGLDG
ITPINVPAGDKPKGIMPEANTCLVLHGVIYFLNFSNICVESWNKYSGRCTFYGCKG
LVGRPKSLSVKVKLFKPCVLCALIVEGDARIHNNAENACFVLKGMALIKHNVVCG
VSDOTMRRFVTCADQNCHTLKTVHIVSHSRHCVPVCDHNMFRCTIHLGRGMFRPS
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PVLNVTELRSDHLTSLCLRTDYESSDEDDN"
2071. .2073
/citation=[6]
/replace="gcg"
2417. .2418
/citation=[6]

Query Match 75.0%; Score 18; DB 14; Length 34125;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TGAAGGGCTTCATGTTCC 22
|||||
Db 3998 TGAAGGGCTTCATGTTCC 4015

RESULT 7
AC132177 238483 bp DNA linear HTG 10-OCT-2002
AC132177/c Rattus norvegicus clone CH230-165B1, WORKING DRAFT SEQUENCE, 6
LOCUS
DEFINITION Rattus norvegicus clone CH230-165B1, WORKING DRAFT SEQUENCE, 6
unordered pieces.
AC132177 AC132177.4 GI:23683197
VERSION
KEYWORDS HTG; HTGS, PHASE1; HTGS, DRAFT; HTGS, FULLTOP.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 238483)
AUTHORS Muzny,D., Marie,, Metzker,M.Lee,, Abramzon,S., Adams,C., Alder,J.,
Allen,C., Allen,H., Alsbrooks,S., Amin,A., Anguiano,D.,
Anyalebechi,V., Aoyagi,A., Ayodeji,M., Baca,E., Baden,H.,
Baldwin,D., Bandaranaike,D., Barber,M., Barnstead,M., Benahmed,F.,
Biswalo,K., Blair,J., Blankenburg,K., Blyth,P., Brown,M.,
Bryant,N., Buhay,C., Burch,P., Burrell,K., Calderon,E.,
Cardenas,V., Carter,K., Cavazos,I., Ceasar,H., Center,A.,
Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Y., Chen,Z., Chu,J.,
Cleveland,C., Cockrell,R., Cox,C., Coyle,M., Cree,A., D'Souza,L.,
Davila,M.L., Davis,C., Davy-Carroll,L., De Anda,C., Dederich,D.,
Delgado,O., Denson,S., Deramo,C., Ding,Y., Dinh,H., Divya,K.,
Draper,H., Dugan-Rocha,S., Dunn,A., Durbin,K., Duval,B., Eaves,K.,
Egan,A., Escotto,M., Eugene,C., Evans,C.A., Falls,T., Fan,G.,

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Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P., Frazer, C.M., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Garza, M., Gregorovich, E., Geer, K., Gill, R., Grady, M., Guerra, T., Guevara, M., Gunaratne, P., Haaland, W., Hamill, C., Hamilton, C., Hamilton, J., Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J., Hernandez, R., Hines, S., Hladun, S.L., Hodgson, A., Hogue, M., Hollins, B., Howells, S., Huly, S., Hume, J., Idlebird, D., Jackson, A., Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jolivet, A., Karpathy, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C., Kowis, C., Kratt, C.L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J., Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J., Lorensu, L., Louised, H., Lozano, R.J., Lu, X., Ma, J., Maheshwari, M., Mahindartne, M., Mahmoud, M., Malloy, K., Mangum, A., Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, E., Mawhinney, S., McLeod, M.P., McNeill, T.Z., Meenen, E., Milosavljevic, A., Miner, G.S., Minja, E., Montemayor, J., Moore, S., Morgan, M., Morris, K., Morris, S., Munidasa, M., Murphy, M., Nair, L., Nankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S., Parks, K., Nwankemeh, O., Okwuonu, G., Olarnpunsagoon, A., Pal, S., Parks, K., Pasternak, S., Paul, H., Perez, A., Perez, L., Primus, E., Pu, L., Plopper, F., Polindexter, A., Popovic, D., Primus, E., Pu, L., Puzo, M., Quiroz, J., Rachlin, E., Reeves, K., Regier, M.A., Reigh, R., Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F., Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S.J., Sanders, W., Savory, G., Scherer, S., Scott, G., Shatsman, S., Shen, H., Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smajs, D., Snead, A., Sodergren, E., Song, X.-Z., Sorelle, R., Sosa, J., Steimle, M., Strong, R., Sutton, A., Svatek, A., Taber, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Usmani, K., Valas, R., Vera, V., Villasana, D., Waldron, L., Walker, B., Wang, J., Wang, Q., Wang, S., Warren, J., Warren, R., Wei, X., White, F., Williams, G., Willson, R., Wleczky, R., Wooden, H., Worley, K., Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von Niederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O., Weinstock, G. and Gibbs, R.A.

Direct Submission  
Unpublished  
2 (bases 1 to 238483)  
Rat Genome Sequencing Consortium.  
Submitted (30-AUG-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA  
3 (bases 1 to 238483)  
Rat Genome Sequencing Consortium.  
Submitted (10-OCT-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA  
On Oct 10, 2002 this sequence version replaced gi:22725823.  
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.

----- Genome Center  
Center: Baylor College of Medicine  
Center code: BCM  
Web site: http://www.hgsc.bcm.tmc.edu/  
Contact: hgsc-help@bcm.tmc.edu  
----- Project Information  
Center project name: GOVP  
Center clone name: CH230-165B1  
----- Summary Statistics  
Assembly program: Phrap; version 0.990329

Consensus quality: 22924 bases at least Q40  
Consensus quality: 22513 bases at least Q30  
Consensus quality: 226732 bases at least Q20  
Estimated insert size: 226330; sum-of-contigs estimation  
Quality coverage: 7x in Q20 bases; sum-of-contigs estimation

-----  
\* NOTE: Estimated insert size may differ from sequence length  
\* (see http://www.hgsc.bcm.tmc.edu/docs/genbank\_draft\_data.html).  
\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 6 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.  
\* 1 3207: contig of 3207 bp in length  
\* 3208 3307: gap of unknown length  
\* 3308 184048: contig of 180741 bp in length  
\* 184049 184148: gap of unknown length  
\* 184149 197235: contig of 13087 bp in length  
\* 197236 197335: gap of unknown length  
\* 197336 227086: contig of 29751 bp in length  
\* 227087 227186: gap of unknown length  
\* 227187 228436: contig of 1250 bp in length  
\* 228437 228536: gap of unknown length  
\* 228537 238483: contig of 9947 bp in length.

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/mol\_type="genomic DNA"  
/db\_xref="taxon:10116"  
/clone="CH230-165B1"  
194764..195895  
misc\_feature  
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195946..197235  
misc\_feature  
/note="wgs\_contig"

ORIGIN  
Query Match 75.0%; Score 18; DB 2; Length 238483;  
Best Local Similarity 100.0%; Pred. No. 3.8;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GAAGGGCTTCATGTTCCA 23  
DB 13365 GAAGGGCTTCATGTTCCA 13348

RESULT 8  
AC087634  
LOCUS  
DEFINITION Homo sapiens chromosome 15, clone RP11-302D8 map 15, LOW-PASS  
SEQUENCE SAMPLING.  
AC087634  
AC087634.1 GI:12229409  
VERSION  
HTG: HTGS PHASE0.  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE  
1 (bases 1 to 60456)  
AUTHORS Birren, B., Linton, L., Nusbaum, C. and Lander, E.  
TITLE  
Homo sapiens chromosome 15, clone RP11-302D8  
JOURNAL  
Unpublished  
REFERENCE  
2 (bases 1 to 60456)  
AUTHORS Birren, B., Linton, L., Nusbaum, C., Allen, N., Anderson, S., Barna, N., Bastien, V., Boguslavsky, L., Bouckgalter, B., Brown, A., Camarata, J., Campopiano, A., Choquet, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArrellano, K., Dewar, K., Diaz, J.S., Dodge, S., Fero, S., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Heaford, A., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Karatas, A., LaRocque, K., Lamazares, R., Landers, I.,

Lehoczyk, J., Levine, R., Liu, G., MacClean, C., Macdonald, P.,  
 Marquis, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K.,  
 McPeeters, R., Meldrum, J., Meneus, L., Mihova, T., Mienga, V.,  
 Murphy, T., Naylor, J., Nguyen, C., Norbu, C., Norman, C.H.,  
 O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K.,  
 Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R.,  
 Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M.,  
 Roy, A., Santos, R., Schauer, S., Schuback, R., Seaman, S., Severy, P.,  
 Sougne, C., Spencer, B., Stange-Thomann, N., Stojanovic, N.,  
 Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J.,  
 Trauers, M., Travis, N., Trigglio, J., Vassiliev, H., Viel, R., Vo, A.,  
 Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G., Zainoun, J.,  
 Zembek, L., Zimmer, A. and Zody, M.

Direct Submission  
 Submitted (15-JAN-2001) Whitehead Institute/MIT Center for Genome  
 Research, 320 Charles Street, Cambridge, MA 02141, USA  
 All repeats were identified using RepeatMasker:  
 Smit, A.F.A. & Green, P. (1996-1997)  
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

----- Genome Center  
 Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIBR  
 Web site: <http://www-seq.wi.mit.edu>

Contact: [sequence\\_submissions@genome.wi.mit.edu](mailto:sequence_submissions@genome.wi.mit.edu)

----- Project Information

Center project name: L11917

Center Clone name: 302\_D\_8

-----  
 \* NOTE: This record contains 72 individual  
 \* sequencing reads that have not been assembled into  
 \* contigs. Runs of N are used to separate the reads  
 \* and the order in which they appear is completely  
 \* arbitrary. Low-pass sequence sampling is useful for  
 \* identifying clones that may be gene-rich and allows  
 \* overlap relationships among clones to be deduced.  
 \* However, it should not be assumed that this clone  
 \* will be sequenced to completion. In the event that  
 \* the record is updated, the accession number will  
 \* be preserved.

1 785: contig of 785 bp in length  
 \* 786 885: gap of 100 bp  
 \* 886 1621: contig of 736 bp in length  
 \* 1622 1721: gap of 100 bp  
 \* 1722 2493: contig of 772 bp in length  
 \* 2494 2593: gap of 100 bp  
 \* 2594 3335: contig of 742 bp in length  
 \* 3336 3435: gap of 100 bp  
 \* 3436 4147: contig of 712 bp in length  
 \* 4148 4247: gap of 100 bp  
 \* 4248 4982: contig of 735 bp in length  
 \* 4983 5082: gap of 100 bp  
 \* 5083 5805: contig of 723 bp in length  
 \* 5806 5905: gap of 100 bp  
 \* 5906 6635: contig of 730 bp in length  
 \* 6636 6735: gap of 100 bp  
 \* 6736 7460: contig of 725 bp in length  
 \* 7461 7560: gap of 100 bp  
 \* 7561 8283: contig of 723 bp in length  
 \* 8284 8383: gap of 100 bp  
 \* 8384 9142: contig of 759 bp in length  
 \* 9143 9242: gap of 100 bp  
 \* 9243 9975: contig of 733 bp in length  
 \* 9976 10075: gap of 100 bp  
 \* 10076 10813: contig of 738 bp in length  
 \* 10814 10913: gap of 100 bp  
 \* 10914 11649: contig of 736 bp in length  
 \* 11650 11749: gap of 100 bp  
 \* 11750 12481: contig of 732 bp in length  
 \* 12482 12581: gap of 100 bp  
 \* 12582 13315: contig of 734 bp in length  
 \* 13316 13415: gap of 100 bp  
 \* 13416 14151: contig of 736 bp in length  
 \* 14152 14251: gap of 100 bp

14252 14975: contig of 724 bp in length  
 \* 14976 15075: gap of 100 bp  
 \* 15076 15814: contig of 739 bp in length  
 \* 15815 15914: gap of 100 bp  
 \* 15915 16622: contig of 748 bp in length  
 \* 16663 16762: gap of 100 bp  
 \* 16763 17532: contig of 770 bp in length  
 \* 17533 17632: gap of 100 bp  
 \* 17633 18362: contig of 730 bp in length  
 \* 18363 18462: gap of 100 bp  
 \* 18463 19220: contig of 758 bp in length  
 \* 18463 19320: gap of 100 bp  
 \* 19321 20051: contig of 731 bp in length  
 \* 20052 20151: gap of 100 bp  
 \* 20152 20880: contig of 729 bp in length  
 \* 20881 20980: gap of 100 bp  
 \* 20981 21750: contig of 770 bp in length  
 \* 21751 21850: gap of 100 bp  
 \* 21851 22606: contig of 756 bp in length  
 \* 22607 22706: gap of 100 bp  
 \* 22707 23469: contig of 763 bp in length  
 \* 23470 23569: gap of 100 bp  
 \* 23570 24318: contig of 749 bp in length  
 \* 24319 24418: gap of 100 bp  
 \* 24419 25159: contig of 741 bp in length  
 \* 25160 25259: gap of 100 bp  
 \* 25260 25993: contig of 734 bp in length  
 \* 25994 26093: gap of 100 bp  
 \* 26094 26846: contig of 753 bp in length  
 \* 26847 26946: gap of 100 bp  
 \* 26947 27651: contig of 705 bp in length  
 \* 27652 27751: gap of 100 bp  
 \* 27752 28487: contig of 736 bp in length  
 \* 28488 28587: gap of 100 bp  
 \* 28588 29324: contig of 737 bp in length  
 \* 29325 29424: gap of 100 bp  
 \* 29425 30193: contig of 769 bp in length  
 \* 30194 30293: gap of 100 bp  
 \* 30294 31035: contig of 742 bp in length  
 \* 31036 31135: gap of 100 bp  
 \* 31136 31889: contig of 754 bp in length  
 \* 31890 31989: gap of 100 bp  
 \* 31990 32731: contig of 742 bp in length  
 \* 32732 32831: gap of 100 bp  
 \* 32832 33569: contig of 738 bp in length  
 \* 33570 33669: gap of 100 bp  
 \* 33670 34415: contig of 746 bp in length  
 \* 34416 34515: gap of 100 bp  
 \* 34516 35272: contig of 757 bp in length  
 \* 35273 35372: gap of 100 bp  
 \* 35373 36095: contig of 723 bp in length  
 \* 36096 36195: gap of 100 bp  
 \* 36196 36912: contig of 717 bp in length  
 \* 36913 37012: gap of 100 bp  
 \* 37013 37770: contig of 758 bp in length  
 \* 37771 37870: gap of 100 bp  
 \* 37871 38611: contig of 741 bp in length  
 \* 38612 38711: gap of 100 bp  
 \* 38712 39462: contig of 751 bp in length  
 \* 39463 39562: gap of 100 bp  
 \* 39563 40324: contig of 762 bp in length  
 \* 40325 40424: gap of 100 bp  
 \* 40425 41225: contig of 801 bp in length  
 \* 41226 41325: gap of 100 bp  
 \* 41326 42063: contig of 738 bp in length  
 \* 42064 42163: gap of 100 bp  
 \* 42164 42879: contig of 716 bp in length  
 \* 42880 43712: contig of 733 bp in length  
 \* 43713 43812: gap of 100 bp  
 \* 43813 44509: contig of 697 bp in length  
 \* 44510 44609: gap of 100 bp  
 \* 44610 45341: contig of 732 bp in length

TITLE  
 JOURNAL

COMMENT

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* 45342 45441: gap of 100 bp
* 45442 contig of 727 bp in length
* 46168: gap of 100 bp
* 46268: contig of 100 bp
* 46269 contig of 752 bp in length
* 47021 47120: gap of 100 bp
* 47121 47867: contig of 747 bp in length
* 47868 47867: gap of 100 bp
* 47968 48712: contig of 745 bp in length
* 48713 48812: gap of 100 bp
* 48813 49531: contig of 719 bp in length
* 49532 49631: gap of 100 bp
* 49632 50374: gap of 743 bp in length
* 50375 50474: gap of 100 bp
* 50475 51198: contig of 724 bp in length
* 51199 51298: gap of 100 bp
* 51299 52122: contig of 724 bp in length
* 52123 52888: contig of 766 bp in length
* 52889 52988: gap of 100 bp
* 52989 53725: contig of 737 bp in length
* 53726 53825: gap of 100 bp
* 53826 54566: contig of 741 bp in length
* 54567 54666: gap of 100 bp
* 54667 55445: contig of 779 bp in length
* 55446 55445: gap of 100 bp
* 55446 56281: contig of 736 bp in length
* 56282 56381: gap of 100 bp
* 56382 57126: contig of 745 bp in length
* 57127 57226: gap of 100 bp
* 57227 57965: contig of 739 bp in length
* 57966 58065: gap of 100 bp

Query Match 70.8%; Score 17; DB 2; Length 60456;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 AAGGGCTTCATGTTCCA 23
Db 9925 AAGGGCTTCATGTTCCA 9941
|||||||

RESULT 9
AL805925/c
LOCUS AL805925 104244 bp DNA linear ROD 24-AUG-2002
DEFINITION Mouse DNA sequence from clone RP23-210E20 on chromosome X, complete
sequence.
ACCESSION AL805925
VERSION AL805925.6 GI:22531408
KEYWORDS HTG.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 104244)
Johnson, C.
Direct Submission
Submitted (24-AUG-2002) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Aug 27, 2002 this sequence version replaced gi:22416054.
----- Genome Center
Center: Wellcome Trust Sanger Institute
Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
-----
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence was finished as follows otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest. The following
abbreviations are used to associate primary accession numbers given
in the feature table with their source databases: Em:, EMBL; SW:,
SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP
database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP23-210E20 is
from the RPCI-23 Mouse PAC Library
constructed by the group of Pieter de Jong.
For further details see http://www.chori.org/bacpac/home.htm
VECTOR: pBACE3.6.

FEATURES
Location/Qualifiers
source
1..104244
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
/chromosome="X"
/clone="RP23-210E20"
/clone_lib="RPCI-23"

ORIGIN
Query Match 70.8%; Score 17; DB 10; Length 104244;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CTGAAGGGCTTCATGTT 20
Db 2178 CTGAAGGGCTTCATGTT 2162
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RESULT 10
AL954170
LOCUS AL954170 138152 bp DNA linear ROD 13-AUG-2003
DEFINITION Mouse DNA sequence from clone RP23-467H15 on chromosome 2, complete
sequence.
ACCESSION AL954170
VERSION AL954170.4 GI:33636222
KEYWORDS HTG.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 138152)
North, P., Leaves, N., Greyststrong, J., Coppola, M., Manjunath, S.,
Russell, E., Smith, M., Strachan, G., Tofts, C., Boal, S., Cobley, V.,
Hunter, G., Kimberley, C., Thomas, D., Cave-Berry, L., Weston, P. and
Botcherby, M.R.M.
Direct Submission
Submitted (13-AUG-2003) Mouse Sequencing Group, HGMP-RC, Hinxton,
Cambridge, CB10 1SB, UK. E-mail enquiries:- mrbotche@hgmp.mrc.ac.uk
or pnorth@hgmp.mrc.ac.uk
HGMP-RC part of the UK Mouse Sequencing Consortium
On Aug 13, 2003 this sequence version replaced gi:32567581.
----- Genome Center
Center: UK Medical Research Council
Center code: UK-MRC
Web site: http://mrcseq.har.mrc.ac.uk
Contact: mouseq@har.mrc.ac.uk
-----
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence was finished as follows otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such

```

as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em, EMBL; Sw, SWISSPROT; Tr, TREMBL; Wp, WORMPEP; Information on the WORMPEP database can be found at [http://www.sanger.ac.uk/Projects/C\\_elegans/wormpep](http://www.sanger.ac.uk/Projects/C_elegans/wormpep) RP23-467H15 is from the RPCI-23 Mouse BAC library

constructed by the group of Pieter de Jong.

VECTOR: pBACe3.6

Sequence from the Mouse Genome Sequencing Consortium whole genome shotgun may have been used to confirm this sequence. Sequence data from the whole genome shotgun alone has only been used where it has a phred quality of at least 30.

## FEATURES

source

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1. .138152
   Location/Qualifiers
     /organism="Mus musculus"
     /mol_type="genomic DNA"
     /db_xref="taxon:10090"
     /chromosomes="2"
     /clone="RP23-467H15"
     /clone_lib="RPCI-23"

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## ORIGIN

```

Query Match      70.8%; Score 17; DB 10; Length 138152;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 5 TGAAGGGCTTCATGTC 21

|||||

Db 137153 TGAAGGGCTTCATGTC 137169

## RESULT 11

BX248232/c

LOCUS

```

DEFINITION      BX248232             152804 bp    DNA    linear    HTG 07-NOV-2003
                  Danio rerio clone CH211-23215, WORKING DRAFT SEQUENCE, 3 unordered
                  pieces.

```

ACCESSION

BX248232.6 GI:38228942

VERSION

HTG; HTGS PHASE1; HTGS ACTIVEFIN; HTGS\_DRAFT; HTGS\_FULLTOP.

KEYWORDS

Danio rerio (zebrafish)

SOURCE

```

ORGANISM
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
  Cypriniformes; Cyprinidae; Danio.
  1 (bases 1 to 152804)
  Giselle.H.

```

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

```

Submitted (06-NOV-2003) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
zfish-help@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Nov 7, 2003 this sequence version replaced gi:38141652.
----- Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: zfish-help@sanger.ac.uk
----- Project Information
Center project name: zC23215
----- Summary Statistics
Assembly program: XGAP4; version 4.5
Chemistry: Dye-terminator; 100% of reads
Consensus quality: 152578 bases at least Q40
Consensus quality: 152597 bases at least Q30
Consensus quality: 152598 bases at least Q20
Insert size: 152604; sum-of-contigs
Insert size: 151454; 2.1% error; agarose-fp
Quality coverage: 10.26x in Q20 bases; sum-of-contigs Quality
Coverage: 9.69x in Q20 bases; agarose-fp

```

```

-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 3 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

```

```

* 1 86810: contig of 86810 bp in length
* 86811 86910: gap of 100 bp
* 86911 138019: contig of 51109 bp in length
* 138020 138119: gap of 100 bp
* 138120 152804: contig of 14685 bp in length.

```

## FEATURES

source

```

1. .152804
   Location/Qualifiers
     /organism="Danio rerio"
     /mol_type="genomic DNA"
     /db_xref="taxon:7955"
     /clone="CH211-23215"
     /clone_lib="CHORI-211"
     1. .86810
     /note="assembly_fragment:02232
     fragment_chain:1"
     86911. .138019
     /note="assembly_fragment:00979
     fragment_chain:1"
     138120. .152804
     /note="assembly_fragment:01208
     fragment_chain:1"

```

## ORIGIN

```

Query Match      70.8%; Score 17; DB 2; Length 152804;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 4 CTGAAGGGCTTCATGTT 20

|||||

Db 137376 CTGAAGGGCTTCATGTT 137360

## RESULT 12

AC109200/c

LOCUS

```

DEFINITION      AC109200             162077 bp    DNA    linear    HTG 19-NOV-2003
                  Mus musculus chromosome 8 clone RP23-26G21 map 8, WORKING DRAFT
                  SEQUENCE, 6 ordered pieces.

```

ACCESSION

AC109200.5 GI:38424184

VERSION

HTG; HTGS PHASE2; HTGS\_DRAFT; HTGS\_FULLTOP.

KEYWORDS

Mus musculus (house mouse)

SOURCE

```

ORGANISM
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
  1 (bases 1 to 162077)
  Birren.B., Nusbaum.C. and Lander.E.

```

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

```

Submitted (06-NOV-2003) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
zfish-help@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Nov 7, 2003 this sequence version replaced gi:38141652.
----- Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: zfish-help@sanger.ac.uk
----- Project Information
Center project name: zC23215
----- Summary Statistics
Assembly program: XGAP4; version 4.5
Chemistry: Dye-terminator; 100% of reads
Consensus quality: 152578 bases at least Q40
Consensus quality: 152597 bases at least Q30
Consensus quality: 152598 bases at least Q20
Insert size: 152604; sum-of-contigs
Insert size: 151454; 2.1% error; agarose-fp
Quality coverage: 10.26x in Q20 bases; sum-of-contigs Quality
Coverage: 9.69x in Q20 bases; agarose-fp

```

Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J.,  
 Roberti, M., Roy, A., Santos, R., Schauer, S., Schuback, R., Seaman, S.,  
 Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N.,  
 Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J.,  
 Thomas, K., Travers, M., Travis, N., Trigilio, J., Vassiliev, H.,  
 Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G.,  
 Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

Direct Submission  
 Submitted (03-FEB-2002) Whitehead Institute/MIT Center for Genome  
 Research, 320 Charles Street, Cambridge, MA 02141, USA  
 3 (bases 1 to 162077)

Birren, B., Nuebaum, C., Lander, E., Abouelheil, A., Allen, N.,  
 Anderson, M., Arachchi, H. M., Barna, N., Bastien, V., Bloom, T.,  
 Boguslavsky, L., Boukhgalter, B., Camarata, J., Chang, J., Choepel, Y.,  
 Collymore, A., Cook, A., Cooke, P., Corum, B., DeArellano, K.,  
 Diaz, J. S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Faro, S.,  
 Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S.,  
 Graham, L., Grand-Pierre, N., Hafez, N., Hagopian, D., Hagos, B.,  
 Hall, J., Horton, L., Hulne, W., Iliev, I., Johnson, R., Jones, C.,  
 Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R.,  
 Lindblad-Toh, K., Liu, G., Lui, X., Mabbitt, R., MacLean, C.,  
 MacDonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M.,  
 Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J.,  
 Nguyen, C., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P.,  
 O'Neill, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N.,  
 Rachupka, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P.,  
 Roman, J., Schauer, S., Schuback, R., Seaman, S., Severy, P., Smith, C.,  
 Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M.,  
 Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M.,  
 Vassiliev, H., Venkataraman, V. S., Viel, R., Vo, A., Wilson, B., Wu, X.,  
 Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

Direct Submission  
 Submitted (19-NOV-2003) Whitehead Institute/MIT Center for Genome  
 Research, 320 Charles Street, Cambridge, MA 02141, USA  
 On Nov 19, 2003 this sequence version replaced gi:21313786.  
 All repeats were identified using RepeatMasker:  
 Smit, A.F.A. & Green, P. (1996-1997)  
 http://ftp.genome.washington.edu/RM/RepeatMasker.html

----- Genome Center  
 Center: Whitehead Institute/ MIT Center for Genome Research  
 Center code: WIBR  
 Web site: http://www-seq.wi.mit.edu  
 Contact: sequence\_submissions@genome.wi.mit.edu  
 ----- Project Information  
 Center project name: L20459  
 Center clone name: 26 G 21  
 ----- Summary Statistics  
 Sequencing vector: Plasmid; n/a; 100% of reads  
 Chemistry: Dye-terminator Big Dye; 100% of reads  
 Assembly program: Phrap; version 0.960731  
 Consensus quality: 160977 bases at least Q40  
 Consensus quality: 161390 bases at least Q30  
 Consensus quality: 161524 bases at least Q20  
 Insert size: 157000; agarose-ftp  
 Insert size: 161577; sum-of-contigs  
 Quality coverage: 13.8 in Q20 bases; agarose-ftp  
 Quality coverage: 13.4 in Q20 bases; sum-of-contigs

-----

\* NOTE: This is a 'working draft' sequence. It currently  
 \* consists of 6 contigs. Gaps between the contigs  
 \* are represented as runs of N. The order of the pieces  
 \* is believed to be correct as given, however the sizes  
 \* of the gaps between them are based on estimates that have  
 \* provided by the submitter.  
 \* This sequence will be replaced  
 \* by the finished sequence as soon as it is available and  
 \* the accession number will be preserved.  
 \* 1 53642: contig of 53642 bp in length  
 \* 53643 53742: gap of 100 bp  
 \* 53743 54202: contig of 460 bp in length  
 \* 54203 54302: gap of 100 bp  
 \* 54303 55174: contig of 872 bp in length  
 \* 55175 55274: gap of 100 bp

TITLE  
 JOURNAL  
 REFERENCE  
 AUTHORS

TITLE  
 JOURNAL  
 COMMENT

\* 55275 127105: contig of 71831 bp in length  
 \* 127106 127205: gap of 100 bp  
 \* 127206 152575: contig of 25370 bp in length  
 \* 152576 152675: gap of 100 bp  
 \* 152676 162077: contig of 9402 bp in length.

FEATURES  
 source  
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 /mol\_type="genomic DNA"  
 /db\_xref="taxon:10090"  
 /chromosome="8"  
 /map="8"  
 /clone\_lib="RPCI-23 Female Mouse BAC"  
 1..53642  
 /note="assembly\_fragment"  
 clone\_end:SP6  
 vector\_side:left  
 53743..54202  
 /note="assembly\_fragment"  
 54303..55174  
 /note="assembly\_fragment"  
 55275..127105  
 /note="assembly\_fragment"  
 127206..152575  
 /note="assembly\_fragment"  
 152676..162077  
 /note="assembly\_fragment"  
 clone\_end:T7  
 vector\_side:right

misc\_feature

misc\_feature

misc\_feature

misc\_feature

misc\_feature

ORIGIN

Query Match 70.8%; Score 17; DB 2; Length 162077;  
 Best Local Similarity 100.0%; Pred. No. 16;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 AGGGCTTCATGTTCCAC 24  
 |||||  
 DB 95213 AGGGCTTCATGTTCCAC 95197

RESULT 13  
 AL606494

LOCUS Mouse DNA sequence from clone RP23-198B6 on chromosome 2, complete  
 DEFINITION sequence.  
 ACCESSION AL606494.3 GI:32567580  
 VERSION AL606494  
 KEYWORDS HTG.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus

REFERENCE  
 AUTHORS North, P., Leaves, N., Greystrom, J., Coppola, M., Manjunath, S.,  
 Russell, E., Smith, M., Strachan, G., Tofts, C., Boal, E., Cobley, V.,  
 Hunter, G., Kimberley, C., Thomas, D., Cave-Berry, L., Weston, P. and  
 Botcherby, M. R. M.  
 Direct Submission  
 Submitted (12-JUL-2003) Mouse Sequencing Group, HGMP-RC, Hinxton,  
 Cambridge, CB10 1SB, UK. E-mail enquiries:- mrbotche@hgmp.mrc.ac.uk  
 or pnorth@hgmp.mrc.ac.uk  
 HGMP-RC part of the UK Mouse Sequencing Consortium  
 On Jul 12, 2003 this sequence version replaced gi:15723837.  
 ----- Genome Center  
 Center: UK Medical Research Council  
 Center code: UK-MRC  
 Web site: http://mrcseq.har.mrc.ac.uk  
 Contact: mouseq@har.mrc.ac.uk  
 -----

TITLE  
 JOURNAL

REMARK  
 COMMENT

During sequence assembly data is compared from overlapping clones.  
 Where differences are found these are annotated as variations  
 together with a note of the overlapping clone name. Note that the

variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em: EMBL; Sw: SWISSPROT; Tr: TREMBL; Wp: WORMPEP; Information

on the WORMPEP database can be found at

[http://www.sanger.ac.uk/Projects/C\\_elegans/wormpep](http://www.sanger.ac.uk/Projects/C_elegans/wormpep) RP23-198B6 is

from the RP23-23 Mouse BAC library

constructed by the group of Pieter de Jong.

For further details see <http://www.chori.org/bacpac/home.htm>

VECTOR: pBACE3.6

Sequence from the Mouse Genome Sequencing Consortium whole genome shotgun may have been used to confirm this sequence. Sequence data from the whole genome shotgun alone has only been used where it has a phred quality of at least 30.

#### FEATURES

source

```
1. .184317
   /organism="Mus musculus"
   /mol_type="genomic DNA"
   /db_xref="taxon:10090"
   /chromosomes="2"
   /clone="RP23-198B6"
   /clone_lib="RPCI-23"
```

#### ORIGIN

Query Match 70.8%; Score 17; DB 10; Length 184317;

Best Local Similarity 100.0%; Pred. No. 15;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TGAAGGCTTCATGTC 21

|||||

Db 1732 TGAAGGCTTCATGTC 1748

#### RESULT 14

AC096363

LOCUS

DEFINITION Rattus norvegicus 1 BAC CH230-54P17 (Children's Hospital Oakland

Research Institute) complete sequence.

AC096363

VERSION

KEYWORDS

SOURCE Rattus norvegicus (Norway rat)

#### ORGANISM

Rattus norvegicus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
Rattus.

REFERENCE 1 (bases 1 to 215356)

#### AUTHORS

Muzny,D,Marie., Metzker,M.Lee., Abramson,S., Adams,C., Alder,J.,  
Allen,C., Allen,H., Alsbrooks,S., Amin,A., Anguiano,D.,  
Anyalebechi,V., Aoyagi,A., Ayodeji,M., Baca,E., Baden,H.,  
Baldwin,D., Bandaranaike,D., Barber,M., Barnstead,M., Benahmed,F.,  
Biswalo,K., Blair,J., Blankenburg,K., Blyth,P., Brown,M.,  
Bryant,N., Buhay,C., Burch,P., Burrell,K., Calderon,E.,  
Cardenas,V., Carter,K., Cavazos,I., Caesar,H., Center,A.,  
Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Y., Chen,Z., Chu,J.,  
Cleveland,C., Cockrell,R., Cox,C., Coyle,M., Cree,A., D'Souza,L.,  
Davila,M.L., Davis,C., Davy-Carroll,L., De Anda,C., Dederich,D.,  
Delgado,O., Denson,S., Deramo,C., Ding,Y., Dinh,H., Divya,K.,  
Draper,H., Dugan-Rocha,S., Dunn,A., Durbin,K., Duval,B., Eaves,K.,  
Egan,A., Escoto,M., Eugene,C., Evans,C.A., Falls,T., Fan,G.,  
Fernandez,S., Finley,M., Flagg,N., Forbes,L., Foster,M., Foster,P.,  
Fraser,C.M., Gabisi,A., Ganta,R., Garcia,A., Garner,T., Garza,M.,  
Gebregorgis,E., Geer,K., Gill,R., Grady,M., Guerra,W., Guevara,W.,

Gunaratne,P., Haaland,W., Hamil,C., Hamilton,C., Hamilton,K.,  
Harvey,Y., Haylak,P., Hawes,A., Henderson,N., Hernandez,M.,  
Hernandez,R., Hines,S., Hladun,S.L., Hodgson,A., Hogues,J.,  
Hollins,B., Howells,S., Hulyk,S., Hume,J., Idlebird,D., Jackson,A.,  
Jackson,L., Jacob,L., Jiang,H., Johnson,B., Johnson,R., Jolivet,A.,  
Karpachy,S., Kelly,S., Kelly,S., Khan,Z., King,L., Kovar,C.,  
Kowis,C., Kraft,C.L., Lebow,H., Levan,J., Lewis,L., Li,Z., Liu,J.,  
Liu,J., Liu,W., Liu,Y., London,P., Longacre,S., Lopez,J.,  
Lorensheva,L., Louseghed,H., Lozado,R.J., Lu,X., Ma,J.,  
Maheshwari,M., Mahindartne,M., Mahmoud,M., Malloy,K., Mangum,A.,  
Mangum,B., Mapua,P., Martin,K., Martin,R., Martinez,E.,  
Mawhney,S., Mcleod,M., Mcneill,T., Meenen,E., Milosavljevic,A.,  
Miner,G., Minja,E., Montemayor,J., Moore,S., Morgan,M., Morris,K.,  
Morris,S., Munidasa,M., Murphy,M., Nair,L., Nankervis,C., Neal,D.,  
Newton,N., Nguyen,N., Norris,S., Nwaokemele,O., Okwuonu,G.,  
Olanpunsogun,A., Pal,S., Parks,K., Pasternak,S., Paul,H.,  
Perez,A., Perez,L., Pfannkuch,C., Plopper,F., Poindexter,A.,  
Popovic,D., Primus,E., Pu,L.-L., Puazo,M., Quiroz,J., Rachlin,E.,  
Reeves,K., Regier,M.A., Reigh,R., Reilly,B., Reilly,M., Ren,Y.,  
Reuter,M., Richards,S., Riggs,P., Rives,C., Rodkey,T., Rojas,A.,  
Rose,M., Rose,R., Ruiz,S.J., Sanders,W., Savery,G., Scherer,S.,  
Scott,G., Shatsman,S., Shen,H., Shetty,J., Shvartsbeyn,A.,  
Sisson,I., Sitter,C.D., Smajd,D., Snead,A., Sodergren,E.,  
Svatek,A., Tabor,P., Taylor,C., Taylor,T., Thomas,N., Thomas,A.,  
Tingey,A., Trejos,Z., Usmani,K., Valas,R., Vera,V., Villasana,D.,  
Waldron,L., Walker,B., Wang,J., Wang,Q., Wang,S., Warren,J.,  
Warren,R., Wei,X., White,F., Williams,G., Willson,R., Wleczyk,R.,  
Wooden,H., Worley,K., Wright,D., Wright,R., Wu,J., Yakub,S.,  
Yen,J., Yoon,L., Yoon,V., Yu,F., Zhang,J., Zhou,J., Zhou,X.,  
Zhao,S., Dunn,D., von Niederhausern,A., Weiss,R., Smith,D.R.,  
Holt,R.A., Smith,H.O., Weinstock,G. and Gibbs,R.A.

#### Direct Submission

Unpublished

2 (bases 1 to 215356)

REFERENCE

Worley,K.C.

Direct Submission

JOURNAL

Submitted (17-SEP-2001) Human Genome Sequencing Center, Department  
of Molecular and Human Genetics, Baylor College of Medicine, One  
Baylor Plaza, Houston, TX 77030, USA

3 (bases 1 to 215356)

REFERENCE

AUTHORS

TITLE

JOURNAL

Rat Genome Sequencing Consortium.  
Submitted (10-MAY-2003) Human Genome Sequencing Center, Department  
of Molecular and Human Genetics, Baylor College of Medicine, One  
Baylor Plaza, Houston, TX 77030, USA

4 (bases 1 to 215356)

REFERENCE

AUTHORS

JOURNAL

Direct Submission

Worley,K.C.

Submitted (01-JUL-2003) Human Genome Sequencing Center, Department  
of Molecular and Human Genetics, Baylor College of Medicine, One  
Baylor Plaza, Houston, TX 77030, USA

#### COMMENT

On Jul 1, 2003 this sequence version replaced gi:30521822.  
Sequencing is completed to a minimum standard of double strand  
coverage with a minimum of 2 clones and 2 reads with no ambiguities  
or 2 chemistries with a minimum of 2 clones and 3 reads with no  
ambiguities. If the sequence quality does not meet this standard,  
it will be indicated in the annotation.

#### FEATURES

source

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1. .215356
   /organism="Rattus norvegicus"
   /mol_type="genomic DNA"
   /db_xref="taxon:10116"
   /chromosomes="1"
   /clone="CH230-54P17"
   /rpt_family="LIMC2"
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   /rpt_family="PB1D9"
   /rpt_family="MTD"
   /rpt_family="LIMC2"
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repeat_region complement(1795..1839)
repeat_region /rpt_family="PB1D7"
repeat_region 1897..2013
repeat_region /rpt_family="PB1D9"
repeat_region 2030..2186
repeat_region /rpt_family="B3"
repeat_region 2187..2246
repeat_region /rpt_family="(CA)n"
repeat_region 2247..2259
repeat_region /rpt_family="B3"
repeat_region 2279..2348
repeat_region /rpt_family="(TG)n"
repeat_region complement(2411..2531)
repeat_region /rpt_family="B1F"
repeat_region complement(2485..2539)
repeat_region /rpt_family="B4A"
repeat_region 2540..2690
repeat_region /rpt_family="RLTR28B"
repeat_region 2660..2885
repeat_region /rpt_family="RLTR28"
repeat_region complement(2904..3118)
repeat_region /rpt_family="B3"
repeat_region 3120..3148
repeat_region /rpt_family="(TTTTG)n"
repeat_region 3164..3238
repeat_region /rpt_family="PB1D7"
repeat_region complement(4251..4341)
repeat_region /rpt_family="RSINE1"
repeat_region complement(4340..4439)
repeat_region /rpt_family="B3A"
repeat_region complement(4459..4662)
repeat_region /rpt_family="B3A"
repeat_region 5152..5367
repeat_region /rpt_family="ID_B1"
repeat_region 5385..5596
repeat_region /rpt_family="B4A"
repeat_region 5591..5937
repeat_region /rpt_family="MTC"
repeat_region 5938..5989
repeat_region /rpt_family="B4A"
repeat_region 6078..6129
repeat_region /rpt_family="ID_B1"
repeat_region 6130..6147
repeat_region /rpt_family="BC1_Rn"
repeat_region 6155..6291
repeat_region /rpt_family="RSINE1"
repeat_region 6320..6354
repeat_region /rpt_family="(A)n"
repeat_region 7540..7750
repeat_region /rpt_family="ID_B1"
repeat_region 7760..7963
repeat_region /rpt_family="B3"
repeat_region 7985..8082
repeat_region /rpt_family="ID_Rn"
repeat_region 8431..8495
repeat_region /rpt_family="tRNA-Ala-GCV_"
repeat_region 8502..8526
repeat_region /rpt_family="(TG)n"
repeat_region 8527..8541
repeat_region /rpt_family="AT_rich"
repeat_region 8542..8624
repeat_region /rpt_family="ID_Rn"
repeat_region 8625..8662
repeat_region /rpt_family="(CAA)n"
repeat_region 8673..8689
repeat_region /rpt_family="AT_rich"
repeat_region complement(8721..8992)
repeat_region /rpt_family="B4A"
repeat_region 9344..9521
repeat_region /rpt_family="B3A"
repeat_region 9524..9547
repeat_region /rpt_family="(CA)n"
repeat_region complement(9562..9669)

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9678..9960
/rpt_family="MTC"
complement(9976..10126)
/rpt_family="RSINE1"
10127..10227
/rpt_family="B3A"
10232..10308
/rpt_family="B1F"
10773..10893
/rpt_family="B1_Rn"
11195..11233
/rpt_family="MIR"
11234..11265
/rpt_family="(CAAT)n"
11266..11454
/rpt_family="MIR"
complement(11501..11784)
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12161..12250
/rpt_family="L3"
16193..16220
/rpt_family="GC_rich"
16933..16988
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complement(17099..17245)

Query Match 70.8%; Score 17; DB 10; Length 215356;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GCTGAAGGGCTTCATGT 19
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RESULT 15
AC102091/c
LOCUS
DEFINITION Mus musculus clone RP23-9K20, WORKING DRAFT SEQUENCE, 5 unordered
pieces.
ACCESSION AC102091
VERSION AC102091.3 GI:27884970
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Birren,B., Nusbaum,C. and Lander,E.
1 (bases 1 to 215958)
Mus musculus, clone RP23-9K20
Unpublished
REFERENCE 2 (bases 1 to 215958)
AUTHORS Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
Anderson,S., Barna,N., Bastien,V., Boguslavsky,L., Boukhgalter,B.,
Brown,A., Camarata,J., Campopiano,A., Chang,J., Chazaro,B.,
Choepe,Y., Colangelo,M., Collins,S., Collymore,A., Cook,A.,
Cooke,P., Dearellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S.,
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Jones,C., Kamat,A., Karatas,A., Kells,C., LaRocque,K.,
Lamazaras,R., Landers,T., Lehoczy,J., Levine,R., Liu,G.,
MacLean,C., Macdonald,P., Major,J., Marquis,N., Matthews,C.,
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Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D.,
Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Pollara,V.,
Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P.,
Roman,J., Roaetti,M., Roy,A., Santos,R., Schauer,S., Schupback,R.,
Seaman,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N.,
Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J.,
Topham,K., Travers,M., Travis,N., Trigilio,J., Vassiliev,H.,

```

Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,  
 Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.  
 Direct Submission  
 Submitted (23-NOV-2001) Whitehead Institute/MIT Center for Genome  
 Research, 320 Charles Street, Cambridge, MA 02141, USA  
 3 (bases 1 to 215958)  
**REFERENCE**  
**AUTHORS**  
 Anderson,S., Arachchi,H.M., Barna,N., Bastien,V., Bloom,T.,  
 Boquslavskiy,L., Boukhalter,B., Camarata,J., Chang,J., Choepel,Y.,  
 Collymore,A., Cook,A., Cooke,P., Corum,B., DeArellano,K.,  
 Diaz,J.S., Dodge,S., Dooley,K., Dorris,L., Erickson,J., Faro,S.,  
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 Spencer,B., Stange-Thomann,N., Stojanovic,N., Stubbs,M.,  
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 Vassiliev,H., Venkataraman,V.S., Viel,R., Vo,A., Wilson,B., Wu,X.,  
 Wyman,D., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.  
 Direct Submission  
 Submitted (24-JAN-2003) Whitehead Institute/MIT Center for Genome  
 Research, 320 Charles Street, Cambridge, MA 02141, USA  
 On Jan 24, 2003 this sequence version replaced gi:22381287.  
**COMMENT**  
 All repeats were identified using RepeatMasker:  
 Smit, A.F.A. & Green, P. (1996-1997)  
 http://ftp.genome.washington.edu/RM/RepeatMasker.html

# TITLE JOURNAL

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 Job time : 511.783 secs

# ORIGIN

## COMMENT

Center: Whitehead Institute/ MIT Center for Genome Research  
 Center code: WIBR  
 Web site: http://www-seq.wi.mit.edu  
 Contact: sequence\_submissions@genome.wi.mit.edu  
 ----- Project Information  
 Center project name: L18028  
 Center clone name: 9\_K\_20  
 ----- Summary Statistics  
 Sequencing vector: Plasmid; n/a; 100% of reads  
 Chemistry: Dye-terminator Big Dye; 100% of reads  
 Assembly program: Phrap; version 0.960731  
 Consensus quality: 214869 bases at least Q40  
 Consensus quality: 215183 bases at least Q30  
 Consensus quality: 215314 bases at least Q20  
 Insert size: 220000; agarose-fp  
 Insert size: 215558; sum-of-contigs  
 Quality coverage: 11.4 in Q20 bases; agarose-fp  
 Quality coverage: 11.6 in Q20 bases; sum-of-contigs

\* NOTE: This is a 'working draft' sequence. It currently  
 \* consists of 5 contigs. The true order of the pieces  
 \* is not known and their order in this sequence record is  
 \* arbitrary. Gaps between the contigs are represented as  
 \* runs of N, but the exact sizes of the gaps are unknown.  
 \* This record will be updated with the finished sequence  
 \* as soon as it is available and the accession number will  
 \* be preserved.

\* 1 16300: contig of 16300 bp in length  
 \* 16301 16400: gap of 100 bp  
 \* 16401 122337: contig of 105937 bp in length  
 \* 122338 122437: gap of 100 bp  
 \* 122438 139749: contig of 17312 bp in length  
 \* 139750 139849: gap of 100 bp  
 \* 139850 211515: contig of 71666 bp in length  
 \* 211516 211615: gap of 100 bp  
 \* 211616 215958: contig of 4343 bp in length.

# FEATURES

## source

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 26, 2004, 14:55:11 ; Search time 107.037 Seconds  
(without alignments)  
952.539 Million cell updates/sec

Title: US-09-121-239-18

Perfect score: 24

Sequence: 1 CCGCTGAGGGTTCATGTTCCAC 24

Scoring table: OLIGO\_NUC

Gapop 60.0 , Gapext 60.0

Searched: 3373863 seqs, 2124039041 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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- 3: Geneseqn2000s:\*
- 4: Geneseqn2001as:\*
- 5: Geneseqn2001bs:\*
- 6: Geneseqn2002s:\*
- 7: Geneseqn2003as:\*
- 8: Geneseqn2003bs:\*
- 9: Geneseqn2003cs:\*
- 10: Geneseqn2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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2	24	100.0	24	3	Aaz60855 Oligonucl
3	24	100.0	24	3	Aaz60858 Oligonucl
4	24	100.0	24	3	Aaz60856 Oligonucl
5	24	100.0	299	3	Aaz60864 Region su
6	24	100.0	3380	7	Abz18520 Group III
7	18	75.0	34125	6	Abn54940 Mouse spl
8	16	66.7	65	6	Abn54940 Mouse spl
9	16	66.7	751	4	Aai194531 Human neu
10	16	66.7	1044	4	Aas54224 Pseudomon
11	16	66.7	1044	7	ACA42504 Prokaryot
12	16	66.7	2278	3	Aaz289962 Corn ADA2
13	16	66.7	2599	3	Aaz256382-Escherich
14	16	66.7	3460	2	Aav36957 Nucleotid
15	16	66.7	3460	2	Aaz34989 Human cel
16	16	66.7	3460	6	Abx84482 Human cDN
17	16	66.7	6699	7	Abx08804 Angiogene
18	16	66.7	6699	7	Abx76302 Lung canc
19	16	66.7	185035	6	Abt10147 Human bre
20	16	66.7	185035	7	ACA64951 Human FBN
21	15	62.5	23	2	Aat56765 Human bcr
22	15	62.5	23	2	Aat56766 Human bcr
23	15	62.5	33	2	Aat10497 ABL oncog

C	24	15	62.5	33	2	AAT10495	Aat10495 BCR-ABL o
C	25	15	62.5	40	2	AAQ57147	AaQ57147 Chromosom
C	26	15	62.5	47	2	AAQ66785	AaQ66785 Ribozyme
C	27	15	62.5	52	2	AAT12637	Aat12637 T7 promot
C	28	15	62.5	60	2	AAT29713	Aat29713 Chronic m
C	29	15	62.5	62	2	AAQ66774	AaQ66774 L6(1)31 r
C	30	15	62.5	63	6	ABS73178	DNA encod
C	31	15	62.5	80	2	AAQ34631	Human Phl
C	32	15	62.5	80	2	AAV20460	Human bcr
C	33	15	62.5	205	6	ABL87455	Human ova
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C	37	15	62.5	436	7	ABX40048	Bovine ES
C	38	15	62.5	483	7	ADA71111	Rice gene
C	39	15	62.5	549	6	ABS73314	DNA encod
C	40	15	62.5	729	7	ABZ66719	Orthosomy
C	41	15	62.5	921	5	AAS85025	DNA encod
C	42	15	62.5	922	6	ABS73180	DNA encod
C	43	15	62.5	1024	7	ABZ82900	Toxicolog
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## ALIGNMENTS

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ID AAZ60857 standard; DNA; 24 BP.  
AC AAZ60857;  
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DT 16-MAY-2000 (first entry)  
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DE Oligonucleotide used to detect bcr b3-abl fusion transcripts.  
KW Fusion transcript; translocation; bcr b3 region; abl gene;  
KW amplification assay; detection assay; medical diagnosis;  
KW clinical monitoring; chimeric RNA; fusion RNA; condition marker;  
KW disease marker; cancer; leukemia; ss.  
XX  
OS Synthetic.  
XX  
PN WO2000005418-A1.  
XX  
PD 03-FEB-2000.  
XX  
PF 23-JUL-1999; 99WO-US016832.  
XX  
PR 23-JUL-1998; 98US-00121239.  
XX  
(GENP-) GEN-PROBE INC.  
PI Harvey RC, Eastman PS;  
XX  
DR WPI; 2000-182730/16.  
XX  
XX Novel methods for preparing RNA from biological samples, used for the  
detection and measurement of nucleic acids and fusion nucleic acids.  
Claim 19; Page 43; 49pp; English.  
XX  
XX Oligonucleotides AAZ60840-62 and AAZ60865-66 are used in the method of  
the invention to detect fusion transcripts produced from a translocation  
between the bcr b3 region and the abl gene. The specification describes a  
method for detecting a fusion nucleic acid (particularly chimeric mRNA  
species), in a biological sample. The method comprises contacting a  
sample of fusion nucleic acid with primers, amplifying the hybridized  
fusion nucleic acid, and detecting the target hybrid. The method is used  
for the sample and rapid preparation of RNA from a biological sample,  
particularly from the cytoplasm of eukaryotic cells, which is suitable  
for use in an amplification and detection assay. The methods are used for

CC the analysis and detection of nucleic acids in biological samples. The  
 CC methods are useful in the human medical and veterinary fields, for  
 CC medical diagnoses and clinical monitoring of a patient's response to  
 CC therapy where a disease or medical condition is associated with a  
 CC particular type and/or level of mRNA present in the sample. The methods  
 CC are also useful for detecting or quantifying fusion or chimeric RNA  
 CC species, and for detecting a translocation as a marker for a given  
 CC condition or disease, e.g. translocations associate with cancers,  
 CC particularly forms of leukemia

XX Sequence 24 BP; 4 A; 8 C; 6 G; 6 T; 0 U; 0 Other;  
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 AC AAZ60855;  
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 XX Fusion transcript; translocation; bcr b3 region; abl gene;  
 KW amplification assay; detection assay; medical diagnosis;  
 KW clinical monitoring; chimeric RNA; fusion RNA; condition marker;  
 KW disease marker; cancer; leukemia; ss.  
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 OS Synthetic.  
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 PN WO200005418-A1.  
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 PD 03-FEB-2000.  
 PF 23-JUL-1999; 99WO-US016832.  
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 PR 23-JUL-1998; 98US-00121239.  
 XX  
 PA (GENP-) GEN-PROBE INC.  
 XX  
 PI Harvey RC, Eastman PS;  
 XX  
 DR WPI; 2000-182730/16.  
 XX  
 PT Novel methods for preparing RNA from biological samples, used for the  
 PT detection and measurement of nucleic acids and fusion nucleic acids.  
 PS  
 PS Claim 19; Page 42; 49pp; English.  
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 CC Oligonucleotides AAZ60840-62 and AAZ60865-66 are used in the method of  
 CC the invention to detect fusion transcripts produced from a translocation  
 CC between the bcr b3 region and the abl gene. The specification describes a  
 CC method for detecting a fusion nucleic acid (particularly chimeric mRNA  
 CC species), in a biological sample. The method comprises contacting a  
 CC sample of fusion nucleic acid with primers, amplifying the hybridized  
 CC fusion nucleic acid, and detecting the target hybrid. The method is used  
 CC for the simple and rapid preparation of RNA from a biological sample,  
 CC particularly from the cytoplasm of eukaryotic cells, which is suitable  
 CC for use in an amplification and detection assay. The methods are used for  
 CC the analysis and detection of nucleic acids in biological samples. The  
 CC methods are useful in the human medical and veterinary fields, for  
 CC medical diagnoses and clinical monitoring of a patient's response to  
 CC therapy where a disease or medical condition is associated with a  
 CC particular type and/or level of mRNA present in the sample. The methods  
 CC are also useful for detecting or quantifying fusion or chimeric RNA  
 CC species, and for detecting a translocation as a marker for a given  
 CC condition or disease, e.g. translocations associate with cancers,  
 CC particularly forms of leukemia

CC species, and for detecting a translocation as a marker for a given  
 CC condition or disease, e.g. translocations associate with cancers,  
 CC particularly forms of leukemia

XX Sequence 24 BP; 6 A; 6 C; 8 G; 4 T; 0 U; 0 Other;  
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 KW amplification assay; detection assay; medical diagnosis;  
 KW clinical monitoring; chimeric RNA; fusion RNA; condition marker;  
 KW disease marker; cancer; leukemia; ss.  
 XX  
 OS Synthetic.  
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 PN WO200005418-A1.  
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 XX  
 PA (GENP-) GEN-PROBE INC.  
 XX  
 PI Harvey RC, Eastman PS;  
 XX  
 DR WPI; 2000-182730/16.  
 XX  
 PT Novel methods for preparing RNA from biological samples, used for the  
 PT detection and measurement of nucleic acids and fusion nucleic acids.  
 PS  
 PS Claim 19; Page 43; 49pp; English.  
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 CC Oligonucleotides AAZ60840-62 and AAZ60865-66 are used in the method of  
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 CC method for detecting a fusion nucleic acid (particularly chimeric mRNA  
 CC species), in a biological sample. The method comprises contacting a  
 CC sample of fusion nucleic acid with primers, amplifying the hybridized  
 CC fusion nucleic acid, and detecting the target hybrid. The method is used  
 CC for the simple and rapid preparation of RNA from a biological sample,  
 CC particularly from the cytoplasm of eukaryotic cells, which is suitable  
 CC for use in an amplification and detection assay. The methods are used for  
 CC the analysis and detection of nucleic acids in biological samples. The  
 CC methods are useful in the human medical and veterinary fields, for  
 CC medical diagnoses and clinical monitoring of a patient's response to  
 CC therapy where a disease or medical condition is associated with a  
 CC particular type and/or level of mRNA present in the sample. The methods  
 CC are also useful for detecting or quantifying fusion or chimeric RNA  
 CC species, and for detecting a translocation as a marker for a given  
 CC condition or disease, e.g. translocations associate with cancers,  
 CC particularly forms of leukemia

XX Sequence 24 BP; 4 A; 8 C; 6 G; 0 T; 6 U; 0 Other;  
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AC AAZ60856;
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XX 16-MAY-2000 (first entry)
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XX Oligonucleotide used to detect bcr b3-abl fusion transcripts.
XX
XX Fusion transcript; translocation; bcr b3 region; abl gene;
KW amplification assay; detection assay; medical diagnosis;
KW clinical monitoring; chimeric RNA; fusion RNA; condition marker;
KW disease marker; cancer; leukemia; ss.
XX
XX Synthetic.
XX
XX WO200005418-A1.
XX
XX 03-FEB-2000.
XX
XX 23-JUL-1999; 99WO-US016832.
XX
XX 23-JUL-1998; 98US-00121239.
XX
XX (GENP-) GEN-PROBE INC.
XX
XX Harvey RC, Eastman PS;
XX
XX WPI; 2000-182730/16.
XX
XX Novel methods for preparing RNA from biological samples, used for the
XX detection and measurement of nucleic acids and fusion nucleic acids.
XX
XX Claim 19; Page 42; 49pp; English.
XX
XX Oligonucleotides AAZ60840-62 and AAZ60865-66 are used in the method of
XX the invention to detect fusion transcripts produced from a translocation
XX between the bcr b3 region and the abl gene. The specification describes a
XX method for detecting a fusion nucleic acid (particularly chimeric mRNA
XX sample) in a biological sample. The method comprises contacting a
XX sample of fusion nucleic acid with primers, amplifying the hybridized
XX fusion nucleic acid, and detecting the target hybrid. The method is used
XX for the simple and rapid preparation of RNA from a biological sample,
XX particularly from the cytoplasm of eukaryotic cells, which is suitable
XX for use in an amplification and detection assay. The methods are used for
XX the analysis and detection of nucleic acids in biological samples. The
XX methods are useful in the human medical and veterinary fields, for
XX medical diagnoses and clinical monitoring of a patient's response to
XX therapy where a disease or medical condition is associated with a
XX particular type and/or level of mRNA present in the sample. The methods
XX are also useful for detecting or quantifying fusion or chimeric RNA
XX species, and for detecting a translocation as a marker for a given
XX condition or disease, e.g. translocations associate with cancers,
XX particularly forms of leukemia
XX
XX Sequence 24 BP; 6 A; 6 C; 8 G; 0 T; 4 U; 0 Other;

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 KW immune response; virology; immunology; microbiology; molecular biology;  
 KW recombinant DNA technology; gene; ss.  
 KW  
 XX Homo sapiens.  
 OS  
 XX WO200278516-A2.  
 PN  
 XX 10-OCT-2002.  
 PD  
 XX 28-MAR-2002; 2002WO-US010421.  
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 XX 30-MAR-2001; 2001US-0280255P.  
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 XX 28-AUG-2001; 2001US-0315563P.  
 PR  
 XX 09-JAN-2002; 2002US-0347313P.  
 XX  
 XX (CORI-) CORIXA CORP.  
 PA  
 XX Wang T, Wang S, Bangur CS, Gaiger A;  
 PI  
 XX WPI; 2003-058387/05.  
 DR  
 XX  
 XX New immunogenic polynucleotides or polypeptides useful for diagnosing,  
 PT preventing and treating cancer expressing CT or CP mRNA antigens, and in  
 PT virology, immunology, microbiology, molecular biology and recombinant DNA  
 PT techniques.  
 PT  
 XX Claim 1; SEQ ID NO 946; 207pp; English.  
 PS  
 XX ABQ1575 to ABQ20506 represent isolated polynucleotide (I) sequences, and  
 CC ABQ5446 to ABQ54472 represent protein (II) sequences, from the present  
 CC invention. (I) and (II) have cytosolic activity and can be used in gene  
 CC therapy and vaccines. (I), (II), antibodies and compositions from the  
 CC present invention are useful for diagnosing, preventing and treating  
 CC cancer, which expresses CT or CP mRNA antigens. They are useful for  
 CC stimulating immune response. They can also be useful in virology,  
 CC immunology, microbiology, molecular biology and recombinant DNA  
 CC techniques. N.B. The sequence data for this patent did not form part of  
 CC the printed specification, but was obtained in electronic format directly  
 CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
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 DB 80 CCGCTGAAGGGCTTCATGTTCCAC 57  
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 AC  
 XX ABS69903;  
 XX  
 XX 21-NOV-2002 (first entry)  
 DT  
 XX Human adenovirus type 12 genome sequence.  
 DE  
 XX Vector; adenovirus; adeno-associated; adenosine deaminase gene; receptor;  
 KW adenosine deaminase deficiency; severe combined immune deficiency; PAH;  
 KW beta-chain; haemoglobin gene; beta-thalassaemia; sickle cell disease;

KW low density lipoprotein gene; familial hypercholesterolaemia;  
 KW hypoxanthine-guanine phosphoribosyltransferase; Lesch-Nyhan syndrome;  
 KW phenylalanine hydroxylase gene; gene therapy; phenylketonuria;  
 KW dystrophin gene; muscular dystrophy; cystic fibrosis; immunostimulant;  
 KW human cystic fibrosis transmembrane conductance regulator gene;  
 KW antianemic; antilipemic; nontropic; cytostatic; dermatological;  
 KW human adenovirus genome; ds.  
 KW  
 XX Human adenovirus type 12.  
 OS  
 XX US2002102731-A1.  
 PN  
 XX 01-AUG-2002.  
 PD  
 XX 12-FEB-2001; 2001US-00782378.  
 PF  
 XX 02-OCT-2000; 2000US-0237747P.  
 XX  
 XX (UYN ) UNIV NEW YORK STATE RES FOUND.  
 PA  
 XX Hearing P, Bahou WF, Sandalon Z, Gnatenko DV;  
 PI  
 XX WPI; 2002-690619/74.  
 XX  
 XX Producing vector, by introducing vector having nucleotide sequence,  
 PT adenovirus inverted terminal repeats and packaging sequence, and adeno-  
 PT associated virus terminal repeat, into cell, and culturing cell.  
 PT  
 XX Disclosure; Page 135-150; 191pp; English.  
 PS  
 XX The present invention relates to a new method of producing a vector. The  
 CC method involves introducing recombinant vector having nucleotide sequence  
 CC (NS) having 5' and 3' end, left and right inverted terminal repeats of  
 CC adenovirus flanking NS, adenovirus packaging sequence linked to inverted  
 CC terminal repeat, and adeno-associated virus terminal repeat linked to 3'  
 CC end of NS, into cell expressing adenovirus early gene lacking from vector  
 CC ; and culturing cell to produce another vector. The method is useful for  
 CC generating vectors, especially mAd vectors. The method is useful in  
 CC transferring nucleotide sequences of interest into a cell, for gene  
 CC transfer applications (e.g. gene therapy) in vitro, ex vivo and in vivo.  
 CC The nucleotide sequences are useful for treating diseases associated with  
 CC it, i.e. adenosine deaminase gene associated with adenosine deaminase  
 CC deficiency with severe combined immune deficiency, beta-chain of  
 CC haemoglobin gene associated with beta-thalassaemia and sickle cell  
 CC disease, receptor for low density lipoprotein gene associated with  
 CC familial hypercholesterolaemia, hypoxanthine-guanine  
 CC phosphoribosyltransferase associated with Lesch-Nyhan syndrome,  
 CC phenylalanine hydroxylase (PAH) gene associated with phenylketonuria,  
 CC dystrophin gene associated with muscular dystrophy, and human cystic  
 CC fibrosis transmembrane conductance regulator gene associated with cystic  
 CC fibrosis. The present nucleic acid sequence represents a human adenovirus  
 CC genome sequence that was used in the methods of the invention  
 CC  
 XX Sequence 34125 BP; 9330 A; 8012 C; 7864 G; 8919 T; 0 U; 0 Other;  
 SQ  
 Query Match 75.0%; Score 18; DB 6; Length 34125;  
 Best Local Similarity 100.0%; Pred. No. 0.95;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 5 TGAAGGGCTTCATGTTCC 22  
 DB 3998 TGAAGGGCTTCATGTTCC 4015  
 RESULT 8  
 ID ABN54940/c  
 XX ABN54940 standard; DNA; 65 BP.  
 AC  
 XX ABN54940;  
 XX  
 XX 15-JUL-2002 (first entry)  
 DT  
 XX Mouse spliced transcript detection oligonucleotide SEQ ID NO:27688.  
 DE

```

XX Human; mouse; rat; splice transcript; detection; RNA transcript;
KW splice variant; transcriptome; oligonucleotide library; ss.
XX
XX OS Mus musculus.
XX
XX PN WO200210449-A2.
XX
XX PD 07-FEB-2002.
XX
XX PF 20-JUL-2001; 2001WO-IB001903.
XX
XX PR 28-JUL-2000; 2000US-0221607P.
XX
XX PR 02-MAY-2001; 2001US-0287724P.
XX
XX PA (COMP-) COMPUGEN INC.
XX
XX PI Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;
XX
XX WPI; 2002-257383/30.
XX
XX New oligonucleotide libraries comprising oligonucleotides which
PT selectively hybridize to mRNAs transcribed from a transcription unit of a
PT genome, useful for detecting tissue-, pathology-, and developmental-
PT specific genes.
XX
XX Example 1; SEQ ID NO 27688; 47pp; English.
XX
XX The present invention describes oligonucleotide libraries for detecting
CC messenger RNAs that populate a (sub-)transcriptome, where the (sub-)
CC transcriptome comprises messenger RNAs transcribed from multiple
CC transcription units that populate a genome. The library comprises several
CC oligonucleotides, each capable of hybridising selectively to a set of
CC messenger RNAs transcribed from a given transcription unit of the genome,
CC which encodes one or more messenger RNA splice variants. The
CC oligonucleotide libraries are useful for detecting mRNAs from a
CC biological sample, in expression profiling studies, in qualitatively or
CC quantitatively characterising the corresponding transcriptome, and in
CC detecting RNA transcripts and splice variants of human or animal
CC transcriptomes. The libraries may also be used as specialised mini
CC libraries to detect transcripts of a sub-transcriptome under a particular
CC biological or pathological state, and so allowing the detection of tissue
CC - and pathology-specific genes such as those genes only expressed in
CC specific tissue under a specific pathological condition; to detect
CC developmental specific genes; and to detect RNA transcripts and splice
CC variants of a transcriptome of a patient suffering from a particular
CC disorder. ABN27253 to ABN59589 represent oligonucleotide sequences from
CC rats, humans and mice, which are used in the exemplification of the
CC present invention. N.B. The sequence data for this patent did not form
CC part of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 65 BP; 18 A; 16 C; 19 G; 12 T; 0 U; 0 Other;
Query Match 66.7%; Score 16; DB 6; Length 65;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GGGCTTCATGTTCCAC 24
DB 22 GGGCTTCATGTTCCAC 7

RESULT 9
AAI94531
ID AAI94531 standard; cDNA; 751 BP.
XX
XX AC AAI94531;
XX
XX DT 13-NOV-2001 (first entry)
XX
XX DE Human neuroblastoma expressed polynucleotide SEQ ID NO 606.
XX

```

```

KW Human; neuroblastoma; malignancy; cancer; tumour marker; N-myc; TrkA; ss.
XX
XX OS Homo sapiens.
XX
XX PN WO200166719-A1.
XX
XX PD 13-SEP-2001.
XX
XX PF 02-MAR-2001; 2001WO-JP001629.
XX
XX PR 07-MAR-2000; 2000JP-00159195.
XX
XX PA (CHIB-) CHIBA PREFECTURE.
XX
XX PA (HISM) HISAMITSU PHARM CO LTD.
XX
XX PI Nakagawara A;
XX
XX WPI; 2001-565584/63.
XX
XX Nucleic acids originating in gene expressed in human neuroblastoma,
PT useful as probe or primer in diagnosing prognosis of human neuroblastoma,
PT malignancy and susceptibility indicator or tumor marker for anti-cancer
PT agents.
XX
XX Claim 1; Page 485; 2979pp; Japanese.
XX
XX The invention relates to novel genes (AAI93926-AAI97963) expressed in
CC human neuroblastoma. The nucleic acids are applicable as a probe or
CC primer in diagnosing the prognosis of human neuroblastoma, malignancy and
CC susceptibility indicators or tumour markers for anti-cancer agents. The
CC gene information for diagnosing prognosis is related to factors similar
CC to that for N-myc and TrkA genes
XX
XX Sequence 751 BP; 176 A; 176 C; 215 G; 157 T; 0 U; 27 Other;
Query Match 66.7%; Score 16; DB 4; Length 751;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GCTGAAGGGCTTCATG 18
DB 548 GCTGAAGGGCTTCATG 563

RESULT 10
AAS54224/c
ID AAS54224 standard; DNA; 1044 BP.
XX
XX AC AAS54224;
XX
XX DT 13-FEB-2002 (first entry)
XX
XX DE Pseudomonas aeruginosa DNA for cellular proliferation protein #355.
XX
XX KW Antisense; ds; prokaryotic cellular proliferation gene; antibiotic;
KW antibacterial; drug design.
XX
XX OS Pseudomonas aeruginosa.
XX
XX PN WO200170955-A2.
XX
XX PD 27-SEP-2001.
XX
XX PF 21-MAR-2001; 2001WO-US009180.
XX
XX PR 21-MAR-2000; 2000US-0191078P.
XX
XX PR 23-MAY-2000; 2000US-0206848P.
XX
XX PR 26-MAY-2000; 2000US-0207277P.
XX
XX PR 23-OCT-2000; 2000US-0242578P.
XX
XX PR 27-NOV-2000; 2000US-0253625P.
XX
XX PR 22-DEC-2000; 2000US-0257931P.
XX
XX PR 16-FEB-2001; 2001US-0269308P.
XX

```

PA (ELIT-) ELITRA PHARM INC.  
 XX Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;  
 PI Yamamoto RT, Xu HH;  
 XX WPI: 2001-611495/70.  
 DR P-PSDB; AAU36365.  
 XX New polynucleotides for the identification and development of  
 PT antibiotics, comprise sequences of antisense nucleic acids.  
 XX  
 PS Claim 27; SEQ ID NO 7861; 511pp; English.  
 XX The invention relates to antisense inhibitors of genes essential to  
 CC prokaryotic cellular proliferation, their use in identifying the genes,  
 CC their use in the discovery of novel antibiotics, the essential genes  
 CC themselves and the encoded proteins. The prokaryotes used are Escherichia  
 CC coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae,  
 CC Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also  
 CC useful for the identification of potential new targets for antibiotic  
 CC development. The antisense nucleic acids can also be used to identify  
 CC proteins used in proliferation, to express these proteins, and to obtain  
 CC antibodies capable of binding to the expressed proteins. The proteins can  
 CC be used to screen compounds in rational drug discovery programmes. The  
 CC antisense nucleic acid sequence is also useful to screen for homologous  
 CC nucleic acids which are required for cell proliferation in a wide variety  
 CC of organisms. The present sequence encodes an essential prokaryotic  
 CC cellular proliferation protein. Note: The sequence data for this patent  
 CC did not form part of the printed specification, but was obtained in  
 CC electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 1044 BP; 159 A; 373 C; 334 G; 178 T; 0 U; 0 Other;  
 Query Match 66.7%; Score 16; DB 4; Length 1044;  
 Best Local Similarity 100.0%; Pred. No. 13;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CCGCTGAAGGGCTTCA 16  
 DB 812 CCGCTGAAGGGCTTCA 797  
 RESULT 11  
 ACA42504/c  
 ID ACA42504 standard; DNA; 1044 BP.  
 XX  
 AC ACA42504;  
 XX  
 DT 19-JUN-2003 (first entry)  
 DE Prokaryotic essential gene #24161.  
 XX  
 KW Antisense; ds; prokaryotic essential gene; cell proliferation;  
 KW drug design; gene.  
 OS Pseudomonas aeruginosa.  
 XX  
 PN WO200277183-A2.  
 XX  
 PD 03-OCT-2002.  
 XX  
 PF 21-MAR-2002; 2002WO-US009107.  
 XX  
 PR 21-MAR-2001; 2001US-00815242.  
 PR 06-SEP-2001; 2001US-00948993.  
 PR 25-OCT-2001; 2001US-0342923P.  
 PR 08-FEB-2002; 2002US-00072851.  
 PR 06-MAR-2002; 2002US-0362699P.  
 XX  
 PA (ELIT-) ELITRA PHARM INC.  
 XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;

PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;  
 XX WPI: 2003-029926/02.  
 DR P-PSDB; ABU38634.  
 XX  
 PT New antisense nucleic acids, useful for identifying proteins or screening  
 PT for homologous nucleic acids required for cellular proliferation to  
 PT isolate candidate molecules for rational drug discovery programs.  
 XX  
 PS Claim 14; SEQ ID NO 30374; 1766pp; English.  
 XX The invention relates to an isolated nucleic acid comprising any one of  
 CC the 6213 antisense sequences given in the specification where expression  
 CC of the nucleic acid inhibits proliferation of a cell. Also included are:  
 CC (1) a vector comprising a promoter operably linked to the nucleic acid  
 CC encoding a polypeptide whose expression is inhibited by the antisense  
 CC nucleic acid; (2) a host cell containing the vector; (3) an isolated  
 CC antisense nucleic acid; (4) an antibody capable of specifically binding  
 CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular  
 CC proliferation or the activity of a gene in an operon required for  
 CC proliferation; (7) identifying a compound that influences the activity of  
 CC the gene product or that has an activity against a biological pathway  
 CC required for proliferation, or that inhibits cellular proliferation; (8)  
 CC identifying a gene required for cellular proliferation or the biological  
 CC pathway in which a proliferation-required gene or its gene product lies  
 CC or a gene on which the test compound that inhibits proliferation of an  
 CC organism acts; (9) manufacturing an antibiotic; (10) profiling a  
 CC compound's activity; (11) a culture comprising strains in which the gene  
 CC product is overexpressed or underexpressed; (12) determining the extent  
 CC to which each of the strains is present in a culture or collection of  
 CC strains; or (13) identifying the target of a compound that inhibits the  
 CC proliferation of an organism. The antisense nucleic acids are useful for  
 CC identifying proteins or screening for homologous nucleic acids required  
 CC for cellular proliferation to isolate candidate molecules for rational  
 CC drug discovery programs, or for screening homologous nucleic acids  
 CC required for proliferation in cells other than S. aureus, S. typhimurium,  
 CC K. pneumoniae or P. aeruginosa. The present sequence is one of the target  
 CC prokaryotic essential genes. Note: The sequence data for this patent did  
 CC not form part of the printed specification, but was obtained in  
 CC electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 1044 BP; 159 A; 373 C; 334 G; 178 T; 0 U; 0 Other;  
 Query Match 66.7%; Score 16; DB 7; Length 1044;  
 Best Local Similarity 100.0%; Pred. No. 13;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CCGCTGAAGGGCTTCA 16  
 DB 812 CCGCTGAAGGGCTTCA 797  
 RESULT 12  
 AAZ89962/c  
 ID AAZ89962 standard; cDNA; 2278 BP.  
 XX  
 AC AAZ89962;  
 XX  
 DT 05-MAY-2000 (first entry)  
 XX  
 DE Corn ADA2 transcription co-activator nucleotide sequence.  
 XX  
 KW ADA2; transcription co-activator; adaptor; plant breeding; corn; ss;  
 KW transgenic plant.  
 XX  
 OS Zea mays.  
 XX  
 PN WO200003026-A2.  
 XX  
 PD 20-JAN-2000.  
 XX



```

PF 12-JUL-1999; 99WO-US015664.
XX
PR 13-JUL-1998; 98US-0092659P.
XX
PA (DUPO ) DU PONT DE NEMOURS & CO E I.
XX
PI Cahoon RE, Liu Z, Odell JT, Sakai H;
XX
DR WPI; 2000-160931/14.
XX
DR P-PSDB; AAY78518.
XX
PT New isolated nucleic acid fragment encoding a transcription coactivator
PT in plants and seeds useful as a probe to isolate genes encoding
PT homologous proteins from other plant species, and as a primer.
XX
PS Claim 3; Page 29-30; 42pp; English.
XX
CC This sequence represents an ADA2 transcription adaptor/co-activator. In
CC yeast ADA2 functionally interacts with the acidic activation domain of
CC transcriptional activators. The invention relates to ADA2 nucleotide and
CC protein sequences, and also to a chimeric gene comprising of the ADA2
CC nucleotide sequence operably linked to a suitable regulatory sequence.
CC The ADA2 nucleotide sequence can be used as a DNA hybridization probe to
CC screen libraries from any desired plant and to isolate cDNAs and genes
CC encoding other ADA2 transcription adaptors, either as cDNAs or genomic
CC DNAs from the same or other plant species. The ADA2 nucleotide sequence
CC is also used as a primer to amplify longer nucleic acid fragments
CC encoding homologous genes from DNA or RNA. The ADA2 nucleotide and
CC peptide sequences are used in the immunological screening of cDNA
CC expression libraries. The nucleotide sequence is used to create
CC transgenic plants in which the protein is present at higher or lower
CC levels than normal or in cell types or developmental stages in which they
CC are not normally found. This would have the effect of altering the level
CC of transcription initiation in those cells. The ADA2 protein is used to
CC prepare antibodies which are useful for detecting them in situ in cells
CC or in vitro in cell extracts. All or a substantial portion of the ADA2
CC nucleotide sequence is used as probes for genetically and physically
CC mapping the genes that they are a part of, and as markers of traits
CC linked to those genes. Such information may be useful in plant breeding
CC in order to develop lines with desired phenotypes. In addition, they are
CC used to probe southern blots containing restriction endonuclease-treated
CC genomic DNAs of a set of individuals representing parent and progeny of a
CC defined genetic cross. Loss of function mutant phenotypes for the cDNA
CC clones identified by target gene disruption or by identifying specific
CC mutants for the genes contained in maize population carrying mutations in
CC all possible genes, are used for producing a plant containing a mutation
CC in the endogenous gene encoding ADA2. This mutant plant can then be used
CC to determine or confirm the natural function of ADA2
XX
SQ Sequence 2278 BP; 669 A; 451 C; 590 G; 561 T; 0 U; 7 Other;
Query Match 66.7%; Score 16; DB 3; Length 2278;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 AAGGCTTCATGTTCC 22
| | | | | | | | | |
Db 1289 AAGGCTTCATGTTCC 1274
RESULT 13
AAZ56382/c
ID AAZ56382 standard; DNA; 2599 BP.
XX
AC AAZ56382;
XX
DT 17-MAR-2000 (first entry)
XX
DE Escherichia coli flagellin protein nucleotide sequence SEQ ID NO:52.
XX
KW Flagellin; fliC; antigen; detection; ds.
XX
OS Escherichia coli.

XX PN WO9961458-A1.
XX
XX 02-DEC-1999.
XX
XX 21-MAY-1999; 99WO-AU000385.
XX
XX 21-MAY-1998; 99AU-00003634.
XX
XX (UNSY ) UNIV SYDNEY.
XX
XX Reeves PR, Wang L;
XX
XX WPI; 2000-072598/06.
XX
XX Novel nucleic acid molecule useful for the detection of flagellated
XX bacterial strains in food, feces, etc.
XX
XX Claim 3; Page 226-227; 245pp; English.
XX
XX AAZ56331 to AAZ56398 represent nucleic acid molecules (I) encoding all or
XX part of an Escherichia coli flagellin protein except a protein expressed
XX by E. coli H1, H7, H12 or H48 type strains. The present invention also
XX describes a method of detecting the presence of E. coli of a particular H
XX serotype in a sample, comprising specifically hybridising a nucleic acid,
XX preferably at least a pair, derived from a flagellating gene, specific
XX for a particular flagellin gene associated with the H serotype, to any
XX E. coli in the sample which contain the gene, and detecting any hybridised
XX molecules identifying the presence of that serotype in the sample. (I)
XX are useful for: (1) detecting the presence of E. coli of H serotype in a
XX sample by hybridising at least one or a pair of (I) to any E. coli in the
XX sample and detecting the hybridised nucleic acid molecules; and (2) for
XX detecting the presence of both O and H-serotypes of E. coli by
XX hybridising at least one or a pair of (I) to any E. coli present in the
XX sample and detecting the hybridised nucleic acid molecules. (I) is
XX particularly useful for detecting the combination of O and H antigen.
XX Hybridised (I) when using at least one (I) is detected by southern blot
XX analysis and, when using a pair of (I), is detected by polymerase chain
XX reaction (PCR). AAZ56399 to AAZ56420 represent primers used in the
XX exemplification of the present invention
XX
SQ Sequence 2599 BP; 708 A; 651 C; 615 G; 625 T; 0 U; 0 Other;
Query Match 66.7%; Score 16; DB 3; Length 2599;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 TGAAGGGCTTCATGTT 20
| | | | | | | | | |
Db 1072 TGAAGGGCTTCATGTT 1057
RESULT 14
AAV36957
ID AAV36957 standard; cDNA; 3460 BP.
XX
AC AAV36957;
XX
DT 26-OCT-1998 (first entry)
XX
DE Nucleotide sequence of human ClqRp gene.
XX
KW Human; Clq receptor protein; ClqRp; phagocytosis; complement;
XX immune system; inflammation; prophylactic; genetic immune deficiency;
XX HIV; cancer; chemotherapy; inhibition; vasculitis; sepsis; fragment;
XX primer; probe; antibody; ss.
XX
OS Homo sapiens.
XX
XX Key Location/Qualifiers
XX Key 149..2107
XX CDS /tag= a
XX FT /product= "ClqRp gene product"
XX FT

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OM nucleic - nucleic search, using sw model

Run on: May 26, 2004, 16:02:51 ; Search time 20.2274 Seconds  
(without alignments)  
659.454 Million cell updates/sec

Title: US-09-121-239-18

Perfect score: 24

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Gapop 60.0 , Gapext 60.0

Searched: 682709 seqs, 277475446 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	16	66.7	306	4	US-09-252-991A-6328
C 2	16	66.7	897	4	US-09-252-991A-6056
C 3	16	66.7	1536	4	US-09-252-991A-6218
C 4	16	66.7	3460	2	US-08-751-305-1
C 5	15	62.5	23	1	US-08-363-233B-21
C 6	15	62.5	23	1	US-08-363-233B-22
C 7	15	62.5	33	3	US-08-793-408-9
C 8	15	62.5	33	3	US-08-793-408-11
C 9	15	62.5	33	3	US-09-139-762A-9
C 10	15	62.5	33	3	US-09-139-762A-11
C 11	15	62.5	47	3	US-08-448-446B-12
C 12	15	62.5	62	3	US-08-448-446B-1
C 13	15	62.5	80	1	US-08-152-621-7
C 14	15	62.5	80	1	US-08-306-691B-38
C 15	15	62.5	80	5	PCT-US92-05035-7
C 16	15	62.5	204	5	PCT-US93-06251-5
C 17	15	62.5	257	1	US-08-152-621-1
C 18	15	62.5	257	1	US-08-306-691B-36
C 19	15	62.5	257	5	PCT-US92-05035-1
C 20	15	62.5	1918	4	US-09-252-991A-3290
C 21	15	62.5	2115	4	US-09-252-991A-3388
C 22	15	62.5	3623	1	US-08-306-691B-35
C 23	15	62.5	30001	1	US-08-125-468-1
C 24	15	62.5	30001	2	US-08-474-933-1
C 25	14	58.3	23	1	US-08-152-621-34
C 26	14	58.3	23	1	US-08-363-233B-24
C 27	14	58.3	23	1	US-08-363-233B-25

C 28	14	58.3	23	5	PCT-US92-05035-34
C 29	14	58.3	25	4	US-09-168-947-31
C 30	14	58.3	26	1	US-08-152-621-29
C 31	14	58.3	26	1	US-08-152-621-33
C 32	14	58.3	26	1	US-08-306-691B-1
C 33	14	58.3	26	1	US-08-306-691B-2
C 34	14	58.3	26	3	US-09-341-955-1
C 35	14	58.3	26	4	US-09-779-881-1
C 36	14	58.3	26	5	PCT-US92-05035-29
C 37	14	58.3	26	5	PCT-US92-05035-33
C 38	14	58.3	26	5	PCT-US93-07541-12
C 39	14	58.3	26	5	PCT-US93-07541-25
C 40	14	58.3	42	2	US-08-768-177-3
C 41	14	58.3	42	3	US-08-991-675A-3
C 42	14	58.3	56	1	US-07-940-652-14
C 43	14	58.3	56	1	US-07-940-652-19
C 44	14	58.3	56	1	US-08-255-553-14
C 45	14	58.3	56	1	US-08-255-553-19

ALIGNMENTS

RESULT 1  
US-09-252-991A-6328/c  
; Sequence 6328, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252.991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 6328  
; LENGTH: 306  
; TYPE: DNA  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-6328

Query Match 66.7%; Score 16; DB 4; Length 306;  
Best Local Similarity 100.0%; Pred. No. 2.4;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCGCTGAAGGGCTTCA 16  
Db 74 CCGCTGAAGGGCTTCA 59

RESULT 2  
US-09-252-991A-6056  
; Sequence 6056, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252.991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 6056  
; LENGTH: 897  
; TYPE: DNA

```
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-6056

Query Match
Best Local Similarity 66.7%; Score 16; DB 4; Length 897;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGCTGAAGGGCTTCA 16
   |||||
Db 19 CCGCTGAAGGGCTTCA 34

RESULT 3
US-09-252-991A-6218
; Sequence 6218, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 6218
; LENGTH: 1536
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-6218

Query Match
Best Local Similarity 66.7%; Score 16; DB 4; Length 1536;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGCTGAAGGGCTTCA 16
   |||||
Db 1319 CCGCTGAAGGGCTTCA 1334

RESULT 4
US-08-751-305-1
; Sequence 1, Application US/08751305
; Patent No. 5965439
; GENERAL INFORMATION:
; APPLICANT: Tenner et al., Andrea J.
; TITLE OF INVENTION: HOST DEFENSE ENHANCEMENT
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/751,305
; FILING DATE: 18-NOV-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Wetherell, Jr., John R.
; REGISTRATION NUMBER: 31,678
; REFERENCE/DOCKET NUMBER: 07306/012001
; TELEPHONE: 619/678-5070
```

```
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3460 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 149..2105
; ORIGIN:
US-08-751-305-1

Query Match
Best Local Similarity 66.7%; Score 16; DB 2; Length 3460;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGCTGAAGGGCTTCA 16
   |||||
Db 476 CCGCTGAAGGGCTTCA 491

RESULT 5
US-08-363-233B-21/c
; Sequence 21, Application US/08363233B
; Patent No. 5714383
; GENERAL INFORMATION:
; APPLICANT: Thompson, James D.
; TITLE OF INVENTION: METHOD AND REAGENT FOR TREATING CHRONIC
; TITLE OF INVENTION: MYELOGENOUS LEUKEMIA
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSEQ for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/363,233B
; FILING DATE: December 23, 1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION DATA: including application
; PRIOR APPLICATION DATA: described below: 2
; APPLICATION NUMBER: 07/882,822
; FILING DATE: May 14, 1992
; APPLICATION NUMBER: 08/193,922
; FILING DATE: February 7, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 209/165
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 23 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; ORIGIN:
US-08-363-233B-21

Query Match
Best Local Similarity 62.5%; Score 15; DB 1; Length 23;
Matches 15; Conservative 100.0%; Pred. No. 9.1;
```

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCGCTGAAGGGCTTC 15  
Db 18 CCGCTGAAGGGCTTC 4

## RESULT 6

US-08-363-233B-22/c  
; Sequence 22, Application US/08363233B  
; Patent No. 5714383

## ; GENERAL INFORMATION:

; APPLICANT: Thompson, James D.

; TITLE OF INVENTION: METHOD AND REAGENT FOR TREATING CHRONIC

; MYELOGENOUS LEUKEMIA

; NUMBER OF SEQUENCES: 39

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Lyon & Lyon

; STREET: 633 West Fifth Street

; CITY: Suite 4700

; STATE: Los Angeles

; COUNTRY: California

; ZIP: U.S.A.

; ZIP: 90071-2066

## ; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

; MEDIUM TYPE: storage

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: IBM P.C. DOS 5.0

; SOFTWARE: PastSeq for Windows 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/363.233B

; FILING DATE: December 23, 1994

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; PRIOR APPLICATION DATA: including application

; PRIOR APPLICATION DATA: described below: 2

; APPLICATION NUMBER: 07/882,822

; FILING DATE: May 14, 1992

; APPLICATION NUMBER: 08/193,922

; FILING DATE: February 7, 1994

; ATTORNEY/AGENT INFORMATION:

; NAME: Warburg, Richard J.

; REGISTRATION NUMBER: 32,327

; REFERENCE/DOCKET NUMBER: 209/165

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (213) 489-1600

; TELEFAX: (213) 955-0440

; TELEX: 67-3510

; INFORMATION FOR SEQ ID NO: 22:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 23 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

US-08-363-233B-22

## Query Match

Best Local Similarity 62.5%; Score 15; DB 1; Length 23;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCGCTGAAGGGCTTC 15  
Db 17 CCGCTGAAGGGCTTC 3

## RESULT 7

US-08-793-408-9/c

; Sequence 9, Application US/08793408

; Patent No. 6007988

## ; GENERAL INFORMATION:

; APPLICANT: Choo, Yen

; APPLICANT: Klug, Aaron

; CURRENT APPLICATION DATA:

; TITLE OF INVENTION: MYELOGENOUS LEUKEMIA

; NUMBER OF SEQUENCES: 39

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Lyon & Lyon

; STREET: 633 West Fifth Street

; CITY: Suite 4700

; STATE: Los Angeles

; COUNTRY: California

; ZIP: U.S.A.

; ZIP: 90071-2066

## ; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

; MEDIUM TYPE: storage

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: IBM P.C. DOS 5.0

; SOFTWARE: PastSeq for Windows 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/363.233B

; FILING DATE: December 23, 1994

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; PRIOR APPLICATION DATA: including application

; PRIOR APPLICATION DATA: described below: 2

; APPLICATION NUMBER: 07/882,822

; FILING DATE: May 14, 1992

; APPLICATION NUMBER: 08/193,922

; FILING DATE: February 7, 1994

; ATTORNEY/AGENT INFORMATION:

; NAME: Warburg, Richard J.

; REGISTRATION NUMBER: 32,327

; REFERENCE/DOCKET NUMBER: 209/165

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (213) 489-1600

; TELEFAX: (213) 955-0440

; TELEX: 67-3510

; INFORMATION FOR SEQ ID NO: 22:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 23 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

US-08-363-233B-22

## Query Match

Best Local Similarity 62.5%; Score 15; DB 1; Length 23;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

## RESULT 8

US-08-793-408-11/c

; Sequence 11, Application US/08793408

; Patent No. 6007988

## ; GENERAL INFORMATION:

; APPLICANT: Choo, Yen

; APPLICANT: Klug, Aaron

; CURRENT APPLICATION DATA:

; TITLE OF INVENTION: MYELOGENOUS LEUKEMIA

; NUMBER OF SEQUENCES: 39

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Lyon & Lyon

; STREET: 633 West Fifth Street

; CITY: Suite 4700

; STATE: Los Angeles

; COUNTRY: California

; ZIP: U.S.A.

; ZIP: 90071-2066

## ; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

; MEDIUM TYPE: storage

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: IBM P.C. DOS 5.0

; SOFTWARE: PastSeq for Windows 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/363.233B

; FILING DATE: December 23, 1994

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; PRIOR APPLICATION DATA: including application

; PRIOR APPLICATION DATA: described below: 2

; APPLICATION NUMBER: 07/882,822

; FILING DATE: May 14, 1992

; APPLICATION NUMBER: 08/193,922

; FILING DATE: February 7, 1994

; ATTORNEY/AGENT INFORMATION:

; NAME: Warburg, Richard J.

; REGISTRATION NUMBER: 32,327

; REFERENCE/DOCKET NUMBER: 209/165

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (213) 489-1600

; TELEFAX: (213) 955-0440

; TELEX: 67-3510

; INFORMATION FOR SEQ ID NO: 22:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 23 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

US-08-363-233B-22

## Query Match

Best Local Similarity 62.5%; Score 15; DB 1; Length 23;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

## RESULT 9

US-08-793-408-11/c

; Sequence 11, Application US/08793408

; Patent No. 6007988

## ; GENERAL INFORMATION:

; APPLICANT: Choo, Yen

; APPLICANT: Klug, Aaron

; CURRENT APPLICATION DATA:

; TITLE OF INVENTION: MYELOGENOUS LEUKEMIA

; NUMBER OF SEQUENCES: 39

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Lyon & Lyon

; STREET: 633 West Fifth Street

; CITY: Suite 4700

; STATE: Los Angeles

; COUNTRY: California

; ZIP: U.S.A.

; ZIP: 90071-2066

## ; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

; MEDIUM TYPE: storage

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: IBM P.C. DOS 5.0

; SOFTWARE: PastSeq for Windows 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/363.233B

; FILING DATE: December 23, 1994

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; PRIOR APPLICATION DATA: including application

; PRIOR APPLICATION DATA: described below: 2

; APPLICATION NUMBER: 07/882,822

; FILING DATE: May 14, 1992

; APPLICATION NUMBER: 08/193,922

; FILING DATE: February 7, 1994

; ATTORNEY/AGENT INFORMATION:

; NAME: Warburg, Richard J.

; REGISTRATION NUMBER: 32,327

; REFERENCE/DOCKET NUMBER: 209/165

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (213) 489-1600

; TELEFAX: (213) 955-0440

; TELEX: 67-3510

; INFORMATION FOR SEQ ID NO: 22:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 23 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

US-08-363-233B-22

## Query Match

Best Local Similarity 62.5%; Score 15; DB 1; Length 23;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

## RESULT 10

US-08-793-408-11/c

; Sequence 11, Application US/08793408

; Patent No. 6007988

## ; GENERAL INFORMATION:

; APPLICANT: Choo, Yen

; APPLICANT: Klug, Aaron

; CURRENT APPLICATION DATA:

; TITLE OF INVENTION: MYELOGENOUS LEUKEMIA

; NUMBER OF SEQUENCES: 39

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Lyon & Lyon

; STREET: 633 West Fifth Street

; CITY: Suite 4700

; STATE: Los Angeles

; COUNTRY: California

; ZIP: U.S.A.

; ZIP: 90071-2066

## ; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

; MEDIUM TYPE: storage

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: IBM P.C. DOS 5.0

; SOFTWARE: PastSeq for Windows 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/363.233B

; FILING DATE: December 23, 1994

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; PRIOR APPLICATION DATA: including application

; PRIOR APPLICATION DATA: described below: 2

; APPLICATION NUMBER: 07/882,822

; FILING DATE: May 14, 1992

; APPLICATION NUMBER: 08/193,922

; FILING DATE: February 7, 1994

; ATTORNEY/AGENT INFORMATION:

; NAME: Warburg, Richard J.

; REGISTRATION NUMBER: 32,327

; REFERENCE/DOCKET NUMBER: 209/165

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (213) 489-1600

; TELEFAX: (213) 955-0440

; TELEX: 67-3510

; INFORMATION FOR SEQ ID NO: 22:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 23 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

US-08-363-233B-22

## Query Match

Best Local Similarity 62.5%; Score 15; DB 1; Length 23;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

## RESULT 11

US-08-793-408-11/c

; Sequence 11, Application US/08793408

; Patent No. 6007988

## ; GENERAL INFORMATION:

; APPLICANT: Choo, Yen

; APPLICANT: Klug, Aaron

; CURRENT APPLICATION DATA:

; TITLE OF INVENTION: MYELOGENOUS LEUKEMIA

; NUMBER OF SEQUENCES: 39

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Lyon & Lyon

; STREET: 633 West Fifth Street

; CITY: Suite 4700

; STATE: Los Angeles

; COUNTRY: California

; ZIP: U.S.A.

; ZIP: 90071-2066

## ; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

; MEDIUM TYPE: storage

; COMPUTER: IBM Compatible

APPLICATION NUMBER: US/08/793,408  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/GB95/01949  
FILING DATE: 17-AUG-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9514698.1  
FILING DATE: 18-JUL-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9422534.9  
FILING DATE: 08-NOV-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9416880.4  
FILING DATE: 20-AUG-1994  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 33 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-793-408-11

Query Match 62.5%; Score 15; DB 3; Length 33;  
Best Local Similarity 100.0%; Pred. No. 9.1;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGCTGAAGGGCTTC 15  
DB 30 CCGCTGAAGGGCTTC 16

## RESULT 9

US-09-139-762A-9/c  
Sequence 9, Application US/09139762A  
Patent No. 6013453

GENERAL INFORMATION:  
APPLICANT: Choo, Yen  
APPLICANT: Klug, Aaron  
APPLICANT: Sanchez Garcia, Isidro  
TITLE OF INVENTION: Improvements in or Relating to  
TITLE OF INVENTION: Binding Proteins for Recognition of DNA  
NUMBER OF SEQUENCES: 125  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pillsbury Madison & Sutro, L.L.P.  
STREET: 1100 New York Avenue, N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20005-3918

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Word Perfect  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/139,762A  
FILING DATE:

CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/793,408  
FILING DATE: 02-JUN-1997  
APPLICATION NUMBER: PCT/GB95/01949  
FILING DATE: 17-AUG-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9514698.1  
FILING DATE: 18-JUL-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9422534.9  
FILING DATE: 08-NOV-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9416880.4  
FILING DATE: 20-AUG-1994

INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 33 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-139-762A-9

Query Match 62.5%; Score 15; DB 3; Length 33;  
Best Local Similarity 100.0%; Pred. No. 9.1;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGCTGAAGGGCTTC 15  
DB 30 CCGCTGAAGGGCTTC 16

## RESULT 10

US-09-139-762A-11/c  
Sequence 11, Application US/09139762A  
Patent No. 6013453

GENERAL INFORMATION:  
APPLICANT: Choo, Yen  
APPLICANT: Klug, Aaron  
APPLICANT: Sanchez Garcia, Isidro  
TITLE OF INVENTION: Improvements in or Relating to  
TITLE OF INVENTION: Binding Proteins for Recognition of DNA  
NUMBER OF SEQUENCES: 125  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pillsbury Madison & Sutro, L.L.P.  
STREET: 1100 New York Avenue, N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20005-3918

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Word Perfect  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/139,762A  
FILING DATE:

CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/793,408  
FILING DATE: 02-JUN-1997  
APPLICATION NUMBER: PCT/GB95/01949  
FILING DATE: 17-AUG-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9514698.1  
FILING DATE: 18-JUL-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9422534.9  
FILING DATE: 08-NOV-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9416880.4  
FILING DATE: 20-AUG-1994

INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 33 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-139-762A-11

Query Match 62.5%; Score 15; DB 3; Length 33;  
Best Local Similarity 100.0%; Pred. No. 9.1;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGCTGAAGGGCTTC 15  
DB 30 CCGCTGAAGGGCTTC 16

RESULT 11  
US-08-448-446B-12/c  
; Sequence 12, Application US/08448446B  
; Patent No. 6080851  
; GENERAL INFORMATION:  
; APPLICANT: Pachuk et al.  
; TITLE OF INVENTION: Compounds and Methods for the Treatment  
; OF INVENTION: of Leukemias  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Woodcock Washburn  
; ADDRESSEE: Kurtz Mackiewicz & No. 6080851iris  
; STREET: One Liberty Place - 46th Floor  
; CITY: Philadelphia  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19103  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE  
; COMPUTER: IBM PS/2  
; OPERATING SYSTEM: PC-DOS  
; SOFTWARE: WORDPERFECT 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/448,446B  
; FILING DATE: July 10, 1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/989,852  
; FILING DATE: December 4, 1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Doreen Yatko Trujillo  
; REGISTRATION NUMBER: 35,719  
; REFERENCE/DOCKET NUMBER: APOL-0020  
; TELECOMMUNICATION INFORMATION: C  
; TELEPHONE: (215) 568-3100  
; TELEFAX: (215) 568-3439  
; INFORMATION FOR SEQ ID NO: 12:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 47  
; TYPE: Nucleic Acid  
; STRANDEDNESS: Single  
; TOPOLOGY: Linear  
; ANTI-SENSE:  
; US-08-448-446B-12  
Query Match 62.5%; Score 15; DB 3; Length 47;  
Best Local Similarity 100.0%; Pred. No. 9.1;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 CCGCTGAAGGCTTC 15  
Db 30 CCGCTGAAGGCTTC 16  
RESULT 12  
US-08-448-446B-1/c  
; Sequence 1, Application US/08448446B  
; Patent No. 6080851  
; GENERAL INFORMATION:  
; APPLICANT: Pachuk et al.  
; TITLE OF INVENTION: Compounds and Methods for the Treatment  
; OF INVENTION: of Leukemias  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Woodcock Washburn  
; ADDRESSEE: Kurtz Mackiewicz & No. 6080851iris  
; STREET: One Liberty Place - 46th Floor  
; CITY: Philadelphia  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19103

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE  
; COMPUTER: IBM PS/2  
; OPERATING SYSTEM: PC-DOS  
; SOFTWARE: WORDPERFECT 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/448,446B  
; FILING DATE: July 10, 1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/989,852  
; FILING DATE: December 4, 1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Doreen Yatko Trujillo  
; REGISTRATION NUMBER: 35,719  
; REFERENCE/DOCKET NUMBER: APOL-0020  
; TELECOMMUNICATION INFORMATION: C  
; TELEPHONE: (215) 568-3100  
; TELEFAX: (215) 568-3439  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 62  
; TYPE: Nucleic Acid  
; STRANDEDNESS: Single  
; TOPOLOGY: Linear  
; ANTI-SENSE: No  
; US-08-448-446B-1  
Query Match 62.5%; Score 15; DB 3; Length 62;  
Best Local Similarity 100.0%; Pred. No. 9;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 CCGCTGAAGGCTTC 15  
Db 45 CCGCTGAAGGCTTC 31  
RESULT 13  
US-08-152-621-7/c  
; Sequence 7, Application US/08152621  
; Patent No. 5652222  
; GENERAL INFORMATION:  
; APPLICANT: Calabretta, Bruno  
; APPLICANT: Gewirtz, Alan M.  
; TITLE OF INVENTION: Selective Inhibition of  
; OF INVENTION: Leukemic Cell Proliferation by bcr-abl  
; TITLE OF INVENTION: Antisense Oligonucleotides  
; NUMBER OF SEQUENCES: 34  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SEIDEL, GONDA, LAVORGNA  
; ADDRESSEE: & MONACO, P.C.  
; STREET: 1800 Two Penn Center  
; CITY: Philadelphia  
; STATE: Pennsylvania  
; COUNTRY: U.S.A.  
; ZIP: 19102  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.50 inch, 720 KB  
; COMPUTER: IBM PS/2  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: Wordperfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/152,621  
; FILING DATE: No. 5652222ember 15, 1993  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/718,302  
; FILING DATE: June 18, 1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Monaco, Daniel A.  
; REGISTRATION NUMBER: 30,480  
; REFERENCE/DOCKET NUMBER: 6056-120 (CT.) 1  
; TELECOMMUNICATION INFORMATION:

TELEPHONE: (215) 568-8383  
TELEFAX: (215) 568-5549  
TELEX: No. 565222e  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 80 Nucleotides  
TYPE: nucleic acid  
STRANDEDNESS: single stranded  
TOPOLOGY: linear  
US-08-152-621-7

Query Match 62.5%; Score 15; DB 1; Length 80;  
Best Local Similarity 100.0%; Pred. No. 9;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGCTGAAGGGCTTC 15  
DB 45 CCGCTGAAGGGCTTC 31

RESULT 14  
US-08-306-691B-38/c  
Sequence 38, Application US/08306691B  
GENERAL INFORMATION:  
APPLICANT: Calabretta, Bruno  
APPLICANT: Skorski, Tomasz  
TITLE OF INVENTION: ANTISENSE  
TITLE OF INVENTION: ANTISENSE  
NUMBER OF SEQUENCES: 55  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Seidel, Gonda, Lavorigna & Monaco, P.C.  
STREET: Two Penn Center, Suite 1800  
CITY: Philadelphia  
STATE: Pennsylvania  
COUNTRY: U.S.A.  
ZIP: 19102

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb  
COMPUTER: IBM PS/2  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: WordPerfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/306,691B  
FILING DATE: September 15, 1994  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Monaco, Daniel A.  
REGISTRATION NUMBER: 30,480  
REFERENCE/DOCKET NUMBER: 8321-8  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (215) 568-8383  
TELEFAX: (215) 568-5549  
TELEX: No. 5734039e  
INFORMATION FOR SEQ ID NO: 38:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 80 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-306-691B-38

Query Match 62.5%; Score 15; DB 1; Length 80;  
Best Local Similarity 100.0%; Pred. No. 9;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGCTGAAGGGCTTC 15  
DB 45 CCGCTGAAGGGCTTC 31

RESULT 15  
PCT-US92-05035-7/c  
Sequence 7, Application PC/TUS9205035  
GENERAL INFORMATION:  
APPLICANT: Calabretta, Bruno  
APPLICANT: Gewirtz, Alan M.  
TITLE OF INVENTION: Selective Inhibition of  
TITLE OF INVENTION: Leukemic Cell Proliferation by bcr-abl  
TITLE OF INVENTION: Antisense Oligonucleotides  
NUMBER OF SEQUENCES: 34  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Temple University - Of The Common-  
ADDRESSEE: wealth System of Higher Education  
STREET: 406 University Services Building  
CITY: Philadelphia  
STATE: Pennsylvania  
COUNTRY: U.S.A.  
ZIP: 19122  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb  
COMPUTER: IBM PS/2  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: WordPerfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US92/05035  
FILING DATE: 19920615  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/718,302  
FILING DATE: June 18, 1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/869,911  
FILING DATE: April 14, 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Monaco, Daniel A.  
REGISTRATION NUMBER: 30,480  
REFERENCE/DOCKET NUMBER: 6056-120 (CIP) 1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (215) 568-8383  
TELEFAX: (215) 568-5549  
TELEX: None  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 80 Nucleotides  
TYPE: NUCLEIC ACID  
STRANDEDNESS: single stranded  
TOPOLOGY: linear  
PCT-US92-05035-7

Query Match 62.5%; Score 15; DB 5; Length 80;  
Best Local Similarity 100.0%; Pred. No. 9;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGCTGAAGGGCTTC 15  
DB 45 CCGCTGAAGGGCTTC 31

Search completed: May 27, 2004, 02:25:15  
Job time : 20.2274 secs



GenCore version 5.1.6.  
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OM nucleic - nucleic search, using sw model

Run on: May 27, 2004, 11:30:47 ; Search time 126.301 Seconds  
(without alignments)  
864.392 Million cell updates/sec

Title: US-09-121-239-18

Perfect score: 24

Sequence: 1 CCGTGAAGGCTTCATGTTCCAC 24

Scoring table: OLIGO NUC

Gapop 60.0 , Gapext 60.0

Searched: 2960401 seqs, 2274450654 residues

Word size : 0

Total number of hits satisfying chosen parameters: 5920802

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published Applications NA.\*

- 1: /cgn2\_6/ptodata/2/pubpna/US07\_PUBCOMB.seq.\*
- 2: /cgn2\_6/ptodata/2/pubpna/PCT\_NEW\_PUB.seq.\*
- 3: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq.\*
- 4: /cgn2\_6/ptodata/2/pubpna/US06\_PUBCOMB.seq.\*
- 5: /cgn2\_6/ptodata/2/pubpna/US07\_NEW\_PUB.seq.\*
- 6: /cgn2\_6/ptodata/2/pubpna/PCTUS\_PUBCOMB.seq.\*
- 7: /cgn2\_6/ptodata/2/pubpna/US08\_NEW\_PUB.seq.\*
- 8: /cgn2\_6/ptodata/2/pubpna/US08\_PUBCOMB.seq.\*
- 9: /cgn2\_6/ptodata/2/pubpna/US09A\_PUBCOMB.seq.\*
- 10: /cgn2\_6/ptodata/2/pubpna/US09B\_PUBCOMB.seq.\*
- 11: /cgn2\_6/ptodata/2/pubpna/US09C\_PUBCOMB.seq.\*
- 12: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq.\*
- 13: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq2.\*
- 14: /cgn2\_6/ptodata/2/pubpna/US10A\_PUBCOMB.seq.\*
- 15: /cgn2\_6/ptodata/2/pubpna/US10B\_PUBCOMB.seq.\*
- 16: /cgn2\_6/ptodata/2/pubpna/US10C\_PUBCOMB.seq.\*
- 17: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq.\*
- 18: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq.\*
- 19: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Query	DB	ID	Description
C 1	24	100.0	3450	16	US-10-457-954-5	Sequence 5, Appli
C 2	18	75.0	34125	9	US-09-782-378A-25	Sequence 25, Appli
C 3	16	66.7	65	10	US-09-908-975-27688	Sequence 27688, A
C 4	16	66.7	310	15	US-10-029-386-26614	Sequence 26614, A
C 5	16	66.7	555	15	US-10-029-386-12914	Sequence 12914, A
C 6	16	66.7	1044	9	US-09-815-242-7861	Sequence 7861, Ap
C 7	16	66.7	1044	13	US-10-282-122A-30374	Sequence 30374, A
C 8	16	66.7	1424	13	US-10-425-114-523	Sequence 523, App
C 9	16	66.7	1951	15	US-10-029-386-22997	Sequence 22997, A
C 10	16	66.7	6699	13	US-10-211-462-130	Sequence 130, App
C 11	16	66.7	6699	15	US-10-021-660-15	Sequence 15, Appl
C 12	16	66.7	85076	16	US-10-085-117-97	Sequence 97, Appl
C 13	16	66.7	126413	13	US-10-087-192-1831	Sequence 1831, Ap
C 14	15	62.5	24	13	US-10-382-634-21	Sequence 21, Appl

C	15	62.5	24	15	US-10-349-320-20	Sequence 20, Appl
	16	62.5	205	9	US-09-867-701-10433	Sequence 10433, A
	17	62.5	436	9	US-09-960-352-5213	Sequence 5213, Ap
	18	62.5	489	13	US-10-424-599-43483	Sequence 43483, A
C	19	62.5	491	13	US-10-424-599-7082	Sequence 7082, Ap
	20	62.5	499	13	US-10-027-632-85551	Sequence 85551, A
	21	62.5	499	16	US-10-027-632-85551	Sequence 85551, A
	22	62.5	729	13	US-10-107-431-100	Sequence 100, App
C	23	62.5	773	13	US-10-027-632-133705	Sequence 133705, A
C	24	62.5	773	16	US-10-027-632-133705	Sequence 133705, A
	25	62.5	1133	13	US-10-425-114-4855	Sequence 4855, Ap
	26	62.5	1163	13	US-10-027-632-118039	Sequence 118039, A
	27	62.5	1163	13	US-10-027-632-118040	Sequence 118040, A
	28	62.5	1163	16	US-10-027-632-118039	Sequence 118039, A
	29	62.5	1163	16	US-10-027-632-118040	Sequence 118040, A
C	30	62.5	1590	16	US-10-369-493-27261	Sequence 27261, A
	31	62.5	1749	13	US-10-282-122A-25460	Sequence 25460, A
C	32	62.5	1765	13	US-10-424-599-103532	Sequence 103532, A
	33	62.5	1806	9	US-09-815-242-4015	Sequence 4015, Ap
	34	62.5	1806	13	US-10-282-122A-7373	Sequence 7373, Ap
	35	62.5	2482	13	US-10-363-480-1	Sequence 49, Appli
C	36	62.5	3393	15	US-10-263-480-1	Sequence 1, Appli
	37	62.5	3606	16	US-10-214-529-6	Sequence 6, Appli
C	38	62.5	3840	15	US-10-204-041-3	Sequence 3, Appli
	39	62.5	5527	9	US-09-880-107-3710	Sequence 3710, Ap
C	40	62.5	5744	16	US-10-439-703-5	Sequence 5, Appli
	41	62.5	38734	10	US-09-373-658-30	Sequence 30, Appli
	42	62.5	38734	11	US-09-989-687-30	Sequence 30, Appli
	43	62.5	45055	13	US-10-107-431-277	Sequence 277, App
C	44	62.5	84539	9	US-09-962-436-36	Sequence 36, Appli
	45	62.5	212231	13	US-10-087-192-1126	Sequence 1126, Ap

ALIGNMENTS

RESULT 1  
US-10-457-954-5/c  
; Sequence 5, Application US/10457954  
; Publication No. US20040005623A1  
; GENERAL INFORMATION:  
; APPLICANT: Longley, B. Jack  
; TITLE OF INVENTION: Method of determining tumor sensitivities to therapeutic drugs  
; FILE REFERENCE: 960296.98890  
; CURRENT APPLICATION NUMBER: US/10/457,954  
; CURRENT FILING DATE: 2003-06-10  
; PRIOR APPLICATION NUMBER: 60/387,370  
; PRIOR FILING DATE: 2002-06-10  
; PRIOR APPLICATION NUMBER: 60/387,406  
; PRIOR FILING DATE: 2002-06-10  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 5  
; LENGTH: 3450  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(3447)  
; FEATURE:  
; NAME/KEY: misc\_structure  
; LOCATION: (730)..(765)  
; OTHER INFORMATION: encode amino acids 244-255 for forming the sides of the enzymatic  
; OTHER INFORMATION: pocket  
; FEATURE:  
; NAME/KEY: misc\_structure  
; LOCATION: (931)..(1077)  
; OTHER INFORMATION: encode amino acids 311-359 for forming the sides of the enzymatic  
; OTHER INFORMATION: pocket  
; FEATURE:  
; NAME/KEY: misc\_structure  
; LOCATION: (1141)..(1206)  
; OTHER INFORMATION: encode amino acids 381-402 for forming the enzymatic pocket's

OTHER INFORMATION: activation loop  
US-10-457-954-5

Query Match 100.0%; Score 24; DB 16; Length 3450;  
Best Local Similarity 100.0%; Pred. No. 0.00011;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGCTGAAGGCTTCATGTTCCAC 24  
DB 150 CCGCTGAAGGCTTCATGTTCCAC 127

RESULT 2

US-09-782-378A-25  
Sequence 25 Application US/09782378A  
Patent No. US20020102731A1  
GENERAL INFORMATION:  
APPLICANT: Hearing, Patrick  
APPLICANT: Bahou, Wadie  
APPLICANT: Sandalon, Ziv  
APPLICANT: Gnatenko, Dmitri  
TITLE OF INVENTION: Adenoviral Vectors  
FILE REFERENCE: STONYB-04970  
CURRENT APPLICATION NUMBER: US/09/782,378A  
CURRENT FILING DATE: 2001-02-12  
PRIOR APPLICATION NUMBER: 60/237,747  
PRIOR FILING DATE: 2000-10-02  
NUMBER OF SEQ ID NOS: 27  
SOFTWARE: Patentin version 3.0  
SEQ ID NO 25  
LENGTH: 34125  
TYPE: DNA  
ORGANISM: Human adenovirus type 12  
US-09-782-378A-25

Query Match 75.0%; Score 18; DB 9; Length 34125;  
Best Local Similarity 100.0%; Pred. No. 0.41;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TGAAGGCTTCATGTTCC 22  
DB 3998 TGAAGGCTTCATGTTCC 4015

RESULT 3

US-09-908-975-27688/c  
Sequence 27688 Application US/09908975  
Publication No. US20030165843A1  
GENERAL INFORMATION:  
APPLICANT: SHOSHAN, Avi  
APPLICANT: WASSERMAN, Alon  
APPLICANT: MINTZ, Eli  
APPLICANT: MINTZ, Liat  
TITLE OF INVENTION: FAIGLER, Samchon  
TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICE  
FILE REFERENCE: 36688-0005  
CURRENT APPLICATION NUMBER: US/09/908,975  
CURRENT FILING DATE: 2001-07-20  
PRIOR APPLICATION NUMBER: US 60/287,724  
PRIOR FILING DATE: 2001-05-02  
PRIOR APPLICATION NUMBER: US 60/221,607  
PRIOR FILING DATE: 2000-07-28  
NUMBER OF SEQ ID NOS: 32337  
SOFTWARE: Patentin version 3.0  
SEQ ID NO 27688  
LENGTH: 65  
TYPE: DNA  
ORGANISM: Mus musculus  
US-09-908-975-27688

Query Match 66.7%; Score 16; DB 10; Length 65;  
Best Local Similarity 100.0%; Pred. No. 7.9;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GGGCTTCATGTTCCAC 24  
DB 22 GGGCTTCATGTTCCAC 7

RESULT 4

US-10-029-386-26614/c  
Sequence 26614 Application US/10029386  
Publication No. US20030194704A1  
GENERAL INFORMATION:  
APPLICANT: Penn, Sharron G.  
APPLICANT: Rank, David R.  
APPLICANT: Hanzel, David K.  
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G  
TITLE OF INVENTION: EXPRESSION ANALYSIS TWO  
FILE REFERENCE: AEOMICA-X-2  
CURRENT APPLICATION NUMBER: US/10/029,386  
CURRENT FILING DATE: 2001-12-20  
NUMBER OF SEQ ID NOS: 34288  
SOFTWARE: Anomax Sequence Listing Engine vers. 1.1  
SEQ ID NO 26614  
LENGTH: 310  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: MAP TO CHR20.3  
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.2  
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 3.5  
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.5  
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.9  
OTHER INFORMATION: SWISSPROT HIT: P07204, EVALUE 2.00e-08  
OTHER INFORMATION: NT HIT: g112742414, EVALUE 0.00e+00  
OTHER INFORMATION: EST\_HUMAN HIT: B1907890.1, EVALUE 0.00e+00  
US-10-029-386-26614

Query Match 66.7%; Score 16; DB 15; Length 310;  
Best Local Similarity 100.0%; Pred. No. 7.5;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGCTGAAGGCTTCA 16  
DB 62 CCGCTGAAGGCTTCA 47

RESULT 5

US-10-029-386-12914/c  
Sequence 12914 Application US/10029386  
Publication No. US20030194704A1  
GENERAL INFORMATION:  
APPLICANT: Penn, Sharron G.  
APPLICANT: Rank, David R.  
APPLICANT: Hanzel, David K.  
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G  
TITLE OF INVENTION: EXPRESSION ANALYSIS TWO  
FILE REFERENCE: AEOMICA-X-2  
CURRENT APPLICATION NUMBER: US/10/029,386  
CURRENT FILING DATE: 2001-12-20  
NUMBER OF SEQ ID NOS: 34288  
SOFTWARE: Anomax Sequence Listing Engine vers. 1.1  
SEQ ID NO 12914  
LENGTH: 555  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: MAP TO CHR20.3  
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.2  
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 3.5  
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.5  
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.9  
OTHER INFORMATION: SWISSPROT HIT: P07204, EVALUE 4.00e-08  
OTHER INFORMATION: NT HIT: g112742414, EVALUE 0.00e+00

OTHER INFORMATION: EST\_HUMAN HIT: B1907890.1, EVALUATE 0.00e+00  
US-10-029-386-12914

Query Match 66.7%; Score 16; DB 15; Length 555;  
Best Local Similarity 100.0%; Pred. No. 7.3; Indels 0; Gaps 0;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGCTGAAGGGCTTCA 16  
DB 90 CCGCTGAAGGGCTTCA 75

## RESULT 6

US-09-815-242-7861/c  
Sequence 7861, Application US/09815242  
Patent No. US20020061569A1

## GENERAL INFORMATION:

APPLICANT: Haselbeck, Robert  
APPLICANT: Ohlsen, Kari L.  
APPLICANT: Zyskind, Judith W.  
APPLICANT: Wall, Daniel  
APPLICANT: Trawick, John D.  
APPLICANT: Carr, Grant J.  
APPLICANT: Yamamoto, Robert T.  
APPLICANT: Xu, H. Howard

TITLE OF INVENTION: Identification of Essential Genes in

TITLE OF INVENTION: Prokaryotes

FILE REFERENCE: ELITRA.011A

CURRENT APPLICATION NUMBER: US/09/815,242

CURRENT FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR FILING DATE: 2000-03-21

PRIOR APPLICATION NUMBER: 60/206,848

PRIOR FILING DATE: 2000-05-23

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: 60/242,578

PRIOR FILING DATE: 2000-10-23

PRIOR APPLICATION NUMBER: 60/253,625

PRIOR FILING DATE: 2000-11-27

PRIOR APPLICATION NUMBER: 60/257,931

PRIOR FILING DATE: 2000-12-22

PRIOR APPLICATION NUMBER: 60/269,308

PRIOR FILING DATE: 2001-02-16

NUMBER OF SEQ ID NOS: 14110

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 7861

LENGTH: 1044

TYPE: DNA

ORGANISM: Pseudomonas aeruginosa

FEATURE:

NAME/KEY: CDS

LOCATION: (1)...(1044)

US-09-815-242-7861

Query Match 66.7%; Score 16; DB 9; Length 1044;  
Best Local Similarity 100.0%; Pred. No. 7.2;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGCTGAAGGGCTTCA 16  
DB 812 CCGCTGAAGGGCTTCA 797

## RESULT 7

US-10-282-122A-30374/c

Sequence 30374, Application US/10282122A

Publication No. US20040029129A1

## GENERAL INFORMATION:

APPLICANT: Wang, Liangsu

APPLICANT: Zamudio, Carlos

APPLICANT: Malone, Cheryl

APPLICANT: Haselbeck, Robert

APPLICANT: Ohlsen, Kari  
APPLICANT: Zyskind, Judith  
APPLICANT: Wall, Daniel  
APPLICANT: Trawick, John  
APPLICANT: Carr, Grant  
APPLICANT: Yamamoto, Robert  
APPLICANT: Forsyth, R.  
APPLICANT: Xu, H.

TITLE OF INVENTION: Identification of Essential Genes in Microorganisms

FILE REFERENCE: ELITRA.034A

CURRENT APPLICATION NUMBER: US/10/282,122A

CURRENT FILING DATE: 2003-02-20

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR FILING DATE: 2000-03-21

PRIOR APPLICATION NUMBER: 60/206,848

PRIOR FILING DATE: 2000-05-23

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: 60/230,335

PRIOR FILING DATE: 2000-09-06

PRIOR APPLICATION NUMBER: 60/230,347

PRIOR FILING DATE: 2000-09-09

PRIOR APPLICATION NUMBER: 60/242,578

PRIOR FILING DATE: 2000-10-23

PRIOR APPLICATION NUMBER: 60/253,625

PRIOR FILING DATE: 2000-11-27

PRIOR APPLICATION NUMBER: 60/257,931

PRIOR FILING DATE: 2000-12-22

PRIOR APPLICATION NUMBER: 60/267,636

PRIOR FILING DATE: 2001-02-09

PRIOR APPLICATION NUMBER: 60/269,308

PRIOR FILING DATE: 2001-02-16

Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 78614

SOFTWARE: PatentIn version 3.1

SEQ ID NO 30374

LENGTH: 1044

TYPE: DNA

ORGANISM: Pseudomonas aeruginosa

US-10-282-122A-30374

Query Match 66.7%; Score 16; DB 13; Length 1044;  
Best Local Similarity 100.0%; Pred. No. 7.2;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGCTGAAGGGCTTCA 16  
DB 812 CCGCTGAAGGGCTTCA 797

## RESULT 8

US-10-425-114-523/c

Sequence 523, Application US/10425114

Publication No. US20040034888A1

## GENERAL INFORMATION:

APPLICANT: Liu, Jingdong

APPLICANT: Zhou, Yihua

APPLICANT: Kovalic, David K.

APPLICANT: Screen, Steven E.

APPLICANT: Tabaska, Jack E.

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

FILE REFERENCE: 38-21(5313)B

CURRENT APPLICATION NUMBER: US/10/425,114

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 73128

SEQ ID NO 523

LENGTH: 1424

TYPE: DNA

ORGANISM: Zea mays

FEATURE:

OTHER INFORMATION: Clone ID: 700076886\_FLI

US-10-425-114-523

Query Match 66.7%; Score 16; DB 13; Length 1424;  
Best Local Similarity 100.0%; Pred. No. 7.1;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 AAGGGCTTCATGTTCC 22  
|||||  
Db 481 AAGGGCTTCATGTTCC 466

RESULT 9

US-10-029-386-22997  
; Sequence 22997, Application US/10029386  
; Publication No. US20030194704A1  
; GENERAL INFORMATION:  
; APPLICANT: Penn, Sharon G.  
; APPLICANT: Rank, David R.  
; TITLE OF INVENTION: HANZEL, David K.  
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR C  
; FILE REFERENCE: AEOMICA-X-2  
; CURRENT APPLICATION NUMBER: US/10/029,386  
; CURRENT FILING DATE: 2001-12-20  
; NUMBER OF SEQ ID NOS: 34288  
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1  
; SEQ ID NO 22997  
; LENGTH: 1951  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: MAP TO AL118508.6  
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.4  
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.83  
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.3  
; OTHER INFORMATION: SWISSPROT HIT: O73775, EVALUE 1.00e-39  
; OTHER INFORMATION: NT HIT: g112742414, EVALUE 0.00e+00  
; OTHER INFORMATION: EST\_HUMAN HIT: B1907890.1, EVALUE 0.00e+00  
US-10-029-386-22997

Query Match 66.7%; Score 16; DB 15; Length 1951;  
Best Local Similarity 100.0%; Pred. No. 7;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGCTGAAGGGCTTCA 16  
|||||  
Db 328 CCGCTGAAGGGCTTCA 343

RESULT 10

US-10-211-462-130  
; Sequence 130, Application US/10211462  
; Publication No. US20040033495A1  
; GENERAL INFORMATION:  
; APPLICANT: Murray, Richard  
; APPLICANT: Glynn, Richard  
; APPLICANT: Watson, Susan R.  
; APPLICANT: Aziz, Natasha  
; APPLICANT: Eos Biotechnology, Inc.  
; TITLE OF INVENTION: Methods of Diagnosis of Angiogenesis, Compositions and  
; FILE REFERENCE: 018501-006200US  
; CURRENT APPLICATION NUMBER: US/10/211,462  
; CURRENT FILING DATE: 2003-02-13  
; PRIOR APPLICATION NUMBER: US 09/784,356  
; PRIOR FILING DATE: 2001-02-14  
; PRIOR APPLICATION NUMBER: US 09/791,390  
; PRIOR FILING DATE: 2001-02-22  
; PRIOR APPLICATION NUMBER: US 60/310,025  
; PRIOR FILING DATE: 2001-08-03  
; PRIOR APPLICATION NUMBER: US 60/334,244  
; PRIOR FILING DATE: 2001-11-29  
; NUMBER OF SEQ ID NOS: 230

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 130

; LENGTH: 6699

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-211-462-130

Query Match 66.7%; Score 16; DB 13; Length 6699;  
Best Local Similarity 100.0%; Pred. No. 6.7;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGCTGAAGGGCTTCA 16  
|||||  
Db 476 CCGCTGAAGGGCTTCA 491

RESULT 11

US-10-021-660-15  
; Sequence 15, Application US/10021660  
; Publication No. US20030152926A1  
; GENERAL INFORMATION:  
; APPLICANT: Murray, Richard  
; APPLICANT: Glynn, Richard  
; APPLICANT: Watson, Susan R.  
; APPLICANT: Eos Biotechnology, Inc.  
; TITLE OF INVENTION: No. US20030152926A1 Methods of Diagnosis of Angiogenesis,  
; TITLE OF INVENTION: Compositions and Methods of Screening for Angiogenesis  
; TITLE OF INVENTION: Modulators  
; FILE REFERENCE: 018501-000710US  
; CURRENT APPLICATION NUMBER: US/10/021,660  
; CURRENT FILING DATE: 2001-12-06  
; PRIOR APPLICATION NUMBER: US/09/784,356  
; PRIOR FILING DATE: 2001-02-14  
; PRIOR APPLICATION NUMBER: US 09/637,977  
; PRIOR FILING DATE: 2000-08-11  
; NUMBER OF SEQ ID NOS: 135  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 15  
; LENGTH: 6699  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-021-660-15

Query Match 66.7%; Score 16; DB 15; Length 6699;  
Best Local Similarity 100.0%; Pred. No. 6.7;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGCTGAAGGGCTTCA 16  
|||||  
Db 476 CCGCTGAAGGGCTTCA 491

RESULT 12

US-10-085-117-97/c  
; Sequence 97, Application US/10085117  
; Publication No. US2003023334A1  
; GENERAL INFORMATION:  
; APPLICANT: Morris, David W.  
; APPLICANT: Engelhard, Eric K.  
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER  
; FILE REFERENCE: 529452000121  
; CURRENT APPLICATION NUMBER: US/10/085,117  
; CURRENT FILING DATE: 2002-02-27  
; PRIOR APPLICATION NUMBER: US 09/798,586  
; PRIOR FILING DATE: 2001-03-02  
; NUMBER OF SEQ ID NOS: 361  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 97  
; LENGTH: 85076  
; TYPE: DNA  
; ORGANISM: Mus musculus  
; FEATURE:  
; NAME/KEY: variation

; LOCATION: (1)...(85076)  
; OTHER INFORMATION: n = any nucleotide  
US-10-085-117-97

Query Match 66.7%; Score 16; DB 16; Length 85076;  
Best Local Similarity 100.0%; Pred. No. 6.2; 0; Indels 0; Gaps 0;  
Matches 16; Conservative 0; Mismatches 0;

Qy 3 GCTGAAGGGCTTCATG 18

Db 30797 GCTGAAGGGCTTCATG 30782

## RESULT 13

US-10-087-192-1831

; Sequence 1831, Application US/10087192

; Publication No. US20020182586A1

; GENERAL INFORMATION:

; APPLICANT: Morris, David W.

; APPLICANT: Engelhard, Eric K.

; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR

; FILE REFERENCE: 529452000122

; CURRENT APPLICATION NUMBER: US/10/087,192

; CURRENT FILING DATE: 2002-03-01

; PRIOR APPLICATION NUMBER: US 09/747,377

; PRIOR FILING DATE: 2000-12-22

; PRIOR APPLICATION NUMBER: US 09/798,586

; PRIOR FILING DATE: 2001-03-02

; NUMBER OF SEQ ID NOS: 2059

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 1831

; LENGTH: 126413

; TYPE: DNA

; ORGANISM: Mus musculus

; FEATURE:

; NAME/KEY: misc\_feature

; LOCATION: (1)...(126413)

; OTHER INFORMATION: n = A,T,C or G

US-10-087-192-1831

Query Match

Best Local Similarity 66.7%; Score 16; DB 13; Length 126413;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 GGGCTTCATGTTCCAC 24

Db 101481 GGGCTTCATGTTCCAC 101496

## RESULT 14

US-10-382-634-21/c

; Sequence 21, Application US/10382634

; Publication No. US20040038921A1

; GENERAL INFORMATION:

; APPLICANT: Kreutzer, Roalnd

; TITLE OF INVENTION: Composition and Method for Inhibiting Expression of a Target Gene

; FILE REFERENCE: 20200/2062

; CURRENT APPLICATION NUMBER: US/10/382,634

; CURRENT FILING DATE: 2003-03-07

; PRIOR APPLICATION NUMBER: DE 101 55 280.7

; PRIOR FILING DATE: 2001-10-26

; PRIOR APPLICATION NUMBER: DE 101 58 411.3

; PRIOR FILING DATE: 2001-11-29

; PRIOR APPLICATION NUMBER: DE 101 60 151.4

; PRIOR FILING DATE: 2001-12-07

; PRIOR APPLICATION NUMBER: DE 102 30 996.5

; PRIOR FILING DATE: 2002-07-09

; PRIOR APPLICATION NUMBER: PCT/EP02/00152

; PRIOR FILING DATE: 2002-01-09

; PRIOR APPLICATION NUMBER: PCT/EP02/00151

; PRIOR FILING DATE: 2002-01-09

; PRIOR APPLICATION NUMBER: PCT/EP02/11971

; PRIOR FILING DATE: 2002-10-25  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 21

; LENGTH: 24

; TYPE: DNA

; ORGANISM: artificial sequence

; FEATURE:

; OTHER INFORMATION: PRIMER

US-10-382-634-21

Query Match 62.5%; Score 15; DB 13; Length 24;

Best Local Similarity 100.0%; Pred. No. 32;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCGCTGAAGGGCTTC 15

Db 23 CCGCTGAAGGGCTTC 9

## RESULT 15

US-10-349-320-20/c

; Sequence 20, Application US/10349320

; Publication No. US20030190654A1

; GENERAL INFORMATION:

; APPLICANT: Heidenreich, Olaf

; TITLE OF INVENTION: DOUBLE-STRANDED RNA (dsRNA) AND METHOD OF USE

; FILE REFERENCE: 20200/2112

; CURRENT APPLICATION NUMBER: US/10/349,320

; CURRENT FILING DATE: 2003-01-22

; PRIOR APPLICATION NUMBER: DE 102 02 419.7

; PRIOR FILING DATE: 2002-01-22

; NUMBER OF SEQ ID NOS: 20

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 20

; LENGTH: 24

; TYPE: DNA

; ORGANISM: Artificial sequence

; FEATURE:

; OTHER INFORMATION: Tagman probe

US-10-349-320-20

Query Match

Best Local Similarity 62.5%; Score 15; DB 15; Length 24;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCGCTGAAGGGCTTC 15

Db 23 CCGCTGAAGGGCTTC 9

Search completed: May 27, 2004, 14:58:31

Job time : 126.301 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 26, 2004, 15:22:41 ; Search time 847.385 Seconds

(without alignments)  
845.770 Million cell updates/sec

Title: US-09-121-239-18

Perfect score: 24

Sequence: 1 CCGCTGAAGGCTTCATGTTCCAC 24

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 27513289 seqs, 14931090276 residues

Word size : 0

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

EST:\*

1: em\_estba:\*

2: em\_esthum:\*

3: em\_estin:\*

4: em\_estmu:\*

5: em\_estov:\*

6: em\_estpl:\*

7: em\_estro:\*

8: em\_htc:\*

9: gb\_est1:\*

10: gb\_est2:\*

11: gb\_htc:\*

12: gb\_est3:\*

13: gb\_est4:\*

14: gb\_est5:\*

15: em\_estfun:\*

16: em\_estom:\*

17: em\_gss\_hum:\*

18: em\_gss\_inv:\*

19: em\_gss\_pln:\*

20: em\_gss\_fun:\*

21: em\_gss\_fun:\*

22: em\_gss\_nam:\*

23: em\_gss\_mus:\*

24: em\_gss\_pro:\*

25: em\_gss\_rod:\*

26: em\_gss\_phg:\*

27: em\_gss\_vrl:\*

28: gb\_gss1:\*

29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	24	100.0	404	14	H81820	H81820 Ys68e09.r1
C 2	24	100.0	421	12	BM832613	BM832613 K-EST0107
C 3	24	100.0	544	9	AL707819	AL707819 DKF26686L
4	24	100.0	781	13	BX097261	BX097261 BX097261

5	18	75.0	525	14	CD848190	CD848190 DH0AC002Z
c 6	18	75.0	546	13	BU019091	BU019091 QHE20D24.
7	18	75.0	573	13	BY243155	BY243155 BY243155
c 8	18	75.0	1110	12	BM917206	BM917206 AGENCOURT
9	17	70.8	303	14	CD588643	CD588643 RK047A3H0
10	17	70.8	317	14	CD585274	CD585274 RK030A2C0
11	17	70.8	323	14	CD591703	CD591703 RK050A4G0
12	17	70.8	324	14	CD601328	CD601328 RK132A1C1
13	17	70.8	330	14	CD601373	CD601373 RK132A2C1
14	17	70.8	330	14	CD602150	CD602150 RK140A2F0
15	17	70.8	496	14	CD603852	CD603852 RZ150A3E0
16	17	70.8	500	14	CD585675	CD585675 RK032A1F0
c 17	17	70.8	514	12	BJ063595	BJ063595 BJ063595
18	17	70.8	705	13	BQ617441	BQ617441 fab04C07.
c 19	17	70.8	925	10	BQ120890	BQ120890 601757493
c 20	16	66.7	157	10	AW386252	AW386252 CM4-PT001
c 21	16	66.7	191	10	AW420212	AW420212 fj88g07.Y
c 22	16	66.7	235	9	AI035445	AI035445 ub47a08.X
c 23	16	66.7	256	9	AA881130	AA881130 VZ06905.X
c 24	16	66.7	281	12	BG985652	BG985652 ba02a03.u
25	16	66.7	288	10	BB009502	BB009502 BB009502
26	16	66.7	322	14	CD166258	CD166258 MM1-0002P
c 27	16	66.7	324	10	BB838010	BB838010 BB838010
28	16	66.7	325	10	BF148232	BF148232 UX45F03.X
29	16	66.7	335	10	BF318395	BF318395 UX11E01.X
30	16	66.7	339	12	BM211354	BM211354 C0804F12-
c 31	16	66.7	342	13	BY139003	BY139003 BY139003
c 32	16	66.7	344	10	BB869806	BB869806 BB869806
c 33	16	66.7	347	12	BM211586	BM211586 C0808G06-
c 34	16	66.7	348	13	BY175856	BY175856 BY175856
c 35	16	66.7	354	13	BY310701	BY310701 BY310701
c 36	16	66.7	356	9	AA268399	AA268399 va41h09.r
c 37	16	66.7	359	13	BY020770	BY020770 BY020770
c 38	16	66.7	361	28	AQ037986	AQ037986 CIT-HSP-2
c 39	16	66.7	362	28	AQ040284	AQ040284 CIT-HSP-2
c 40	16	66.7	363	12	BM195340	BM195340 C0308E04-
c 41	16	66.7	363	13	BY304103	BY304103 BY304103
c 42	16	66.7	364	9	AA119050	AA119050 mp62h06.r
c 43	16	66.7	373	13	BY319051	BY319051 BY319051
c 44	16	66.7	377	13	BX636769	BX636769 BX636769
45	16	66.7	378	14	CD538683	CD538683 B0205E11-

#### ALIGNMENTS

RESULT 1  
H81820  
LOCUS  
DEFINITION  
H81820  
404 bp mRNA linear EST 09-NOV-1995  
Ys68e09.r1 Soares retina N2b4HR Homo sapiens cDNA clone  
IMAGE:219976 5', similar to gb:M14752 PROTO-ONCOGENE  
TYROSINE-PROTEIN KINASE ABL (HUMAN); mRNA sequence.  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
H81820.1 GI:1059909  
EST.  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE  
AUTHORS  
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,  
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,  
Parsons, J., Rifkin, L., Rohlffing, T., Soares, M., Tan, F.,  
Trevisan, E., Waterston, R., Williamson, A., Wohldmann, P. and  
Wilson, R.  
TITLE  
JOURNAL  
COMMENT  
The WashU-Merck EST Project  
Unpublished (1995)  
Contact: Wilson RK  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu

High quality sequence stops: 382  
Source: IMAGE Consortium, LLNL.  
This clone is available royalty-free through LLNL ; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.  
Insert Length: 1427 Std Error: 0.00  
Seq primer: M13RP1  
High quality sequence stop: 382.

## FEATURES

source

## ORIGIN

Query Match	100.0%;	Score 24;	DB 14;	Length 404;
Best Local Similarity	100.0%;	Pred. No. 0.0037;		
Matches 24;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	CCGCTGAAGGGCTTCATGTTCCAC	24	
Db	111	CCGCTGAAGGGCTTCATGTTCCAC	134	

## FEATURES

Source

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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="S11SNU1-47-E02"
/sex="M"
/tissue_type="Stomach"
/cell_type="Lymphoblast-like"
/cell_line="SNU-1"
/lab_host="topiof"
/clone_lib="S11SNU1"
/note="Organ: Stomach; Vector: pME18-FL3; Site 1: XhoI; Site 2: XhoI; The poly (A) + RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tobacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including SfiI site by treatment of T4 RNA ligase and the first strand cDNA was synthesized with Superscript II using SfiI oligo-dT primer. After first strand synthesis, RNA was degraded by NaOH treatment and cDNA was amplified by PCR reaction. The PCR products were digested with SfiI and cloned into DraIII- digested pME18-FL3 vector. The obtained cDNA vectors were used for transformation of competent cells E. coli Topiof, by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."

```

## ORIGIN

```

Query Match      100.0%; Score 24; DB 12; Length 421;
Best Local Similarity 100.0%; Pred. No. 0.0037;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGCTGAAGGGCTTCATGTTCCAC 24
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Db 270 CCGCTGAAGGGCTTCATGTTCCAC 247

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## FEATURES

Source



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ORIGIN
Query Match      100.0%; Score 24; DB 9; Length 544;
Best Local Similarity 100.0%; Pred. No. 0.004;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGCTGAAGGGCTTCATGTTCCAC 24
    |||
Db 524 CCGCTGAAGGGCTTCATGTTCCAC 501
    |||

RESULT 4
LOCUS BX097261 781 bp mRNA linear EST 04-FEB-2003
DEFINITION BX097261 Soares retina N2b4HR Homo sapiens cDNA clone
IMAGE:219976; IMAGE:219976, mRNA sequence.
ACCESSION BX097261
VERSION BX097261.1 GI:27843159
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 781)
AUTHORS Ebert, L., Heil, O., Hennig, S., Neubert, P., Partsch, E., Peters, M.,
Radelof, U., Schneider, D. and Korn, B.
TITLE Human Unigeneset - RZPD3
JOURNAL Unpublished (2003)
COMMENT Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
RZPD; IMAGE:219976
RZPDLIB; I.M.A.G.E. cDNA Clone Collection;
http://www.rzpd.de/ClonesCards/cgi-
bin/showLib.pl.cgi?response?libNo=972 Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 101
Fax: +49 30 32639 111
www.rzpd.de
This clone is available royalty-free from RZPD;
contact RZPD (clone@rzpd.de) for further information. Seq primer:
M13r, Primer sequence: TTTACACAGGAAACAGTATGAC.
FEATURES
source
1..781
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:219976"
/sex="male"
/tissue_type="retina"
/dev_stage="55 year old"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares retina N2b4HR"
/notes="Organ: eye; Vector: pT7T3D (Pharmacia) with a
modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTTCACATCTGAGTGGAGCGCGCGCTTTTCTTTTCTTTT 3'],
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT7T3 vector
(Pharmacia). The retinas were obtained from a 55 year old
Caucasian and total cellular poly(A)+ RNA was extracted 6
hrs after their removal. The retina RNA was kindly
provided by Roderick R. McInnes M.D. Ph.D. from the
University of Toronto. Library constructed by Bento
Soares and M.Fatima Bonaudo."

ORIGIN
Query Match      100.0%; Score 24; DB 13; Length 781;
Best Local Similarity 100.0%; Pred. No. 0.0045;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGCTGAAGGGCTTCATGTTCCAC 24
    |||
Db 524 CCGCTGAAGGGCTTCATGTTCCAC 501
    |||

RESULT 5
LOCUS CD848190 525 bp mRNA linear EST 11-JUL-2003
DEFINITION DH0AC002H02FW1 HaDevR2 Helianthus annuus cDNA clone HaDevR2002H02,
mRNA sequence.
ACCESSION CD848190
VERSION CD848190.1 GI:32532012
KEYWORDS EST.
SOURCE Helianthus annuus (common sunflower)
ORGANISM Helianthus annuus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; campanulids; Asterales; Asteraceae; Asteroideae;
Heliantheae; Helianthus.
REFERENCE 1 (bases 1 to 525)
AUTHORS Genoplante, a major partnership french program in plant genomics
TITLE Genoplante, (2003)
JOURNAL Unpublished (2003)
COMMENT Contact: Genoplante
Genoplante
93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplante' (http://www.genoplante.com
and http://genoplante-info.infobiogen.fr).
FEATURES
source
1..525
/organism="Helianthus annuus"
/mol_type="mRNA"
/cultivar="psc8"
/db_xref="taxon:4232"
/clone="HaDevR2002H02"
/tissue_type="terminal bud"
/clone_lib="HaDevR2"

ORIGIN
Query Match      75.0%; Score 18; DB 14; Length 525;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 AAGGCTTCATGTTCCAC 24
    |||
Db 211 AAGGCTTCATGTTCCAC 228
    |||

RESULT 6
LOCUS BU019091 546 bp mRNA linear EST 23-AUG-2002
DEFINITION QHE20D24.yg.ab1 QH EFGHJ sunflower RHA280 Helianthus annuus cDNA
clone QHE20D24, mRNA sequence.
ACCESSION BU019091
VERSION BU019091.1 GI:22454611
KEYWORDS EST.
SOURCE Helianthus annuus (common sunflower)
ORGANISM Helianthus annuus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; campanulids; Asterales; Asteraceae; Asteroideae;
Heliantheae; Helianthus.
REFERENCE 1 (bases 1 to 546)
AUTHORS Kozik, A., Michelmore, R.W., Knapp, S., Matvienko, M., Rieseberg, L.,
Lin, H., van Damme, M., Lavelle, D., Chevalier, P., Ziegler, J.,
Ellison, P., Kolkman, J., Slabaugh, M.S., Livingston, K., Zhou, Y.,
Lai, Z., Church, S., Jackson, L. and Bradford, K.
TITLE Lettuce and Sunflower ESTs from the Compositae Genome Project

```

http://compgenomics.ucdavis.edu/  
 Unpublished (2002)  
 Contact: Alexander Kozik [R.W.Michelmore]  
 Department of Vegetable Crops, R.W.Michelmore Lab  
 University of California at Davis (UCD)  
 Asmudson Hall, UCD, Davis, CA 95616, USA  
 Tel: 1-(530)-742-1742  
 Fax: 1-(530)-752-9659  
 Email: akozikeatgc.org [michelmore@vegmail.ucdavis.edu]  
 singleton, see http://cpgdb.ucdavis.edu/ for details.  
 Plate: QHE20 row: D column: 24.

**TITLE**  
 JOURNAL  
 MEDLINE  
 PUBMED  
 COMMENT

**FEATURES**  
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 1..546  
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 /mol\_type="mRNA"  
 /cultivar="RHA280"  
 /db\_xref="taxon:4232"  
 /clone="QHE20D24"  
 /lab\_host="E.coli"  
 /clone\_lib="QH\_EFGHJ sunflower RHA280"  
 /note="Vector: DBRCDNASFIAB; The library was constructed from 11 different sources of RNA from a single genotype. Separate cDNAs were generated using primers that incorporated unique 5' and 3' tags to distinguish each source of RNA. cDNAs were then pooled, size-fractionated, directionally cloned into a custom medium-copy vector and transfections made with four size classes to minimize size bias. Details of each source of RNA and library construction can be obtained at http://cpgdb.ucdavis.edu/TAG\_TISSUE=roots environmental stress  
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 TAG\_SEQ=ATCTCGCGGG"

**ORIGIN**

Query Match 75.0%; Score 18; DB 13; Length 546;  
 Best Local Similarity 100.0%; Pred. No. 10;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 AAGGGCTTCATGTTCCAC 24  
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 Db 309 AAGGGCTTCATGTTCCAC 292

**RESULT 7**  
 LOCUS  
 BY243155  
 DEFINITION  
 BY243155 RIKEN full-length enriched, visual cortex Mus musculus  
 CDNA clone K230039L14 5', mRNA sequence.  
 BY243155  
 ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Mus musculus (house mouse)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 573)  
 Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S.,  
 Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I.,  
 Kiyosawa,H., Tagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A.,  
 Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C.,  
 Hume,D.A., Quackenbush,J., Schriml,L.M., Kapin,A., Matsuda,H.,  
 Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Bruscia,V.,  
 Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A.,  
 Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T.,  
 Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S.,  
 Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A.,  
 Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A.,  
 Kurochin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R.,  
 Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T.,  
 Numata,K., Okido,T., Pavan,W.J., Perlea,G., Pesole,G.,  
 Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S.,  
 Ravasi,T., Reed,J.C., Reid,D.J., Reid,J., Ring,B.Z., Ringwald,M.,  
 Sandelin,A., Schneider,C., Sempke,C.A., Setou,M., Shimada,K.,

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 /mol\_type="mRNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="K230039L14"  
 /tissue\_type="visual cortex"  
 /clone\_lib="RIKEN full-length enriched, visual cortex"

**ORIGIN**

Query Match 75.0%; Score 18; DB 13; Length 573;  
 Best Local Similarity 100.0%; Pred. No. 11;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGCTGAAGGGCTTCATG 18  
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 Db 462 CGGCTGAAGGGCTTCATG 479

**RESULT 8**  
 BM917206/c

Sultana,R., Tanaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M.,  
 Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y.,  
 Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I.,  
 Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P.,  
 Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M.,  
 Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K.,  
 Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y.,  
 Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K.,  
 Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S.,  
 Rogers,J., Birney,E. and Hayashizaki,Y.  
 Analysis of the mouse transcriptome based on functional annotation  
 of 60,770 full-length cDNAs  
 Nature 420, 563-573 (2002)  
 22354683  
 12466851  
 Contact: Yoshihide Hayashizaki  
 Laboratory for Genome Exploration Research Group, RIKEN Genomic  
 Sciences Center (GSC), Yokohama Institute  
 The Institute of Physical and Chemical Research (RIKEN)  
 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan  
 Tel: 81-45-503-9222  
 Fax: 81-45-503-9216  
 Email: genome-res@sc.riken.go.jp,  
 URL:http://genome.gsc.riken.go.jp/  
 Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S.,  
 Hirozane,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H.,  
 Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R.,  
 Ohno,M., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K.,  
 Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramatsu,M. and  
 Hayashizaki,Y. Direct Submission  
 Computational Analysis of Full-Length Mouse cDNAs Compared with  
 Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)  
 Normalization and subtraction of cap-trapper-selected cDNAs to  
 prepare full-length cDNA libraries for rapid discovery of new  
 genes. Genome Res. 10 (10), 1617-1630 (2000)  
 RIKEN integrated sequence analysis (RISA) system--384-format  
 sequencing pipeline with 384 multicapillary sequencer. Genome Res.  
 10 (11), 1757-1771 (2000)  
 Computer-based methods for the mouse full-length cDNA  
 encyclopedia: real-time sequence clustering for construction of a  
 nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)  
 cDNA library was prepared and sequenced in Mouse Genome  
 Encyclopedia Project of Genome Exploration Research Group in Riken  
 Genomic Sciences Center and Genome Science Laboratory in RIKEN.  
 Division of Experimental Animal Research in Riken contributed to  
 prepare mouse tissues.  
 Tissues were provided by Michela Fagiolini and Takao K. Hensch (  
 Laboratory for Neuronal Circuit Development Brain Science Institute  
 RIKEN 2-1 Hiroosawa,Wako-shi,Saitama 351-0198 Japan ) whose  
 assistance we gratefully acknowledge. Please visit our web site  
 (http://genome.gsc.riken.go.jp) for further details.

```

LOCUS      BM917206                1110 bp      mRNA      linear      EST 12-MAR-2002
DEFINITION AGENCOURT_5702147 NIH_MGC_106 Homo sapiens cDNA clone IMAGE:5483703
5', mRNA sequence.
ACCESSION  BM917206
VERSION     BM917206.1 GI:19367585
KEYWORDS   EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 1110)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
          Email: cgapbs@mail.nih.gov
          Tissue Procurement: Dr. Daniel McVicar, DBS/NCI
          cDNA Library Preparation: Rubin Laboratory
          cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
          DNA Sequencing by: Agencourt Bioscience Corporation
          Clone distribution: MGC clone distribution information can be
          found through the I.M.A.G.E. Consortium/LLNL at:
          http://image.llnl.gov
          Plate: L16M2011 row: m column: 16
          High quality sequence stop: 651.

FEATURES             source
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         /organism="Homo sapiens"
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         /db_xref="IMAGE:5483703"
         /clone="IMAGE:5483703"
         /tissue_type="natural killer cells, cell line"
         /lab_host="DH10B (phage-resistant)"
         /clone_lib="NIH MGC 106"
         /note="Organ: blood; Vector: pOTB7; Site 1: XhoI; Site 2:
         EcoRI; cDNA made by oligo-dT priming. Directionally cloned
         into EcoRI/XhoI sites using the following 5' adaptor:
         GCACAG(G). Library constructed by Ling Hong in the
         laboratory of Gerald M. Rubin (University of California,
         Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
         Superscript II RT (Life Technologies). Note: this is a
         NIH_MGC Library."

ORIGIN
Query Match      75.0%; Score 18; DB 12; Length 1110;
Best Local Similarity 100.0%; Pred. NO. 13;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 GCTGAAGGGCTTCATGTT 20
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DB      823 GCTGAAGGGCTTCATGTT 806

RESULT 9
CD588643
LOCUS      CD588643                303 bp      mRNA      linear      EST 16-JUN-2003
DEFINITION RK047A3H04.T3 Zebrafish Kidney Marrow cDNA library Danio rerio cDNA
clone RK047A3H04 5', mRNA sequence.
ACCESSION  CD588643
VERSION     CD588643.1 GI:31769995
KEYWORDS   EST.
SOURCE      Danio rerio (zebrafish)
ORGANISM    Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
REFERENCE  1 (bases 1 to 303)
AUTHORS   Song, H.D., Wu, X.Y., Sun, X.J., Zhou, Y., Liu, T.X., Zhang, G.W.,
          Sheng, Y., Chen, Y., Ruan, Z., Jiang, C.L., Fan, H.Y., Look, A.T.,
          Zou, L.I. and Chen, Z.
          Gene Expression Profiling in the Zebrafish Kidney Marrow Tissue
          Unpublished (2003)
          Contact: Chen Z.

TITLE     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
JOURNAL   Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
COMMENT   Cypriniformes; Cyprinidae; Danio.

REFERENCE  1 (bases 1 to 303)
AUTHORS   Song, H.D., Wu, X.Y., Sun, X.J., Zhou, Y., Liu, T.X., Zhang, G.W.,
          Sheng, Y., Chen, Y., Ruan, Z., Jiang, C.L., Fan, H.Y., Look, A.T.,
          Zou, L.I. and Chen, Z.
          Gene Expression Profiling in the Zebrafish Kidney Marrow Tissue
          Unpublished (2003)
          Contact: Chen Z.

TITLE     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
JOURNAL   Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
COMMENT   Cypriniformes; Cyprinidae; Danio.

```

```

State Key Lab for Medical Genomics
Shanghai Institute of Hematology, Ruijin Hospital Affiliated to
Shanghai Second Medical University
197 Rui Jin Road II, Shanghai 200025, P. R. China
Tel: 86-21-64740490
Fax: 86-21-64743206
Email: zchen@stn.sh.cn
Seq primer: T3.

FEATURES             source
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         Site 2: EcoRI; Total RNA was extracted from the kidney
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         was separated from total RNA by oligo (dT) cellulose
         chromatography. Library was initially constructed in the
         lambdaZAP Express vector (Stratagene) and in vivo excised
         into pBS-CMV vector."

ORIGIN
Query Match      70.8%; Score 17; DB 14; Length 303;
Best Local Similarity 100.0%; Pred. NO. 32;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 CTGAAGGGCTTCATGTT 20
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DB      111 CTGAAGGGCTTCATGTT 127

RESULT 10
CD585274
LOCUS      CD585274                317 bp      mRNA      linear      EST 16-JUN-2003
DEFINITION RK030A2C01.T3 Zebrafish Kidney Marrow cDNA library Danio rerio cDNA
clone RK030A2C01 5', mRNA sequence.
ACCESSION  CD585274
VERSION     CD585274.1 GI:31766016
KEYWORDS   EST.
SOURCE      Danio rerio (zebrafish)
ORGANISM    Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
REFERENCE  1 (bases 1 to 317)
AUTHORS   Song, H.D., Wu, X.Y., Sun, X.J., Zhou, Y., Liu, T.X., Zhang, G.W.,
          Sheng, Y., Chen, Y., Ruan, Z., Jiang, C.L., Fan, H.Y., Look, A.T.,
          Zou, L.I. and Chen, Z.
          Gene Expression Profiling in the Zebrafish Kidney Marrow Tissue
          Unpublished (2003)
          Contact: Chen Z.

TITLE     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
JOURNAL   Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
COMMENT   Cypriniformes; Cyprinidae; Danio.

REFERENCE  1 (bases 1 to 317)
AUTHORS   Song, H.D., Wu, X.Y., Sun, X.J., Zhou, Y., Liu, T.X., Zhang, G.W.,
          Sheng, Y., Chen, Y., Ruan, Z., Jiang, C.L., Fan, H.Y., Look, A.T.,
          Zou, L.I. and Chen, Z.
          Gene Expression Profiling in the Zebrafish Kidney Marrow Tissue
          Unpublished (2003)
          Contact: Chen Z.

TITLE     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
JOURNAL   Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
COMMENT   Cypriniformes; Cyprinidae; Danio.

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         Site 2: EcoRI; Total RNA was extracted from the kidney
         tissues of mature zebrafish. The poly (A)+ RNA fraction

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was separated from total RNA by oligo (dT) cellulose chromatography. Library was initially constructed in the lambdaZAP Express vector (Stratagene) and in vivo excised into PBS-CMV vector."

## ORIGIN

Query Match 70.8%; Score 17; DB 14; Length 317;  
Best Local Similarity 100.0%; Pred. No. 32;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CTGAAGGGCTTCATGTT 20  
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Db 123 CTGAAGGGCTTCATGTT 139

## RESULT 11

CD591703  
LOCUS  
DEFINITION 323 bp mRNA linear EST 16-JUN-2003  
clone RK065A4G05.T3 Zebrafish Kidney Marrow cDNA library Danio rerio cDNA

ACCESSION  
KEYWORDS  
SOURCE  
ORGANISM

CD591703  
EST.  
Danio rerio (zebrafish)  
Danio rerio  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;  
Cypriniformes; Cyprinidae; Danio.

## REFERENCE

AUTHORS  
Song, H.D., Wu, X.Y., Sun, X.J., Zhou, Y., Liu, T.X., Zhang, G.W.,  
Sheng, Y., Chen, Y., Ruan, Z., Jiang, C.L., Fan, H.Y., Look, A.T.,  
Zou, L.I. and Chen, Z.

## TITLE

Gene Expression Profiling in the Zebrafish Kidney Marrow Tissue

## JOURNAL

COMMENT  
State Key Lab for Medical Genomics  
Shanghai Institute of Hematology, Ruijin Hospital Affiliated to  
Shanghai Second Medical University  
197 Rui Jin Road II, Shanghai 200025, P. R. China

Tel: 86-21-64740490

Fax: 86-21-64743206

Email: zchen@stn.sh.cn

Seq primer: T3.

## FEATURES

## source

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/clone\_lib="Zebrafish Kidney Marrow cDNA library"  
/note="Organ: kidney; Vector: PBS-CMV; Site: 1: XhoI;  
Site: 2: EcoRI; Total RNA was extracted from the kidney  
tissues of mature zebrafish. The poly (A)+ RNA fraction  
was separated from total RNA by oligo (dT) cellulose  
chromatography. Library was initially constructed in the  
lambdaZAP Express vector (Stratagene) and in vivo excised  
into PBS-CMV vector."

## ORIGIN

Query Match 70.8%; Score 17; DB 14; Length 323;  
Best Local Similarity 100.0%; Pred. No. 32;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CTGAAGGGCTTCATGTT 20  
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Db 120 CTGAAGGGCTTCATGTT 136

## RESULT 12

CD601328  
LOCUS  
DEFINITION 324 bp mRNA linear EST 16-JUN-2003  
clone RK132A1C12.T3 Zebrafish Kidney Marrow cDNA library Danio rerio cDNA

clone RK132A1C12 5', mRNA sequence.

CD601328

VERSION GI:31782204

KEYWORDS

SOURCE

## ORGANISM

Danio rerio (zebrafish)  
Danio rerio  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;  
Cypriniformes; Cyprinidae; Danio.

## REFERENCE

AUTHORS  
Song, H.D., Wu, X.Y., Sun, X.J., Zhou, Y., Liu, T.X., Zhang, G.W.,  
Sheng, Y., Chen, Y., Ruan, Z., Jiang, C.L., Fan, H.Y., Look, A.T.,  
Zou, L.I. and Chen, Z.

## TITLE

Gene Expression Profiling in the Zebrafish Kidney Marrow Tissue

## JOURNAL

COMMENT  
Unpublished (2003)  
Contact: Chen Z.  
State Key Lab for Medical Genomics  
Shanghai Institute of Hematology, Ruijin Hospital Affiliated to  
Shanghai Second Medical University  
197 Rui Jin Road II, Shanghai 200025, P. R. China

Tel: 86-21-64740490

Fax: 86-21-64743206

Email: zchen@stn.sh.cn

Seq primer: T3.

## FEATURES

## source

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/note="Organ: kidney; Vector: PBS-CMV; Site: 1: XhoI;  
Site: 2: EcoRI; Total RNA was extracted from the kidney  
tissues of mature zebrafish. The poly (A)+ RNA fraction  
was separated from total RNA by oligo (dT) cellulose  
chromatography. Library was initially constructed in the  
lambdaZAP Express vector (Stratagene) and in vivo excised  
into PBS-CMV vector."

## ORIGIN

Query Match 70.8%; Score 17; DB 14; Length 324;  
Best Local Similarity 100.0%; Pred. No. 33;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CTGAAGGGCTTCATGTT 20  
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Db 111 CTGAAGGGCTTCATGTT 127

## RESULT 13

CD601373  
LOCUS  
DEFINITION 330 bp mRNA linear EST 16-JUN-2003  
clone RK132A2C11.T3 Zebrafish Kidney Marrow cDNA library Danio rerio cDNA

clone RK132A2C11 5', mRNA sequence.

CD601373

VERSION GI:31782249

KEYWORDS

SOURCE

## ORGANISM

Danio rerio (zebrafish)  
Danio rerio  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;  
Cypriniformes; Cyprinidae; Danio.

## REFERENCE

AUTHORS  
Song, H.D., Wu, X.Y., Sun, X.J., Zhou, Y., Liu, T.X., Zhang, G.W.,  
Sheng, Y., Chen, Y., Ruan, Z., Jiang, C.L., Fan, H.Y., Look, A.T.,  
Zou, L.I. and Chen, Z.

## TITLE

Gene Expression Profiling in the Zebrafish Kidney Marrow Tissue

## JOURNAL

COMMENT  
Unpublished (2003)  
Contact: Chen Z.  
State Key Lab for Medical Genomics  
Shanghai Institute of Hematology, Ruijin Hospital Affiliated to  
Shanghai Second Medical University

197 Rui Jin Road II, Shanghai 200025, P. R. China  
Tel: 86-21-64740490  
Fax: 86-21-64743206  
Email: zchen@stn.sh.cn  
Seq primer: T3.

#### FEATURES

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/mol\_type="mrna"  
/db\_xref="taxon:7955"  
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/clone\_lib="Zebrafish Kidney Marrow cDNA library"  
/note="Organ: Kidney; Vector: pBS-CMV; Site\_1: XhoI;  
Site\_2: EcoRI; Total RNA was extracted from the kidney  
tissues of mature zebrafish. The poly (A)+ RNA fraction  
was separated from total RNA by oligo (dT) cellulose  
chromatography. Library was initially constructed in the  
lambdaZAP Express vector (Stratagene) and in vivo excised  
into pBS-CMV vector."

#### ORIGIN

Query Match 70.8%; Score 17; DB 14; Length 330;  
Best Local Similarity 100.0%; Pred. No. 33;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CTGAAGGGCTTCATGTT 20  
|||||  
Db 111 CTGAAGGGCTTCATGTT 127

#### RESULT 14

CD602150  
LOCUS  
DEFINITION  
RK140A2F04.T3 Zebrafish Kidney Marrow cDNA library Danio rerio cDNA  
clone RK140A2F04 5', mRNA sequence.

ACCESSION  
CD602150  
VERSION  
EST.  
SOURCE  
Danio rerio (zebrafish)

#### ORGANISM

Danio rerio  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;  
Cypriniformes; Cyprinidae; Danio.

#### REFERENCE

AUTHORS  
Song,H.D., Wu,X.Y., Sun,X.J., Zhou,Y., Liu,T.X., Zhang,G.W.,  
Sheng,Y., Chen,Y., Ruan,Z., Jiang,C.L., Fan,H.Y., Look,A.T.,  
Zou,L.I. and Chen,Z.

#### TITLE

JOURNAL  
COMMENT  
Gene Expression Profiling in the Zebrafish Kidney Marrow Tissue  
Unpublished (2003)  
Contact: Chen Z.

State Key Lab for Medical Genomics  
Shanghai Institute of Hematology, Ruijin Hospital Affiliated to  
Shanghai Second Medical University  
197 Rui Jin Road II, Shanghai 200025, P. R. China  
Tel: 86-21-64740490  
Fax: 86-21-64743206  
Email: zchen@stn.sh.cn  
Seq primer: T3.

#### FEATURES

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Location/Qualifiers  
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Site\_2: EcoRI; Total RNA was extracted from the kidney  
tissues of mature zebrafish. The poly (A)+ RNA fraction  
was separated from total RNA by oligo (dT) cellulose  
chromatography. Library was initially constructed in the  
lambdaZAP Express vector (Stratagene) and in vivo excised

into pBS-CMV vector."

#### ORIGIN

Query Match 70.8%; Score 17; DB 14; Length 330;  
Best Local Similarity 100.0%; Pred. No. 33;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CTGAAGGGCTTCATGTT 20  
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#### RESULT 15

CD603852  
LOCUS  
DEFINITION  
RZ150A3E05.T3 Zebrafish Kidney Marrow cDNA library Danio rerio cDNA  
clone RZ150A3E05 5', mRNA sequence.

ACCESSION  
CD603852  
VERSION  
EST.  
SOURCE  
Danio rerio (zebrafish)

#### ORGANISM

Danio rerio  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;  
Cypriniformes; Cyprinidae; Danio.

#### REFERENCE

AUTHORS  
Song,H.D., Wu,X.Y., Sun,X.J., Zhou,Y., Liu,T.X., Zhang,G.W.,  
Sheng,Y., Chen,Y., Ruan,Z., Jiang,C.L., Fan,H.Y., Look,A.T.,  
Zou,L.I. and Chen,Z.

#### TITLE

JOURNAL  
COMMENT  
Gene Expression Profiling in the Zebrafish Kidney Marrow Tissue  
Unpublished (2003)  
Contact: Chen Z.

State Key Lab for Medical Genomics  
Shanghai Institute of Hematology, Ruijin Hospital Affiliated to  
Shanghai Second Medical University  
197 Rui Jin Road II, Shanghai 200025, P. R. China  
Tel: 86-21-64740490  
Fax: 86-21-64743206  
Email: zchen@stn.sh.cn  
Seq primer: T3.

#### FEATURES

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Site\_2: EcoRI; Total RNA was extracted from the kidney  
tissues of mature zebrafish. The poly (A)+ RNA fraction  
was separated from total RNA by oligo (dT) cellulose  
chromatography. Library was initially constructed in the  
lambdaZAP Express vector (Stratagene) and in vivo excised  
into pBS-CMV vector."

#### ORIGIN

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Best Local Similarity 100.0%; Pred. No. 37;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CTGAAGGGCTTCATGTT 20  
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Db 180 CTGAAGGGCTTCATGTT 196

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: May 26, 2004, 16:00:31 ; Search time 510.783 Seconds  
(without alignments)  
2036.547 Million cell updates/sec

Title: US-09-121-239-19

Perfect score: 24

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Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 3470272 seqs, 21671516995 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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7: gb\_ph.\*

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

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C 1	24	100.0	24	6	BD222538	Methods f
C 2	24	100.0	24	6	BD222539	Methods f
C 3	24	100.0	24	6	BD222540	Methods f
C 4	24	100.0	24	6	BD222541	Methods f
C 5	24	100.0	299	6	BD222547	Methods f
C 6	18	75.0	34125	14	AT12CGA	XJ3487 Adenovirus
C 7	18	75.0	238483	2	AC132177	AC132177 Rattus no
C 8	17	70.8	60456	2	AC087634	AC087634 Homo sapi
C 9	17	70.8	104244	10	AL805925	AL805925 Mouse DNA
C 10	17	70.8	138152	10	AL954170	AL954170 Mouse DNA
C 11	17	70.8	152804	2	BX248232	BX248232 Danio rer
C 12	17	70.8	162077	2	AC109200	AC109200 Mus muscu
C 13	17	70.8	184317	10	AL606494	AL606494 Mouse DNA
C 14	17	70.8	215356	10	AC096363	AC096363 Rattus no
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C 16	17	70.8	256703	2	AC114076	AC114076 Rattus no
C 17	17	70.8	259220	2	AC097694	AC097694 Rattus no
C 18	16	66.7	404	8	AF082605	AF082605 Leavenwor
C 19	16	66.7	415	8	AF082606	AF082606 Leavenwor
C 20	16	66.7	556	11	G85739	G85739 S209P6356RA
C 21	16	66.7	688	11	G97604	G97604 S209P6432FF
C 22	16	66.7	751	6	BD018368	BD018368 Novel gen
C 23	16	66.7	751	6	BD098306	BD098306 Novel gen
C 24	16	66.7	760	8	AF082603	AF082603 Leavenwor
C 25	16	66.7	1050	10	AF039216	AF039216 Mus muscu
C 26	16	66.7	1109	10	BC005636	BC005636 Mus muscu
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C 28	16	66.7	1599	8	ZMA430386	ZMA430386 Zea mays
C 29	16	66.7	2233	8	AY166687	AY166687 Cryptonec
C 30	16	66.7	2370	8	ZMA430205	ZMA430205 Zea mays
C 31	16	66.7	2577	9	BC028075	BC028075 Homo sapi
C 32	16	66.7	3335	5	AY422997	AY422997 Danio rer
C 33	16	66.7	3337	9	HSA295142	HSA295142 Homo sapi
C 34	16	66.7	3398	5	BC045427	BC045427 Danio rer
C 35	16	66.7	3460	6	AR079398	AR079398 Sequence
C 36	16	66.7	3460	9	HSU94333	HSU94333 Human Clq/M
C 37	16	66.7	4194	10	MUSCTNC	MUSCTNC J04971 M.musculus
C 38	16	66.7	14652	1	AE004799	AE004799 Pseudomon
C 39	16	66.7	48139	9	AC109827	AC109827 Homo sapi
C 40	16	66.7	50436	9	AL391258	AL391258 Human DNA
C 41	16	66.7	60631	1	AF006628	AF006628 Continuation (9 of
C 42	16	66.7	67542	9	AC026422	AC026422 Homo sapi
C 43	16	66.7	70305	1	YPCD1	YPCD1 AL117189 Yersinia
C 44	16	66.7	70504	1	AF053946	AF053946 Yersinia
C 45	16	66.7	70504	1	AF053946	AF053946 Yersinia

ALIGNMENTS

RESULT 1  
BD222538/c  
LOCUS BD222538 24 bp DNA linear PAT 17-JUL-2003  
DEFINITION Methods for detecting and measuring spliced nucleic acids.  
ACCESSION BD222538  
VERSION BD222538.1 GI:33032308  
KEYWORDS JP 2002521037-A/16.  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1 (bases 1 to 24)  
AUTHORS Harvey, R.C. and Eastman, P.S.  
TITLE Methods for detecting and measuring spliced nucleic acids  
JOURNAL Patent: JP 2002521037-A 16 16-JUL-2002;  
GEN PROBE INC

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COMMENT      OS   Artificial Sequence
              PN   JP 2002521037-A/16
              PD   16-JUL-2002
              PP   23-JUL-1999 JP 2000561364
              PR   23-JUL-1998 US 09/121239
              PI   RICHARD C HARVEY, PAUL S EASTMAN
              PC   C12Q1/68, C12N15/09, C12N15/00
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FEATURES      Location/Qualifiers
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Best Local Similarity 75.0%; Pred. No. 0.0025;
Matches 18; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY      1 CCGCUGAAGGGCUUCAUGUCCAC 24
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Db      24 CCGCTGAAGGGCTTCATGTTCCAC 1

RESULT 2
BD222539/c
LOCUS      BD222539      24 bp      RNA      linear      PAT 17-JUL-2003
DEFINITION Methods for detecting and measuring spliced nucleic acids.
ACCESSION  BD222539
VERSION    BD222539.1 GI:33032309
KEYWORDS  JP 2002521037-A/17.
SOURCE    synthetic construct
          artificial sequences.
ORGANISM  1 (bases 1 to 24)
REFERENCE 1 Harvey, R.C. and Eastman, P.S.
          Methods for detecting and measuring spliced nucleic acids
          Patent: JP 2002521037-A 17 16-JUL-2002;
          GEN PROBE INC
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              PD   16-JUL-2002
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              PR   23-JUL-1998 US 09/121239
              PI   RICHARD C HARVEY, PAUL S EASTMAN
              PC   C12Q1/68, C12N15/09, C12N15/00
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Matches 18; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

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Db      24 CCGCTGAAGGGCTTCATGTTCCAC 1

RESULT 3
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LOCUS      BD222540      24 bp      DNA      linear      PAT 17-JUL-2003
DEFINITION Methods for detecting and measuring spliced nucleic acids.
ACCESSION  BD222540
VERSION    BD222540.1 GI:33032310
KEYWORDS  JP 2002521037-A/18.
SOURCE    synthetic construct
          artificial sequences.
ORGANISM  1 (bases 1 to 24)
REFERENCE 1 Harvey, R.C. and Eastman, P.S.
          Methods for detecting and measuring spliced nucleic acids
          Patent: JP 2002521037-A 18 16-JUL-2002;
          GEN PROBE INC
COMMENT    OS   Artificial Sequence
              PN   JP 2002521037-A/18
              PD   16-JUL-2002
              PP   23-JUL-1999 JP 2000561364
              PR   23-JUL-1998 US 09/121239
              PI   RICHARD C HARVEY, PAUL S EASTMAN
              PC   C12Q1/68, C12N15/09, C12N15/00
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Matches 18; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

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RESULT 4
BD222541
LOCUS      BD222541      24 bp      RNA      linear      PAT 17-JUL-2003
DEFINITION Methods for detecting and measuring spliced nucleic acids.
ACCESSION  BD222541
VERSION    BD222541.1 GI:33032311
KEYWORDS  JP 2002521037-A/19.
SOURCE    synthetic construct
          artificial sequences.
ORGANISM  1 (bases 1 to 24)
REFERENCE 1 Harvey, R.C. and Eastman, P.S.
          Methods for detecting and measuring spliced nucleic acids
          Patent: JP 2002521037-A 19 16-JUL-2002;
          GEN PROBE INC
COMMENT    OS   Artificial Sequence
              PN   JP 2002521037-A/19
              PD   16-JUL-2002
              PP   23-JUL-1999 JP 2000561364
              PR   23-JUL-1998 US 09/121239
              PI   RICHARD C HARVEY, PAUL S EASTMAN
              PC   C12Q1/68, C12N15/09, C12N15/00
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Best Local Similarity 75.0%; Pred. No. 0.0025;
Matches 18; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY      1 CCGCUGAAGGGCUUCAUGUCCAC 24
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Db      24 CCGCTGAAGGGCTTCATGTTCCAC 1

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Best Local Similarity 75.0%; Pred. No. 0.0025;
Matches 18; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

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DB 1 CCGCTGAAGGGCTTCATGTTCCAC 24

RESULT 5
BD222547/c
LOCUS BD222547 299 bp DNA linear PAT 17-JUL-2003
DEFINITION Methods for detecting and measuring spliced nucleic acids.
ACCESSION BD222547
VERSION BD222547.1 GI:33032317
KEYWORDS JP 2002521037-A/25.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 299)
AUTHORS Harvey,R.C. and Eastman,P.S.
TITLE Methods for detecting and measuring spliced nucleic acids
JOURNAL Patent: JP 2002521037-A 25 16-JUL-2002;
GEN PROBE INC
OS Homo sapiens (human)
PN JP 2002521037-A/25
PD 16-JUL-2002
PR 23-JUL-1999 JP 2000561364
PR 23-JUL-1998 US 09/121239
PI RICHARD C HARVEY,PAUL S EASTMAN
PC C12Q1/68,C12N15/09,C12N15/00
CC Methods for detecting and measuring spliced nucleic acids FH
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FT Location/Qualifiers
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Best Local Similarity 75.0%; Pred. No. 0.002;
Matches 18; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

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DB 165 CCGCTGAAGGGCTTCATGTTCCAC 142

RESULT 6
AT12CGA
LOCUS AT12CGA 34125 bp DNA linear VRL 17-FEB-1997
DEFINITION Adenovirus type 12 DNA, complete genome.
ACCESSION X73487
VERSION X73487.1 GI:313361
KEYWORDS complete genome; core protein; DNA polymerase; DNA-binding protein;
endoprotease; fiber protein; hexon protein; large T-antigen;
maturation protein; minor core protein; penton protein;
peripentonal hexon-associated protein; promoter; repeat region;
small t-antigen; transcriptional activation.
SOURCE Human adenovirus type 12
ORGANISM Human adenovirus type 12
Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
REFERENCE 1 (bases 1 to 3957)
AUTHORS Tolun,A., Alestrom,P. and Pettersson,U.
TITLE Sequence of inverted terminal repetitions from different
adenoviruses: demonstration of conserved sequences and homology
between SA7 termini and SV40 DNA
JOURNAL Cell 17 (3), 705-713 (1979)
MEDLINE
PUBMED
REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
80001962
225041
2 (bases 1 to 3957)
Sugisaki,H., Sugimoto,K., Takamami,M., Shiroki,K., Saito,I.,
Shimojo,H., Sawada,Y., Uemizu,Y., Uesugi,S. and Fujinaga,K.
Structure and gene organization in the transformed Hind III-G
fragment of Ad12
Cell 20 (3), 777-786 (1980)
JOURNAL
MEDLINE
PUBMED
81022638
6251973
3 (bases 1 to 3957)
Shinagawa,M. and Padmanabhan,R.
Comparative sequence analysis of the inverted terminal repetitions
from different adenoviruses
Proc. Natl. Acad. Sci. U.S.A. 77 (7), 3831-3835 (1980)
JOURNAL
MEDLINE
PUBMED
81054665
6253991
4
Kimura,T., Sawada,Y., Shinawawa,M., Shimizu,Y., Shiroki,K.,
Shimojo,H., Sugisaki,H., Takamami,M., Uemizu,Y. and Fujinaga,K.
Nucleotide sequence of the transforming early region E1b of
adenovirus type 12 DNA: structure and gene organization, and
comparison with those of adenovirus type 5 DNA
Nucleic Acids Res. 9 (23), 6571-6589 (1981)
JOURNAL
MEDLINE
PUBMED
82105565
6275367
5 (bases 24334 to 24703)
Engler,J.A. and van Bree,M.P.
The nucleotide sequence of the gene encoding protein Iva2 in human
adenovirus type 7
Gene 19 (1), 71-80 (1982)
JOURNAL
MEDLINE
PUBMED
83054637
6292051
6 (bases 1488 to 3861)
Kimura,T.
Structure and sequence analysis of the transforming region E1b of
human adenovirus type 12
Sapporo Igaku Zasshi 52, 253-267 (1983)
JOURNAL
MEDLINE
PUBMED
83277521
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7 (bases 20966 to 22966)
Kruijer,W., van Schaik,P.M., Speijer,J.G. and Sussenbach,J.S.
Structure and function of adenovirus DNA binding protein:
comparison of the amino acid sequences of the Ad5 and Ad12 proteins
derived from the nucleotide sequence of the corresponding genes
Virology 128 (1), 140-153 (1983)
JOURNAL
MEDLINE
PUBMED
83277521
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8 (bases 1 to 3957)
van Ormondt,H. and Galibert,F.
Nucleotide sequences of adenovirus DNAs
Curr. Top. Microbiol. Immunol. 110, 73-142 (1984)
JOURNAL
MEDLINE
PUBMED
85002829
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9 (bases 4831 to 10470)
Shu,L.M., Hong,J.S., Wei,Y.F. and Engler,J.A.
Nucleotide sequence of the genes encoded in early region 2b of
human adenovirus type 12
Gene 46 (2-3), 187-195 (1986)
JOURNAL
MEDLINE
PUBMED
87106854
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10 (bases 1 to 530)
Shibata,H., Zheng,J.H., Koikeda,S., Masamune,Y. and Nakanishi,Y.
Cis- and trans-acting factors for transcription of the adenovirus
12 E1A gene
Biochim. Biophys. Acta 1007 (2), 184-191 (1989)
JOURNAL
MEDLINE
PUBMED
89150250
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Juttermann,R., Weyer,U. and Doerfler,W.
Defect of adenovirus type 12 replication in hamster cells: absence
of transcription of viral virus-associated and L1 RNAs
J. Virol. 63 (8), 3535-3540 (1989)
JOURNAL
MEDLINE
PUBMED
89311650

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PUBMED 2746738
REMARK (sites)
REFERENCE 12
AUTHORS Zock, C., Iselt, A. and Doerfler, W.
TITLE A unique mitigator sequence determines the species specificity of
the major late promoter in adenovirus type 12 DNA
JOURNAL J. Virol. 67 (2), 682-693 (1993)
MEDLINE 93124560
PUBMED 8419643
REMARK (sites)
REFERENCE 13
AUTHORS Sprengel, J., Schmitz, B., Heuss-Neitzel, D., Zock, C. and Doerfler, W.
TITLE Nucleotide sequence of human adenovirus type 12 DNA: comparative
functional analysis
JOURNAL J. Virol. 68 (1), 379-389 (1994)
MEDLINE 94076430
PUBMED 8254750
REFERENCE 14 (bases 1 to 34125)
AUTHORS Sprengel, J.
TITLE Direct Submission
JOURNAL Submitted (21-JUN-1993) J. Sprengel, Institute of Genetics/Dept.
Virology, Weyertal 121, 50931 Cologne 41, FRG
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1847..3295
/notes="crossref SWISS-PROT:E1BL_ADE12, P04491"
/codon_start=1
/product="E1B protein, large T-antigen"
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/db_xref="GOA:P04491"
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DVARGEAGGAEPCEGVNMQQVQEGHVLDSGEGPSCADDDKQEKESLKEAAVLIS
RLTVNLMGRPLETYWQELQDFQGMHLQYKYSFEQLKTHLEPWEDECAIKAF
AKLALRPDCSYRITKTITTCAYIINGAIVFVSDTSDRAFRCKMGQMGPGVVGLDG
ITFINVRPAGDKFKGIMPEANTCLVLHGVYFLNFSNICVSESNKYSARCTFYGCWKG
LVGRPKSLSVKCLPEKCVLALIVEGDAHISHNAENACFVLLKGMAILLKHNMYCG
VSDQIMRRFVTCADGNCHTLKTVHIVSHSRHCWPCDDNMFRCITHLGLRGMFRPS
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2071..2073
/citation=[6]
/replace="gcg"
2417..2418
/citation=[6]
Query Match 75.0%; Score 18; DB 14; Length 34125;
Best Local Similarity 66.7%; Pred. No. 4.6;
Matches 12; Conservative 6; Mismatches 0; Indels 0; Gaps 0;
QY 5 UGAAGGGCUCAUGUUC 22
:|||||:|:|:|:|
Db 3998 TGAAGGGCTTCATGTTCC 4015
RESULT 7
AC132177/c 238483 bp DNA linear HTG 10-OCT-2002
LOCUS Rattus norvegicus clone CH230-165B1, WORKING DRAFT SEQUENCE, 6
DEFINITION unordered pieces.
ACCESSION AC132177
VERSION AC132177.4 GI:23683197
KEYWORDS HTG; HTGS PHASE1; HTGS DRAFT; HTGS FULLTOP.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 238483)
AUTHORS Muzny, D. Marie., Metzker, M. Lee., Abramson, S., Adams, C., Alder, J.,
Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D.,
Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H.,
Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F.,
Biswal, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M.,
Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E.,
Cardenas, V., Carter, K., Cavazos, I., Cesar, H., Chen, Z.,
Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J.,
Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L.,
Davila, M. L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D.,
Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K.,
Draper, H., Dugan-Kocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K.,
Egan, A., Escotto, M., Eugene, C., Evans, C. A., Falls, T., Fan, G.,

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Lehoczyk, J., Levine, R., Liu, G., MacLean, C., Macdonald, P.,  
 Marquis, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K.,  
 McPeeters, R., Meldrum, J., Meneus, L., Mihova, T., Mienga, V.,  
 Murphy, T., Naylor, J., Nguyen, C., Norbu, C., Norman, C.H.,  
 O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K.,  
 Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R.,  
 Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M.,  
 Roy, A., Santos, R., Schauer, S., Schuback, R., Seaman, S., Severy, P.,  
 Sougne, C., Spencer, B., Stange-Thomann, N., Stojanovic, N.,  
 Strauss, N., Subramanian, A., Talamas, J., Testaye, S., Theodore, J.,  
 Travers, M., Travis, N., Triglio, J., Vassiliev, H., Viel, R., Vo, A.,  
 Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G., Zainoun, J.,  
 Zembek, L., Zimmer, A. and Zody, M.

Direct Submission  
 Submitted (15-JAN-2001) Whitehead Institute/MIT Center for Genome  
 Research, 320 Charles Street, Cambridge, MA 02141, USA  
 All repeats were identified using RepeatMasker:  
 Smit, A.F.A. & Green, P. (1996-1997)  
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

----- Genome Center  
 Center: Whitehead Institute/ MIT Center for Genome Research  
 Center code: WIBR  
 Web site: <http://www-seq.wi.mit.edu>  
 Contact: [sequence\\_submissions@genome.wi.mit.edu](mailto:sequence_submissions@genome.wi.mit.edu)  
 ----- Project Information  
 Center project name: L11917  
 Center clone name: 302\_D\_8  
 -----

\* NOTE: This record contains 72 individual  
 \* sequencing reads that have not been assembled into  
 \* contigs. Runs of N are used to separate the reads  
 \* and the order in which they appear is completely  
 \* arbitrary. Low-pass sequence sampling is useful for  
 \* identifying clones that may be gene-rich and allows  
 \* overlap relationships among clones to be deduced.  
 \* However, it should not be assumed that this clone  
 \* will be sequenced to completion. In the event that  
 \* the record is updated, the accession number will  
 \* be preserved.

14252 14975: contig of 724 bp in length  
 14976 15075: gap of 100 bp  
 15076 15814: contig of 739 bp in length  
 15815 15914: gap of 100 bp  
 15915 16662: contig of 748 bp in length  
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 16763 17532: contig of 770 bp in length  
 17533 17632: gap of 100 bp  
 17633 18362: contig of 730 bp in length  
 18363 18462: gap of 100 bp  
 18463 19220: contig of 758 bp in length  
 19221 19320: gap of 100 bp  
 19321 20051: contig of 731 bp in length  
 20052 20151: gap of 100 bp  
 20152 20880: contig of 729 bp in length  
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 20981 21750: contig of 770 bp in length  
 21751 21850: gap of 100 bp  
 21851 22706: contig of 756 bp in length  
 22707 22706: gap of 100 bp  
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 23470 23569: gap of 100 bp  
 23570 24318: contig of 749 bp in length  
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 26094 26846: contig of 753 bp in length  
 26847 26946: gap of 100 bp  
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 27652 27751: gap of 100 bp  
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 28488 28587: gap of 100 bp  
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 29325 29424: gap of 100 bp  
 29425 30193: contig of 769 bp in length  
 30194 30293: gap of 100 bp  
 30294 31035: contig of 742 bp in length  
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 31136 31889: contig of 754 bp in length  
 31890 31989: gap of 100 bp  
 31990 32731: contig of 742 bp in length  
 32732 32831: gap of 100 bp  
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 33670 34415: contig of 746 bp in length  
 34416 35272: contig of 757 bp in length  
 35273 35372: gap of 100 bp  
 35373 36095: contig of 723 bp in length  
 36096 36195: gap of 100 bp  
 36196 36912: contig of 717 bp in length  
 36913 37012: gap of 100 bp  
 37013 37770: contig of 758 bp in length  
 37771 37870: gap of 100 bp  
 37871 38611: contig of 741 bp in length  
 38612 38711: gap of 100 bp  
 38712 39462: contig of 751 bp in length  
 39463 39562: gap of 100 bp  
 39563 40324: contig of 762 bp in length  
 40325 40424: gap of 100 bp  
 40426 41325: contig of 801 bp in length  
 41326 42063: contig of 738 bp in length  
 42064 42163: gap of 100 bp  
 42164 42879: contig of 716 bp in length  
 42880 42979: gap of 100 bp  
 42980 43712: contig of 733 bp in length  
 43713 43812: gap of 100 bp  
 43813 44509: contig of 697 bp in length  
 44510 44609: gap of 100 bp  
 44610 45341: contig of 732 bp in length

TITLE  
 JOURNAL  
 COMMENT

\* 45342 45441: gap of 100 bp  
 \* 45442 contig of 727 bp in length  
 \* 46169 46268: gap of 100 bp  
 \* 46269 47020: contig of 752 bp in length  
 \* 47021 47120: gap of 100 bp  
 \* 47121 47867: contig of 747 bp in length  
 \* 47868 47967: gap of 100 bp  
 \* 47968 48712: contig of 745 bp in length  
 \* 48713 48812: gap of 100 bp  
 \* 48813 49531: contig of 719 bp in length  
 \* 49532 49631: gap of 100 bp  
 \* 49632 50374: contig of 743 bp in length  
 \* 50375 50474: gap of 100 bp  
 \* 50475 51198: contig of 724 bp in length  
 \* 51199 51298: gap of 100 bp  
 \* 51299 52022: contig of 724 bp in length  
 \* 52023 52122: gap of 100 bp  
 \* 52123 52888: contig of 766 bp in length  
 \* 52889 52988: gap of 100 bp  
 \* 52989 53725: contig of 737 bp in length  
 \* 53726 53825: gap of 100 bp  
 \* 53826 54566: contig of 741 bp in length  
 \* 54567 54666: gap of 100 bp  
 \* 54667 55445: contig of 779 bp in length  
 \* 55446 55445: gap of 100 bp  
 \* 55446 56281: contig of 736 bp in length  
 \* 56282 56381: gap of 100 bp  
 \* 56382 57126: contig of 745 bp in length  
 \* 57127 57226: gap of 100 bp  
 \* 57227 57965: contig of 739 bp in length  
 \* 57966 58065: gap of 100 bp

Query Match 70.8%; Score 17; DB 2; Length 60456;

Best Local Similarity 70.6%; Pred. No. 17;  
 Matches 12; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 7 AAGGCUUUAUCCCA 23

DB 9925 AAGGCTTCATGTTCCA 9941

# RESULT 9

AL805925/c

LOCUS Mouse DNA sequence from clone RP23-210E20 on chromosome X, complete  
 DEFINITION sequence.

ACCESSION AL805925

VERSION AL805925.6 GI:22531408

KEYWORDS HTG.

SOURCE Mus musculus (house mouse)

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 104244)

Johnson, C.

Direct Submission

Submitted (24-AUG-2002) Wellcome Trust Sanger Institute, Hinxton,

Cambridgeshire, CB10 1SA, UK. E-mail enquiries:

humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk

On Aug 27, 2002 this sequence version replaced gi:22416054.

----- Genome Center

Center: Wellcome Trust Sanger Institute

Center code: SC

Web site: <http://www.sanger.ac.uk>

Contact: humquery@sanger.ac.uk

## COMMENT

During sequence assembly data is compared from overlapping clones.  
 Where differences are found these are annotated as variations  
 together with a note of the overlapping clone name. Note that the  
 variation annotation may not be found in the sequence submission  
 corresponding to the overlapping clone, as we submit sequences with  
 only a small overlap as described above.

This sequence was finished as follows otherwise noted: all

regions were either double-stranded or sequenced with an alternate  
 chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such  
 as compressions and repeats; all regions were covered by at least  
 one plasmid subclone or more than one M13 subclone; and the  
 assembly was confirmed by restriction digest. The following  
 abbreviations are used to associate primary accession numbers given  
 in the feature table with their source databases: Em:, EMBL; SW:,  
 SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP  
 database can be found at  
[http://www.sanger.ac.uk/Projects/C\\_elegans/wormpep](http://www.sanger.ac.uk/Projects/C_elegans/wormpep) RP23-210E20 is  
 from the RPCI-23 Mouse PAC Library  
 constructed by the group of Pieter de Jong.  
 For further details see <http://www.chori.org/bacpac/home.htm>  
 VECTOR: pBACE3.6.

## FEATURES

Location/Qualifiers  
 1..104244  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:10090"  
 /chromosome="X"  
 /clone="RP23-210E20"  
 /clone\_lib="RPCI-23"

## ORIGIN

Query Match 70.8%; Score 17; DB 10; Length 104244;  
 Best Local Similarity 64.7%; Pred. No. 16;  
 Matches 11; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 4 CUGAGGGCUUUAUCCU 20

DB 2178 CTGAAGGGCTTCATGTT 2162

## RESULT 10

AL954170

LOCUS Mouse DNA sequence from clone RP23-467H15 on chromosome 2, complete  
 DEFINITION sequence.

ACCESSION AL954170

VERSION AL954170.4 GI:33636222

KEYWORDS HTG.

SOURCE Mus musculus (house mouse)

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 138152)

North, P., Leaves, N., Greyststrong, J., Coppola, M., Manjunath, S.,  
 Russell, E., Smith, M., Strachan, G., Rotts, C., Roal, E., Cobley, V.,  
 Hunter, G., Kimberley, C., Thomas, D., Cave-Berry, L., Weston, P. and  
 Botcherby, M.R.M.

Direct Submission

Submitted (13-AUG-2003) Mouse Sequencing Group, HGMP-RC, Hinxton,  
 Cambridge, CB10 1SB, UK. E-mail enquiries: - mrbotche@hgmp.mrc.ac.uk  
 or pnoth@hgmp.mrc.ac.uk

HGMP-RC part of the UK Mouse Sequencing Consortium

On Aug 13, 2003 this sequence version replaced gi:32567581.

----- Genome Center

Center: UK Medical Research Council

Center code: UK-MRC

Web site: <http://mrcseq.har.mrc.ac.uk>

Contact: mouseq@har.mrc.ac.uk

## COMMENT

During sequence assembly data is compared from overlapping clones.  
 Where differences are found these are annotated as variations  
 together with a note of the overlapping clone name. Note that the  
 variation annotation may not be found in the sequence submission  
 corresponding to the overlapping clone, as we submit sequences with  
 only a small overlap as described above.  
 This sequence was finished as follows otherwise noted: all  
 regions were either double-stranded or sequenced with an alternate  
 chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such

as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em., EMBL; Sw., SWISSPROT; Tr., TREMBL; Wp., WORMPEP; Information on the WORMPEP database can be found at [http://www.sanger.ac.uk/Projects/C\\_elegans/wormpep](http://www.sanger.ac.uk/Projects/C_elegans/wormpep) RP23-467H15 is from the RPCI-23 Mouse BAC library

constructed by the group of Pieter de Jong.

VECTOR: pBACE3.6

Sequence from the Mouse Genome Sequencing Consortium whole genome shotgun may have been used to confirm this sequence. Sequence data from the whole genome shotgun alone has only been used where it has a phred quality of at least 30.

#### FEATURES

```

source
  1..138152
    Location/Qualifiers
      /organism="Mus musculus"
      /mol_type="genomic DNA"
      /db_xref="taxon:10090"
      /chromosomes="2"
      /clone="RP23-467H15"
      /clone_lib="RPCI-23"

```

#### ORIGIN

```

Query Match      70.8%; Score 17; DB 10; Length 138152;
Best Local Similarity 64.7%; Pred.No. 16;
Matches 11; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

```

QY 5 UGAAGGGCUUCAUGUVC 21

Db 137153 TGAAGGGCTTCATGTC 137169

#### RESULT 11

```

BX248232/c      152804 bp      DNA      linear      HTG 07-NOV-2003
LOCUS
DEFINITION
  Danio rerio clone CH211-23215, WORKING DRAFT SEQUENCE, 3 unordered
  pieces.

```

ACCESSION BX248232.6 GI:38228942

VERSION HTG; HTGS PHASE1; HTGS ACTIVEFIN; HTGS\_DRAFT; HTGS\_FULLTOP.

SOURCE Danio rerio (zebrafish)

#### ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.

#### REFERENCE

1 (bases 1 to 152804)  
 Direct Submission  
 Submitted (06-NOV-2003) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: [zfish-help@sanger.ac.uk](mailto:zfish-help@sanger.ac.uk) Clone requests: [clonerequest@sanger.ac.uk](mailto:clonerequest@sanger.ac.uk)  
 On Nov 7, 2003 this sequence version replaced gi:38141652.

#### COMMENT

----- Genome Center  
 Center: Wellcome Trust Sanger Institute  
 Center code: SC  
 Web site: <http://www.sanger.ac.uk>  
 Contact: [zfish-help@sanger.ac.uk](mailto:zfish-help@sanger.ac.uk)  
 ----- Project Information  
 Center project name: zC23215  
 ----- Summary Statistics  
 Assembly program: XGAP4; version 4.5  
 Chemistry: dye-terminator; 100% of reads  
 Consensus quality: 152578 bases at least Q40  
 Consensus quality: 152597 bases at least Q30  
 Consensus quality: 152598 bases at least Q20  
 Insert size: 152604; sum-of-ctiggs  
 Insert size: 161454; 2.1% error; agarose-fp  
 Quality coverage: 10.26x in Q20 bases; sum-of-ctiggs Quality  
 coverage: 9.69x in Q20 bases; agarose-fp

```

-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 3 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

```

```

* 1 86810: contig of 86810 bp in length
* 86811 86910: gap of 100 bp
* 86911 138019: contig of 51109 bp in length
* 138020 138119: gap of 100 bp
* 138120 152804: contig of 14685 bp in length.

```

#### FEATURES

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source
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      /organism="Danio rerio"
      /mol_type="genomic DNA"
      /db_xref="taxon:7955"
      /clone="CH211-23215"
      /clone_lib="CHORI-211"
      1..86810
        /note="assembly_fragment:02232"
        fragment_chain:1
      86911..138019
        /note="assembly_fragment:00979"
        fragment_chain:1
      138120..152804
        /note="assembly_fragment:01208"
        fragment_chain:1

```

#### misc\_feature

#### misc\_feature

#### misc\_feature

#### ORIGIN

```

Query Match      70.8%; Score 17; DB 2; Length 152804;
Best Local Similarity 64.7%; Pred.No. 16;
Matches 11; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

```

QY 4 CUGAAGGGCUUCAUGUU 20

Db 137376 CTGAAGGGCTTCATGTT 137360

#### RESULT 12

```

AC109200/c      162077 bp      DNA      linear      HTG 19-NOV-2003
LOCUS
DEFINITION
  Mus musculus chromosome 8 clone RP23-26G21 map 8, WORKING DRAFT
  SEQUENCE, 6 ordered pieces.

```

ACCESSION AC109200

VERSION AC109200.5 GI:38424184

KEYWORDS HTG; HTGS PHASE2; HTGS\_DRAFT; HTGS\_FULLTOP.

SOURCE Mus musculus (house mouse)

#### ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 162077)  
 Birren,B., Nussbaum,C. and Lander,E.

#### REFERENCE

AUTHORS Mus musculus chromosome 8, clone RP23-26G21

#### JOURNAL

#### AUTHORS

1 (bases 1 to 162077)  
 Birren,B., Linton,L., Nussbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S., Barna,N., Bastien,V., Boguslavsky,I., Boukhgalter,B., Brown,A., Camarata,J., Campopiano,A., Chang,J., Chazaro,B., Choepel,Y., Collangelo,M., Collins,S., Collamore,A., Cook,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S., Ferreira,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S., Ginde,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N., Hagos,B., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Kamat,A., Karatas,A., Kells,C., LaRoque,K., Lamazares,R., Landers,T., Lehoczy,J., Levine,N., Matthews,C., MacLean,C., MacDonald,P., Major,J., Marquis,N., Matthews,C., McCarthy,M., McEwan,P., McKernan,K., Meldrum,J., Meneus,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Pollara,V., Raymond,C.,

Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodor, J., Topham, K., Travers, M., Travis, N., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

# TITLE JOURNAL

Submitted (03-FEB-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

# REFERENCE AUTHORS

3 (bases 1 to 162077)  
Birren, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N., Anderson, M., Arachchi, H. M., Barna, N., Bastien, V., Bloom, T., Boguslavsky, L., Boukagater, B., Camarata, J., Chang, J., Choepel, Y., Collymore, A., Cook, A., Cooke, P., Corum, B., DeArellano, K., Diaz, J. S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Graham, L., Grand-pierre, N., Hafez, N., Hagopian, D., Hagos, B., Hall, J., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., Lui, X., Mabbitt, R., MacLean, C., Macdonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Rachupka, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Venkataraman, V. S., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

# TITLE JOURNAL

Submitted (19-NOV-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

# COMMENT

On Nov 19, 2003 this sequence version replaced gi:21313786.  
All repeats were identified using RepeatMasker:  
Smit, A. F. A. & Green, P. (1996-1997)  
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

----- Genome Center  
Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIBR

Web site: <http://www-seq.wi.mit.edu>

Contact: [sequence\\_submissions@genome.wi.mit.edu](mailto:sequence_submissions@genome.wi.mit.edu)

----- Project Information

Center project name: L20459

Center clone name: 26 G 21

----- Summary Statistics

Sequencing vector: plasmid; n/a; 100% of reads

Chemistry: Dye-terminator Big Dye; 100% of reads

Assembly program: Phrap; version 0.960731

Consensus quality: 160977 bases at least Q40

Consensus quality: 161390 bases at least Q30

Consensus quality: 161534 bases at least Q20

Insert size: 157000; agarose-fp

Insert size: 161577; sum-of-contigs

Quality coverage: 13.8 in Q20 bases; agarose-fp

Quality coverage: 13.4 in Q20 bases; sum-of-contigs

-----

\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 6 contigs. Gaps between the contigs  
\* are represented as runs of N. The order of the pieces  
\* is believed to be correct as given, however the sizes  
\* of the gaps between them are based on estimates that have  
\* provided by the submitter.

\* This sequence will be replaced  
\* by the finished sequence as soon as it is available and  
\* the accession number will be preserved.

\* 1 53642: contig of 53642 bp in length

\* 53643 53742: gap of 100 bp

\* 53743 54202: contig of 460 bp in length

\* 54203 54302: gap of 100 bp

\* 54303 55174: contig of 872 bp in length

\* 55175 55274: gap of 100 bp

\* 55275 127105: contig of 71831 bp in length  
\* 127106 127205: gap of 100 bp  
\* 127206 125275: contig of 25370 bp in length  
\* 152576 152675: gap of 100 bp  
\* 152676 162077: contig of 9402 bp in length.

# FEATURES source

Location/Qualifiers

1..162077

/organism="Mus musculus"

/mol\_type="genomic DNA"

/db\_xref="taxon:10090"

/chromosome="8"

/map="8"

/clone="RP23-26G21"

/clone\_lib="RPCI-23 Female Mouse BAC"

1..53642

/note="assembly\_fragment"

clone end:SP6

vector\_side:left"

53743..54202

/note="assembly\_fragment"

54303..55174

/note="assembly\_fragment"

55275..127105

/note="assembly\_fragment"

127206..152575

/note="assembly\_fragment"

152676..162077

/note="assembly\_fragment"

clone end:T7

vector\_side:right"

# ORIGIN

Query Match 70.8%; Score 17; DB 2; Length 162077;  
Best Local Similarity 70.6%; Pred. No. 16;  
Matches 12; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

OY 8 AGGGCUCAUGUCCAC 24

|||||:|:|:|:|:|:|

Db 95213 AGGGCTTCATGTTCCAC 95197

# RESULT 13

AL606494

LOCUS

DEFINITION

AL606494

Mouse DNA sequence from clone RP23-198B6 on chromosome 2, complete

sequence.

ACCESSION

AL606494

VERSION

AL606494.3

GI:32567580

KEYWORDS

HTG.

SOURCE

Mus musculus

ORGANISM

Mus musculus

REFERENCE

1 (bases 1 to 162077)

AUTHORS

North, P., Leaves, N., Greystrom, J., Coppola, M., Manjunath, S.,

Russell, E., Smith, M., Strachan, G., Tofts, C., Boal, E., Cobley, V.,

Hunter, G., Kimberley, C., Thomas, D., Cave-Berry, L., Weston, P. and

Botcherby, M. R. M.

Direct Submission

Submitted (12-JUL-2003) Mouse Sequencing Group, HGMP-RC, Hinxton,

Cambridge, CB10 1SB, UK. E-mail enquiries:- [mrbotche@hgmp.mrc.ac.uk](mailto:mrbotche@hgmp.mrc.ac.uk)

or [pnoth@hgmp.mrc.ac.uk](mailto:pnoth@hgmp.mrc.ac.uk)

HGMP-RC part of the UK Mouse Sequencing Consortium

On Jul 12, 2003 this sequence version replaced gi:15723837.

----- Genome Center

Center: UK Medical Research Council

Center code: UK-MRC

Web site: <http://mrcseq.har.mrc.ac.uk>

Contact: [mouse@har.mrc.ac.uk](mailto:mouse@har.mrc.ac.uk)

-----

During sequence assembly data is compared from overlapping clones.

Where differences are found these are annotated as variations

together with a note of the overlapping clone name. Note that the

variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em: EMBL; Sw: SWISSPROT; Tr: TREMBL; Wp: WORMPEP; Information on the WORMPEP database can be found at

[http://www.sanger.ac.uk/Projects/C\\_elegans/wormpep](http://www.sanger.ac.uk/Projects/C_elegans/wormpep) RP23-198B6 is from the RPCI-23 Mouse BAC library

constructed by the group of Pieter de Jong.

For further details see <http://www.chori.org/bacpac/home.htm>

VECTOR: pBACe3.6

Sequence from the Mouse Genome Sequencing Consortium whole genome shotgun may have been used to confirm this sequence. Sequence data from the whole genome shotgun alone has only been used where it has a phred quality of at least 30.

#### FEATURES

source

```
1. .184317
   /organism="Mus musculus"
   /mol_type="genomic DNA"
   /db_xref="taxon:10090"
   /chromosomes="2"
   /clone_lib="RP23-198B6"
   /clone_lib="RPCI-23"
```

#### ORIGIN

Query Match 70.8%; Score 17; DB 10; Length 184317;

Best Local Similarity 64.7%; Pred. No. 15;

Matches 11; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 5 UGAAGGCGUUAUGUUC 21

Db 1732 TGAAGGCTTCAGTTC 1748

#### RESULT 14

AC096363

LOCUS

AC096363 215356 bp DNA linear ROD 01-JUL-2003

DEFINITION Rattus norvegicus 1 BAC CH230-54P17 (Children's Hospital Oakland

Research Institute) complete sequence.

AC096363

VERSION

AC096363.8 GI:32362332

KEYWORDS

HTG.

SOURCE

Rattus norvegicus

ORGANISM

Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;

Rattus.

REFERENCE

AUTHORS

1 (bases 1 to 215356)

Muzny, D. Marie, Metzker, M. Lee, Abramson, S., Adams, C., Alder, J.,

Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D.,

Anylebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H.,

Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F.,

Biswal, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M.,

Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E.,

Cardenas, V., Carter, K., Cavazos, I., Caesar, H., Center, A.,

Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J.,

Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L.,

Davila, M. L., Davis, C., Davy-Carroll, L., De Aram, C., Dederich, D.,

Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K.,

Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K.,

Egan, A., Escotto, M., Eugene, C., Evans, C. A., Falls, T., Fan, G.,

Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P.,

Fraser, C. M., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Garza, M.,

Gebregorgis, E., Geer, K., Gill, R., Grady, M., Guerra, W., Guevara, W.,

Gunaratne, P., Haaland, W., Hamil, C., Hamilton, C., Hamilton, K., Harvey, Y., Haylak, P., Hawes, A., Henderson, N., Hernandez, J., Hernandez, R., Hines, S., Hladun, S. L., Hodgson, A., Hoques, M., Hollins, B., Howells, S., Hulyk, S., Hume, J., Idlebird, D., Jackson, A., Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jolivet, A., Karpathy, S., Kelly, S., Kelly, S., Khan, Z., King, B., Kovar, C., Kowis, C., Kratt, C. L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J., Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J., Maheshwari, M., Mahindartne, M., Mahmoud, M., Malloy, K., Mangum, A., Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, E., Mawhinney, S., McLeod, M., McNeill, T., Meenen, E., Milosavljevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S., Morgan, M., Morris, K., Morris, S., Munidasa, M., Murphy, M., Nair, L., Nankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S., Nwaokemele, O., Okwuonu, G., Olarunpungoon, A., Pal, S., Parks, K., Pasternak, S., Paul, H., Perez, A., Perez, L., Pfannkuch, C., Plopper, F., Poindexter, A., Popovic, D., Primus, E., Pu, L.-L., Puzo, M., Quiroz, J., Rachlin, E., Reeves, K., Regier, M. A., Reigh, R., Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, P., Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S. J., Sanders, W., Savery, G., Scherer, S., Scott, G., Shatsman, S., Shen, H., Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C. D., Smajls, D., Snead, A., Sodergren, E., Song, X.-Z., Sorelle, R., Sosa, J., Steimle, M., Strong, R., Sutton, A., Svatek, A., Tabor, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Usmani, K., Valas, R., Vera, V., Villagana, D., Waldron, L., Walker, B., Wang, J., Wang, Q., Wang, S., Warren, J., Warren, R., Wei, X., White, F., Williams, G., Willson, R., Wlarczyk, R., Wooden, H., Worley, K., Wright, R., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von Niederhausern, A., Weiss, R., Smith, D. R., Holt, R. A., Smith, H. O., Weinstock, G. and Gibbs, R. A.

Direct Submission

Unpublished

2 (bases 1 to 215356)

Worley, K. C.

Direct Submission

Submitted (17-SEP-2001) Human Genome Sequencing Center, Department

of Molecular and Human Genetics, Baylor College of Medicine, One

Baylor Plaza, Houston, TX 77030, USA

3 (bases 1 to 215356)

Rat Genome Sequencing Consortium.

Direct Submission

Submitted (10-MAY-2003) Human Genome Sequencing Center, Department

of Molecular and Human Genetics, Baylor College of Medicine, One

Baylor Plaza, Houston, TX 77030, USA

4 (bases 1 to 215356)

Worley, K. C.

Direct Submission

Submitted (01-JUL-2003) Human Genome Sequencing Center, Department

of Molecular and Human Genetics, Baylor College of Medicine, One

Baylor Plaza, Houston, TX 77030, USA

COMMENT

On Jul 1, 2003 this sequence version replaced gi:30521822.

Sequencing is completed to a minimum standard of double strand

coverage with a minimum of 2 clones and 2 reads with no ambiguities

or 2 chemistries with a minimum of 2 clones and 3 reads with no

ambiguities. If the sequence quality does not meet this standard,

it will be indicated in the annotation.

Location/Qualifiers

1. .215356

/organism="Rattus norvegicus"

/mol\_type="genomic DNA"

/db\_xref="taxon:10116"

/chromosome="1"

/clone="CH230-54P17"

805. .1138

/rpt\_family="LIMC2"

1148. .1232

/rpt\_family="PB1D9"

complement(1386..1506)

/rpt\_family="MTD"

1507. .1734

/rpt\_family="LIMC2"





Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,  
 Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.  
 Direct Submission  
 Submitted (23-NOV-2001) Whitehead Institute/MIT Center for Genome  
 Research, 320 Charles Street, Cambridge, MA 02141, USA  
 3 (bases 1 to 215958)  
 Birren,B., Nusbaum,C., Lander,E., Abouelleil,A., Allen,N.,  
 Anderson,S., Arachchi,H.M., Barna,N., Bastien,V., Bloom,T.,  
 Boguslavskiy,L., Boukhalter,B., Camarata,J., Chang,J., Choepel,Y.,  
 Collymore,A., Cook,A., Cooke,P., Corum,B., DeArillano,K.,  
 Diaz,J.S., Dodge,S., Dooley,K., Dorris,L., Erickson,J., Faro,S.,  
 Ferreira,P., Fitzgerald,M., Gage,D., Galagan,J., Gardyna,S.,  
 Graham,L., Grand-Pierre,N., Hafez,N., Hagopian,B., Hagos,B.,  
 Hall,J., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C.,  
 Kamat,A., Karatas,A., Kells,C., Landers,T., Levine,R.,  
 Lindblad-Toh,K., Liu,G., Lui,A., Mabbitt,R., Maclean,C.,  
 Macdonald,P., Major,J., Manning,J., Matthews,C., McCarthy,M.,  
 Meldrim,J., Meneus,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J.,  
 Nguyen,C., Nicol,R., Norbu,C., O'Connor,T., O'Donnell,P.,  
 O'Neill,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N.,  
 Rachupka,A., Ramasamy,U., Raymond,C., Retta,R., Rise,C., Rogov,P.,  
 Roman,J., Schauer,S., Schupack,R., Seaman,S., Severy,P., Smith,C.,  
 Spencer,B., Stange-Thomann,N., Stojanovic,N., Stubbs,M.,  
 Talamas,J., Tesfaye,S., Theodore,J., Topham,K., Travers,M.,  
 Vassiliev,H., Venkataraman,V.S., Viel,R., Vo,A., Wilson,B., Wu,X.,  
 Wyman,D., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.  
 Direct Submission  
 Submitted (24-JAN-2003) Whitehead Institute/MIT Center for Genome  
 Research, 320 Charles Street, Cambridge, MA 02141, USA  
 On Jan 24, 2003 this sequence version replaced gi:22381287.  
 All repeats were identified using RepeatMasker:  
 Smit, A.F.A. & Green, P. (1996-1997)  
 http://ftp.genome.washington.edu/RM/RepeatMasker.html

TITLE  
 JOURNAL  
 COMMENT

----- Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIBR

Web site: http://www-seq.wi.mit.edu

Contact: sequence\_submissions@genome.wi.mit.edu

----- Project Information

Center project name: L18028

Center clone name: 9\_K\_20

----- Summary Statistics

Sequencing vector: Plasmid; n/a; 100% of reads

Chemistry: Dye-terminator Big Dye; 100% of reads

Assembly program: Phrap; version 0.960731

Consensus quality: 214869 bases at least Q40

Consensus quality: 215183 bases at least Q30

Consensus quality: 215314 bases at least Q20

Insert size: 220000; agarose-fp

Insert size: 215558; sum-of-contigs

Quality coverage: 11.4 in Q20 bases; agarose-fp

Quality coverage: 11.6 in Q20 bases; sum-of-contigs

\*\*\*\*\* NOTE: This is a 'working draft' sequence. It currently  
 \* consists of 5 contigs. The true order of the pieces  
 \* is not known and their order in this sequence record is  
 \* arbitrary. Gaps between the contigs are represented as  
 \* runs of N, but the exact sizes of the gaps are unknown.  
 \* This record will be updated with the finished sequence  
 \* as soon as it is available and the accession number will  
 \* be preserved.

\* 1 16300: contig of 16300 bp in length  
 \* 16301 16400: gap of 100 bp  
 \* 16401 122337: contig of 105937 bp in length  
 \* 122338 122437: gap of 100 bp  
 \* 122438 139749: contig of 17312 bp in length  
 \* 139750 139849: gap of 100 bp  
 \* 139850 211515: contig of 71666 bp in length  
 \* 211516 211615: gap of 100 bp  
 \* 211616 215958: contig of 4343 bp in length.

FEATURES  
 source

Location/Qualifiers  
 1..215958  
 /organism="Mus musculus"

misc\_feature  
 1..16300  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:10090"  
 /clone="RP23-9K20"  
 /clone\_lib="RPCI-23 Female Mouse BAC"  
 /note="assembly\_fragment  
 clone\_end:SP6  
 vector\_side:left"  
 16401..122337  
 /note="assembly\_fragment"  
 122438..139749  
 /note="assembly\_fragment"  
 139850..211515  
 /note="assembly\_fragment"  
 211616..215958  
 /note="assembly\_fragment  
 clone\_end:T7  
 vector\_side:right"

# ORIGIN

Query Match 70.8%; Score 17; DB 2; Length 215958;  
 Best Local Similarity 70.6%; Pred.No.15;  
 Matches 12; Conservative 5; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 GCUGAAGGGGCUCAUGU 19  
 ||:|||||||:|:|:|:  
 Db 106591 GCTGAAGGGGCTTCATGT 106575

Search completed: May 27, 2004, 02:16:51  
 Job time : 510.783 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 26, 2004, 14:55:11 ; Search time 107.037 Seconds  
(without alignments)  
952.539 Million cell updates/sec

Title: US-09-121-239-19

Perfect score: 24

Sequence: 1 CCGUGAAGGCUCAUGUCCAC 24

Scoring table: OLIGO NUC

Gapop 60.0 , Gapext 60.0

Searched: 3373863 seqs, 2124099041 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : N\_Geneseq\_29Jan04.\*

- 1: Geneseqn1980s.\*
- 2: Geneseqn1990s.\*
- 3: Geneseqn2000s.\*
- 4: Geneseqn2001as.\*
- 5: Geneseqn2001bs.\*
- 6: Geneseqn2002s.\*
- 7: Geneseqn2003as.\*
- 8: Geneseqn2003bs.\*
- 9: Geneseqn2003cs.\*
- 10: Geneseqn2004s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	24	100.0	24	3	Aaz60857 Oligonucleotide
2	24	100.0	24	3	Aaz60855 Oligonucleotide
3	24	100.0	24	3	Aaz60858 Oligonucleotide
4	24	100.0	24	3	Aaz60856 Oligonucleotide
5	24	100.0	299	3	Aaz60864 Region su
6	24	100.0	3380	7	Abz18520 Group III
7	18	75.0	34125	6	Abse69903 Human ade
8	16	66.7	65	6	Abn54940 Mouse spl
9	16	66.7	751	4	Aai94531 Human neu
10	16	66.7	1044	4	Aas54224 Pseudomon
11	16	66.7	1044	7	ACA42504 Prokaryot
12	16	66.7	2278	3	Aaz289962 Corn ADA2
13	16	66.7	2599	3	Aaz256382 Escherich
14	16	66.7	3460	2	Aav36957 Nucleotid
15	16	66.7	3460	3	Aaz34989 Human cel
16	16	66.7	3460	6	Abx84482 Human cDN
17	16	66.7	6699	7	Abx08804 Angiogene
18	16	66.7	6699	7	Abx76302 Lung canc
19	16	66.7	185035	6	Abt10147 Human bre
20	16	66.7	185035	7	ACA64951 Human FEN
21	15	62.5	23	2	AAT56765 Human bcr
22	15	62.5	23	2	Aat56766 Human bcr
23	15	62.5	33	2	Aat10497 ABL oncoc

C	24	15	62.5	33	2	AAT10495	Aat10495 BCR-ABL O
C	25	15	62.5	40	2	AAQ57147	Aaq57147 Chromosom
C	26	15	62.5	47	2	AAQ66785	Aaq66785 Ribozyme
C	27	15	62.5	52	2	AAT12637	Aat12637 T7 promot
C	28	15	62.5	60	2	AAT29713	Aat29713 Chronic m
C	29	15	62.5	62	2	AAQ66774	Aaq66774 L6(1)31 r
C	30	15	62.5	63	6	ABS73178	Abse73178 DNA encod
C	31	15	62.5	80	2	AAQ34631	Aaq34631 Human Phl
C	32	15	62.5	80	2	AAV20460	Aav20460 Human bcr
C	33	15	62.5	205	6	ABL87455	Ab187455 Human ova
C	34	15	62.5	257	2	AAQ34625	Aaq34625 Human bcr
C	35	15	62.5	257	2	AAV20458	Aav20458 Human bcr
C	36	15	62.5	423	6	ABS73179	Abse73179 DNA encod
C	37	15	62.5	436	7	ABX40048	Abx40048 Bovine ES
C	38	15	62.5	483	7	ADA71111	Adg71111 Rice gene
C	39	15	62.5	549	6	ABS73314	Abse73314 DNA encod
C	40	15	62.5	729	7	ABZ66719	Abz66719 Orthosomy
C	41	15	62.5	921	5	AAS85025	Aas85025 DNA encod
C	42	15	62.5	922	6	ABS73180	Abse73180 DNA encod
C	43	15	62.5	1024	7	ABZ82900	Abz82900 Toxicolog
C	44	15	62.5	1079	5	AAS85026	Aas85026 DNA encod
C	45	15	62.5	1079	6	ABS73181	Abse73181 DNA encod

ALIGNMENTS

RESULT 1

ID	AAZ60857	standard; DNA; 24 BP.
XX	AAZ60857	
AC	AAZ60857	
DT	16-MAY-2000	(first entry)
XX		
DE	Oligonucleotide used to detect bcr b3-abl fusion transcripts.	
XX		
KW	Fusion transcript; translocation; bcr b3 region; abl gene;	
KW	amplification assay; detection assay; medical diagnosis;	
KW	clinical monitoring; chimeric RNA; fusion RNA; condition marker;	
KW	disease marker; cancer; leukemia; ss.	
XX		
OS	Synthetic.	
XX		
PN	WO200005418-A1.	
XX		
PD	03-FEB-2000.	
XX		
PF	23-JUL-1999; 99WO-US016832.	
XX		
PR	23-JUL-1998; 98US-00121239.	
XX		
PA	(GENP-) GEN-PROBE INC.	
XX		
PI	Harvey RC, Eastman PS;	
XX		
DR	WPI; 2000-182730/16.	
XX		
PT	Novel methods for preparing RNA from biological samples, used for the	
PT	detection and measurement of nucleic acids and fusion nucleic acids.	
XX		

Claim 19; Page 43; 49pp; English.

Oligonucleotides AAZ60840-62 and AAZ60865-66 are used in the method of the invention to detect fusion transcripts produced from a translocation between the bcr b3 region and the abl gene. The specification describes a method for detecting a fusion nucleic acid (particularly chimeric mRNA species), in a biological sample. The method comprises contacting a sample of fusion nucleic acid with primers, amplifying the hybridized fusion nucleic acid, and detecting the target hybrid. The method is used for the simple and rapid preparation of RNA from a biological sample, particularly from the cytoplasm of eukaryotic cells, which is suitable for use in an amplification and detection assay. The methods are used for

CC the analysis and detection of nucleic acids in biological samples. The  
 CC methods are useful in the human medical and veterinary fields, for  
 CC medical diagnoses and clinical monitoring of a patient's response to  
 CC therapy where a disease or medical condition is associated with a  
 CC particular type and/or level of mRNA present in the sample. The methods  
 CC are also useful for detecting or quantifying fusion or chimeric RNA  
 CC species, and for detecting a translocation as a marker for a given  
 CC condition or disease, e.g. translocations associate with cancers,  
 CC particularly forms of leukemia

XX Sequence 24 BP; 4 A; 8 C; 6 G; 6 T; 0 U; 0 Other;  
 SQ Query Match 100.0%; Score 24; DB 3; Length 24;  
 Best Local Similarity 75.0%; Pred. No. 0.00026;  
 Matches 18; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGCUGAAGGCGUUCUUGUCCAC 24  
 ||||:|||||:||||:|||||  
 Db 1 CCGCTGAAGGCTTCATGTTCCAC 24

RESULT 2  
 AAZ60855/c  
 ID AAZ60855 standard; DNA; 24 BP.  
 XX  
 AC AAZ60855;  
 XX  
 DT 16-MAY-2000 (first entry)  
 XX  
 DE Oligonucleotide used to detect bcr b3-abl fusion transcripts.  
 XX  
 KW Fusion transcript; translocation; bcr b3 region; abl gene;  
 KW amplification assay; detection assay; medical diagnosis;  
 KW clinical monitoring; chimeric RNA; fusion RNA; condition marker;  
 KW disease marker; cancer; leukemia; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200005418-A1.  
 XX  
 PD 03-FEB-2000.  
 XX  
 PF 23-JUL-1999; 99WO-US016832.  
 XX  
 PR 23-JUL-1998; 98US-00121239.  
 XX  
 PA (GENP-) GEN-PROBE INC.  
 XX  
 PI Harvey RC, Eastman PS;  
 XX  
 DR WPI; 2000-182730/16.  
 XX  
 PT Novel methods for preparing RNA from biological samples, used for the  
 PT detection and measurement of nucleic acids and fusion nucleic acids.  
 XX  
 PS Claim 19; Page 42; 49pp; English.  
 XX  
 CC Oligonucleotides AAZ60840-62 and AAZ60865-66 are used in the method of  
 CC the invention to detect fusion transcripts produced from a translocation  
 CC between the bcr b3 region and the abl gene. The specification describes a  
 CC method for detecting a fusion nucleic acid (particularly chimeric RNA  
 CC species), in a biological sample. The method comprises contacting a  
 CC sample of fusion nucleic acid with primers, amplifying the hybridized  
 CC fusion nucleic acid, and detecting the target hybrid. The method is used  
 CC for the simple and rapid preparation of RNA from a biological sample,  
 CC particularly from the cytoplasm of eukaryotic cells, which is suitable  
 CC for use in an amplification and detection assay. The methods are used for  
 CC the analysis and detection of nucleic acids in biological samples. The  
 CC methods are useful in the human medical and veterinary fields, for  
 CC medical diagnoses and clinical monitoring of a patient's response to  
 CC therapy where a disease or medical condition is associated with a  
 CC particular type and/or level of mRNA present in the sample. The methods  
 CC are also useful for detecting or quantifying fusion or chimeric RNA  
 CC species, and for detecting a translocation as a marker for a given  
 CC condition or disease, e.g. translocations associate with cancers,  
 CC particularly forms of leukemia

CC species, and for detecting a translocation as a marker for a given  
 CC condition or disease, e.g. translocations associate with cancers,  
 CC particularly forms of leukemia

XX Sequence 24 BP; 6 A; 6 C; 8 G; 4 T; 0 U; 0 Other;  
 SQ Query Match 100.0%; Score 24; DB 3; Length 24;  
 Best Local Similarity 75.0%; Pred. No. 0.00026;  
 Matches 18; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGCUGAAGGCGUUCUUGUCCAC 24  
 ||||:|||||:||||:|||||  
 Db 24 CCGCTGAAGGCTTCATGTTCCAC 1

RESULT 3  
 AAZ60858  
 ID AAZ60858 standard; RNA; 24 BP.  
 XX  
 AC AAZ60858;  
 XX  
 DT 16-MAY-2000 (first entry)  
 XX  
 DE Oligonucleotide used to detect bcr b3-abl fusion transcripts.  
 XX  
 KW Fusion transcript; translocation; bcr b3 region; abl gene;  
 KW amplification assay; detection assay; medical diagnosis;  
 KW clinical monitoring; chimeric RNA; fusion RNA; condition marker;  
 KW disease marker; cancer; leukemia; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200005418-A1.  
 XX  
 PD 03-FEB-2000.  
 XX  
 PF 23-JUL-1999; 99WO-US016832.  
 XX  
 PR 23-JUL-1998; 98US-00121239.  
 XX  
 PA (GENP-) GEN-PROBE INC.  
 XX  
 PI Harvey RC, Eastman PS;  
 XX  
 DR WPI; 2000-182730/16.  
 XX  
 PT Novel methods for preparing RNA from biological samples, used for the  
 PT detection and measurement of nucleic acids and fusion nucleic acids.  
 XX  
 PS Claim 19; Page 43; 49pp; English.  
 XX  
 CC Oligonucleotides AAZ60840-62 and AAZ60865-66 are used in the method of  
 CC the invention to detect fusion transcripts produced from a translocation  
 CC between the bcr b3 region and the abl gene. The specification describes a  
 CC method for detecting a fusion nucleic acid (particularly chimeric RNA  
 CC species), in a biological sample. The method comprises contacting a  
 CC sample of fusion nucleic acid with primers, amplifying the hybridized  
 CC fusion nucleic acid, and detecting the target hybrid. The method is used  
 CC for the simple and rapid preparation of RNA from a biological sample,  
 CC particularly from the cytoplasm of eukaryotic cells, which is suitable  
 CC for use in an amplification and detection assay. The methods are used for  
 CC the analysis and detection of nucleic acids in biological samples. The  
 CC methods are useful in the human medical and veterinary fields, for  
 CC medical diagnoses and clinical monitoring of a patient's response to  
 CC therapy where a disease or medical condition is associated with a  
 CC particular type and/or level of mRNA present in the sample. The methods  
 CC are also useful for detecting or quantifying fusion or chimeric RNA  
 CC species, and for detecting a translocation as a marker for a given  
 CC condition or disease, e.g. translocations associate with cancers,  
 CC particularly forms of leukemia

XX Sequence 24 BP; 4 A; 8 C; 6 G; 0 T; 6 U; 0 Other;

```
Query Match      100.0%; Score 24; DB 3; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.00026;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGCUGAAGGGCUCAUGUCCAC 24
    |||||
DB 1 CCGCUGAAGGGCUCAUGUCCAC 24

RESULT 4
AAZ60856/c
ID AAZ60856 standard; RNA; 24 BP.
XX
AC AAZ60856;
XX
KW Fusion transcript; translocation; bcr b3 region; abl gene;
KW amplification assay; detection assay; medical diagnosis;
KW clinical monitoring; chimeric RNA; fusion RNA; condition marker;
KW disease marker; cancer; leukemia; ss.
XX
OS Synthetic.
XX
FN WO200005418-A1.
XX
PD 03-FEB-2000.
XX
PF 23-JUL-1999; 99WO-US016832.
XX
PR 23-JUL-1998; 98US-00121239.
XX
PA (GENP-) GEN-PROBE INC.
XX
PI Harvey RC, Eastman PS;
XX
WPI; 2000-182730/16.
XX
PT Novel methods for preparing RNA from biological samples, used for the
PT detection and measurement of nucleic acids and fusion nucleic acids.
XX
PS Claim 19; Page 42; 49pp; English.
XX
CC Oligonucleotides AAZ60840-62 and AAZ60865-66 are used in the method of
CC the invention to detect fusion transcripts produced from a translocation
CC between the bcr b3 region and the abl gene. The specification describes a
CC method for detecting a fusion nucleic acid (particularly chimeric mRNA
CC species), in a biological sample. The method comprises contacting a
CC sample of fusion nucleic acid with primers, amplifying the hybridized
CC fusion nucleic acid, and detecting the target hybrid. The method is used
CC for the simple and rapid preparation of RNA from a biological sample,
CC particularly from the cytoplasm of eukaryotic cells, which is suitable
CC for use in an amplification and detection assay. The methods are used for
CC the analysis and detection of nucleic acids in biological samples. The
CC methods are useful in the human medical and veterinary fields, for
CC medical diagnoses and clinical monitoring of a patient's response to
CC therapy where a disease or medical condition is associated with a
CC particular type and/or level of mRNA present in the sample. The methods
CC are also useful for detecting or quantifying fusion or chimeric RNA
CC species, and for detecting a translocation as a marker for a given
CC condition or disease, e.g. translocations associate with cancers,
CC particularly forms of leukemia
XX
SQ Sequence 24 BP; 6 A; 6 C; 8 G; 0 T; 4 U; 0 Other;

Query Match      100.0%; Score 24; DB 3; Length 24;
Best Local Similarity 75.0%; Pred. No. 0.00026;
Matches 18; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGCUGAAGGGCUCAUGUCCAC 24
    |||||
DB 1 CCGCUGAAGGGCUCAUGUCCAC 142

RESULT 6
ABZ18520/c
DB 24 CCGCTGAAGGCTTCATGTTCCAC 1
    RESULT 5
    AAZ60864/c
    ID AAZ60864 standard; DNA; 299 BP.
    XX
    AC AAZ60864;
    XX
    DT 16-MAY-2000 (first entry)
    XX
    DE Region surrounding a splice junction in a normal abl transcript.
    XX
    KW Fusion transcript; translocation; bcr b3 region; abl gene;
    KW amplification assay; detection assay; medical diagnosis;
    KW clinical monitoring; chimeric RNA; fusion RNA; condition marker;
    KW disease marker; cancer; leukemia; ss.
    XX
    OS Unidentified.
    XX
    FN WO200005418-A1.
    XX
    PD 03-FEB-2000.
    XX
    PF 23-JUL-1999; 99WO-US016832.
    XX
    PR 23-JUL-1998; 98US-00121239.
    XX
    PA (GENP-) GEN-PROBE INC.
    XX
    PI Harvey RC, Eastman PS;
    XX
    WPI; 2000-182730/16.
    XX
    PT Novel methods for preparing RNA from biological samples, used for the
    PT detection and measurement of nucleic acids and fusion nucleic acids.
    XX
    PS Disclosure; Fig 3; 49pp; English.
    XX
    CC The present sequence represents a region surrounding a potential splice
    CC junction in a normal abl transcript. The specification describes
    CC oligonucleotides which are used to detect fusion transcripts produced
    CC from a translocation between the bcr b3 region and the abl gene. The
    CC specification also describes a method for detecting a fusion nucleic acid
    CC (particularly chimeric mRNA species), in a biological sample. The method
    CC comprises contacting a sample of fusion nucleic acid with primers,
    CC amplifying the hybridized fusion nucleic acid, and detecting the target
    CC hybrid. The method is used for the simple and rapid preparation of RNA
    CC from a biological sample, particularly from the cytoplasm of eukaryotic
    CC cells, which is suitable for use in an amplification and detection assay.
    CC The methods are used for the analysis and detection of nucleic acids in
    CC biological samples. The methods are useful in the human medical and
    CC veterinary fields, for medical diagnoses and clinical monitoring of a
    CC patient's response to therapy where a disease or medical condition is
    CC associated with a particular type and/or level of mRNA present in the
    CC sample. The methods are also useful for detecting or quantifying fusion
    CC or chimeric RNA species, and for detecting a translocation as a marker
    CC for a given condition or disease, e.g. translocations associate with
    CC cancers, particularly forms of leukemia
    XX
    SQ Sequence 299 BP; 77 A; 70 C; 81 G; 71 T; 0 U; 0 Other;

Query Match      100.0%; Score 24; DB 3; Length 299;
Best Local Similarity 75.0%; Pred. No. 0.00028;
Matches 18; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGCUGAAGGGCUCAUGUCCAC 24
    |||||
DB 165 CCGCTGAAGGCTTCATGTTCCAC 142

RESULT 6
ABZ18520/c
```

ID ABZ18520 standard; cDNA; 3380 BP.  
 AC ABZ18520;  
 XX  
 XX  
 DT 23-JAN-2003 (first entry)  
 XX  
 XX Group III CDNA cancer related clone SEQ ID NO:946.  
 DE  
 XX Human; cancer; tumour; therapy; diagnosis; CT antigen; CP antigen;  
 KW immune response; virology; immunology; microbiology; molecular biology;  
 KW recombinant DNA technology; gene; ss.  
 XX  
 XX Homo sapiens.  
 OS  
 XX WO200278516-A2.  
 PN  
 XX 10-OCT-2002.  
 PD  
 XX 28-MAR-2002; 2002WO-US010421.  
 XX  
 XX 30-MAR-2001; 2001US-0280255P.  
 PR  
 XX 28-AUG-2001; 2001US-0315563P.  
 PR  
 XX 09-JAN-2002; 2002US-0347313P.  
 XX  
 XX (CORI-) CORIXA CORP.  
 PA  
 XX Wang T, Wang S, Bangur CS, Gaiger A;  
 PI  
 XX WPI; 2003-058387/05.  
 DR  
 XX  
 XX New immunogenic polynucleotides or polypeptides useful for diagnosing,  
 PT preventing and treating cancer expressing CT or CP mRNA antigens, and in  
 PT virology, immunology, microbiology, molecular biology and recombinant DNA  
 PT techniques.  
 XX  
 XX Claim 1; SEQ ID NO 946; 207pp; English.  
 PS  
 XX ABQ17575 to ABQ20506 represent isolated polynucleotide (I) sequences, and  
 CC ABP54446 to ABP54472 represent protein (II) sequences, from the present  
 CC invention. (I) and (II) have cytostatic activity and can be used in gene  
 CC therapy and vaccines. (I), (II), antibodies and compositions from the  
 CC present invention are useful for diagnosing, preventing and treating  
 CC cancer, which expresses CT or CP mRNA antigens. They are useful for  
 CC stimulating immune response. They can also be useful in virology,  
 CC immunology, microbiology, molecular biology and recombinant DNA  
 CC techniques. N.B. The sequence data for this patent did not form part of  
 CC the printed specification, but was obtained in electronic format directly  
 CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 3380 BP; 819 A; 1005 C; 989 G; 567 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 24; DB 7; Length 3380;  
 Best Local Similarity 75.0%; Pred. No. 0.00029;  
 Matches 18; Conservative 6; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 CCGCGAAGGGGCUCAUGUCCAC 24  
 DB 80 CCGCTGAGGGCTTCATGTTCCAC 57  
 RESULT 7  
 ID ABS69903  
 XX ABS69903 standard; DNA; 34125 BP.  
 AC ABS69903;  
 XX  
 XX 21-NOV-2002 (first entry)  
 DT  
 XX Human adenovirus type 12 genome sequence.  
 DE  
 XX Vector; adenovirus; adeno-associated; adenosine deaminase gene; receptor;  
 KW adenosine deaminase deficiency; severe combined immune deficiency; PAH;  
 KW beta-chain; haemoglobin gene; beta-thalassaemia; sickle cell disease;

KW low density lipoprotein gene; familial hypercholesterolaemia;  
 KW hypoxanthine-guanine phosphoribosyltransferase; Lesch-Nyhan syndrome;  
 KW phenylalanine hydroxylase gene; gene therapy; phenylketonuria;  
 KW dystrophin gene; muscular dystrophy; cystic fibrosis; immunostimulant;  
 KW human cystic fibrosis transmembrane conductance regulator gene;  
 KW antianemic; antilipemic; nontropic; cytostatic; dermatological;  
 KW human adenovirus genome; ds.  
 XX  
 XX Human adenovirus type 12.  
 OS  
 XX US2002102731-A1.  
 PN  
 XX 01-AUG-2002.  
 PD  
 XX 12-FEB-2001; 2001US-00782378.  
 PF  
 XX 02-OCT-2000; 2000US-0237747P.  
 PR  
 XX (UYN ) UNIV NEW YORK STATE RES FOUND.  
 PA  
 XX Hearing P, Bahou WF, Sandalon Z, Gnatenko DV;  
 PI  
 XX WPI; 2002-690619/74.  
 XX  
 XX Producing vector, by introducing vector having nucleotide sequence,  
 PT adenovirus inverted terminal repeats and packaging sequence, and adeno-  
 PT associated virus terminal repeat, into cell, and culturing cell.  
 XX  
 PS Disclosure; Page 135-150; 191pp; English.  
 XX  
 XX The present invention relates to a new method of producing a vector. The  
 CC method involves introducing recombinant vector having nucleotide sequence  
 CC (NS) having 5' and 3' end, left and right inverted terminal repeats of  
 CC adenovirus flanking NS, adenovirus packaging sequence linked to inverted  
 CC terminal repeat, and adeno-associated virus terminal repeat linked to 3'  
 CC end of NS, into cell expressing adenovirus early gene lacking from vector  
 CC ; and culturing cell to produce another vector. The method is useful for  
 CC generating vectors, especially mAd vectors. The method is useful in  
 CC transferring nucleotide sequences of interest into a cell, for gene  
 CC transfer applications (e.g. gene therapy) in vitro, ex vivo and in vivo.  
 CC The nucleotide sequences are useful for treating diseases associated with  
 CC it, i.e. adenosine deaminase gene associated with adenosine deaminase  
 CC deficiency with severe combined immune deficiency, beta-chain of  
 CC haemoglobin gene associated with beta-thalassaemia and sickle cell  
 CC disease, receptor for low density lipoprotein gene associated with  
 CC familial hypercholesterolaemia, hypoxanthine-guanine  
 CC phosphoribosyltransferase associated with Lesch-Nyhan syndrome,  
 CC phenylalanine hydroxylase (PAH) gene associated with phenylketonuria,  
 CC dystrophin gene associated with muscular dystrophy, and human cystic  
 CC fibrosis transmembrane conductance regulator gene associated with cystic  
 CC fibrosis. The present nucleic acid sequence represents a human adenovirus  
 CC genome sequence that was used in the methods of the invention  
 XX  
 SQ Sequence 34125 BP; 9330 A; 8012 C; 7864 G; 8919 T; 0 U; 0 Other;  
 Query Match 75.0%; Score 18; DB 6; Length 34125;  
 Best Local Similarity 66.7%; Pred. No. 0.95;  
 Matches 12; Conservative 6; Mismatches 0; Indels 0; Gaps 0;  
 OY 5 UGAAGGGCUCAUGUCC 22  
 DB 3998 TGAAGGGCTTCATGTTCC 4015  
 RESULT 8  
 ABNS4940/c  
 ID ABNS4940 standard; DNA; 65 BP.  
 XX  
 XX AC ABNS4940;  
 XX  
 XX 15-JUL-2002 (first entry)  
 DT  
 XX Mouse spliced transcript detection oligonucleotide SEQ ID NO:27688.  
 DE

XX Human; mouse; rat; splice transcript; detection; RNA transcript;  
 KW splice variant; transcriptome; oligonucleotide library; ss.  
 XX  
 OS Mus musculus.  
 PN WO200210449-A2.  
 PD 07-FEB-2002.  
 XX  
 PF 20-JUL-2001; 2001WO-IB001903.  
 XX  
 PR 28-JUL-2000; 2000US-0221607P.  
 PR 02-MAY-2001; 2001US-0287724P.  
 XX  
 PA (COMP-) COMPUGEN INC.  
 XX  
 PI Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;  
 XX  
 DR WPI; 2002-257383/30.  
 XX  
 PT New oligonucleotide libraries comprising oligonucleotides which  
 PT selectively hybridize to mRNAs transcribed from a transcription unit of a  
 PT genome, useful for detecting tissue-, pathology-, and developmental-  
 PT specific genes.  
 XX  
 PS Example 1; SEQ ID NO 27688; 47pp; English.  
 XX  
 CC The present invention describes oligonucleotide libraries for detecting  
 CC messenger RNAs that populate a (sub-)transcriptome, where the (sub-  
 CC )transcriptome comprises messenger RNAs transcribed from multiple  
 CC transcription units that populate a genome. The library comprises several  
 CC oligonucleotides, each capable of hybridizing selectively to a set of  
 CC messenger RNAs transcribed from a given transcription unit of the genome,  
 CC which encodes one or more messenger RNA splice variants. The  
 CC oligonucleotide libraries are useful for detecting mRNAs from a  
 CC biological sample, in expression profiling studies, in qualitatively or  
 CC quantitatively characterizing the corresponding transcriptome, and in  
 CC detecting RNA transcripts and splice variants of human or animal  
 CC transcriptomes. The libraries may also be used as specialised mini  
 CC libraries to detect transcripts of a sub-transcriptome under a particular  
 CC biological or pathological state, and so allowing the detection of tissue  
 CC - and pathology-specific genes such as those genes only expressed in  
 CC specific tissue under a specific pathological condition; to detect  
 CC developmental specific genes; and to detect RNA transcripts and splice  
 CC variants of a transcriptome of a patient suffering from a particular  
 CC disorder. ABN27253 to ABN59589 represent oligonucleotide sequences from  
 CC rats, humans and mice, which are used in the exemplification of the  
 CC present invention. N.B. The sequence data for this patent did not form  
 CC part of the printed specification, but was obtained in electronic format  
 CC directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 65 BP; 18 A; 16 C; 19 G; 12 T; 0 U; 0 Other;  
 Query Match 66.7%; Score 16; DB 6; Length 65;  
 Best Local Similarity 68.8%; Pred. No. 12;  
 Matches 11; Conservative 5; Mismatches 0; Indels 0; Gaps 0;  
 QY 9 GGGCTTCATGTTCCAC 24  
 DB 22 GGGCTTCATGTTCCAC 7  
 RESULT 9  
 AA194531  
 ID AA194531 standard; cDNA; 751 BP.  
 XX  
 AC AA194531;  
 XX  
 DT 13-NOV-2001 (first entry)  
 DE Human neuroblastoma expressed polynucleotide SEQ ID NO 606.  
 XX

KW Human; neuroblastoma; malignancy; cancer; tumour marker; N-myc; TrkA; ss.  
 XX Homo sapiens.  
 XX WO200166719-A1.  
 PD 13-SEP-2001.  
 XX  
 PF 02-MAR-2001; 2001WO-JP001629.  
 XX  
 PR 07-MAR-2000; 2000JP-00159195.  
 XX  
 PA (CHIB-) CHIBA PREFECTURE.  
 PA (HISM ) HISAMITSU PHARM CO LTD.  
 XX  
 PI Nakagawara A;  
 XX  
 DR WPI; 2001-565584/53.  
 XX  
 PT Nucleic acids originating in gene expressed in human neuroblastoma,  
 PT useful as probe or primer in diagnosing prognosis of human neuroblastoma,  
 PT malignancy and susceptibility indicator or tumor marker for anti-cancer  
 PT agents.  
 XX  
 PS Claim 1; Page 485; 2979pp; Japanese.  
 XX  
 CC The invention relates to novel genes (AA193926-AA197963) expressed in  
 CC human neuroblastoma. The nucleic acids are applicable as a probe or  
 CC primer in diagnosing the prognosis of human neuroblastoma, malignancy and  
 CC susceptibility indicators or tumour markers for anti-cancer agents. The  
 CC gene information for diagnosing prognosis is related to factors similar  
 CC to that for N-myc and TrkA genes  
 SQ Sequence 751 BP; 176 A; 176 C; 215 G; 157 T; 0 U; 27 Other;  
 Query Match 66.7%; Score 16; DB 4; Length 751;  
 Best Local Similarity 75.0%; Pred. No. 12;  
 Matches 12; Conservative 4; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 GCUGAAGGGCUUCAUG 18  
 DB 548 GCTGAAGGGCTTCATG 563  
 RESULT 10  
 AA54224/c  
 ID AA54224 standard; DNA; 1044 BP.  
 XX  
 AC AA54224;  
 XX  
 DT 13-FEB-2002 (first entry)  
 XX  
 DE Pseudomonas aeruginosa DNA for cellular proliferation protein #355.  
 XX  
 KW Antisense; ds; prokaryotic cellular proliferation gene; antibiotic;  
 KW antibacterial; drug design.  
 XX  
 OS Pseudomonas aeruginosa.  
 XX  
 PN WO200170955-A2.  
 PD 27-SEP-2001.  
 XX  
 PF 21-MAR-2001; 2001WO-US009180.  
 XX  
 PR 21-MAR-2000; 2000US-0191078P.  
 PR 23-MAY-2000; 2000US-0206848P.  
 PR 26-MAY-2000; 2000US-0207727P.  
 PR 23-OCT-2000; 2000US-0242578P.  
 PR 27-NOV-2000; 2000US-0253625P.  
 PR 22-DEC-2000; 2000US-0257931P.  
 PR 16-FEB-2001; 2001US-0269308P.  
 XX

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PA (ELIT-) ELITRA PHARM INC.
XX
XX Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;
PI Yamamoto RT, Xu HH;
XX
XX WPI; 2001-611495/70.
DR P-PSDB; AAU36365.
XX
XX New polynucleotides for the identification and development of
PT antibiotics, comprise sequences of antisense nucleic acids.
XX
XX Claim 27; SEQ ID NO 7861; 51lpp; English.
XX
XX The invention relates to antisense inhibitors of genes essential to
CC prokaryotic cellular proliferation, their use in identifying the genes,
CC their use in the discovery of novel antibiotics, the essential genes
CC themselves and the encoded proteins. The prokaryotes used are Escherichia
CC coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae,
CC Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also
CC useful for the identification of potential new targets for antibiotic
CC development. The antisense nucleic acids can also be used to identify
CC proteins used in proliferation, to express these proteins, and to obtain
CC antibodies capable of binding to the expressed proteins. The proteins can
CC be used to screen compounds in rational drug discovery programmes. The
CC antisense nucleic acid sequence is also useful to screen for homologous
CC nucleic acids which are required for cell proliferation in a wide variety
CC of organisms. The present sequence encodes an essential prokaryotic
CC cellular proliferation protein. Note: The sequence data for this patent
CC did not form part of the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 1044 BP; 159 A; 373 C; 334 G; 178 T; 0 U; 0 Other;

Query Match 66.7%; Score 16; DB 4; Length 1044;
Best Local Similarity 81.2%; Pred. No. 13;
Matches 13; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGCUGAAGGGCUUCA 16
Db ||||:|||||:|:|

812 CCGCTGAAGGGCTTCA 797

RESULT 11
ACA42504/c
ID ACA42504 standard; DNA; 1044 BP.
XX
XX ACA42504;
XX
XX 19-JUN-2003 (first entry)
XX
XX Prokaryotic essential gene #24161.
XX
XX Antisense; ds; prokaryotic essential gene; cell proliferation;
XX drug design; gene.
XX
XX Pseudomonas aeruginosa.
XX
XX WO20027183-A2.
XX
XX 03-OCT-2002.
XX
XX 21-MAR-2002; 2002WO-US009107.
XX
XX 21-MAR-2001; 2001US-00815242.
XX 06-SEP-2001; 2001US-00948993.
XX 25-OCT-2001; 2001US-0342923P.
XX 08-FEB-2002; 2002US-00072851.
XX 06-MAR-2002; 2002US-0362699P.
XX
XX (ELIT-) ELITRA PHARM INC.
XX
XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
PI

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PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
XX
XX WPI; 2003-029926/02.
DR P-PSDB; ABU38634.
XX
XX New antisense nucleic acids, useful for identifying proteins or screening
PT for homologous nucleic acids required for cellular proliferation to
PT isolate candidate molecules for rational drug discovery programs.
XX
XX Claim 14; SEQ ID NO 30374; 1766pp; English.
XX
XX The invention relates to an isolated nucleic acid comprising any one of
CC the 6213 antisense sequences given in the specification where expression
CC of the nucleic acid inhibits proliferation of a cell. Also included are:
CC (1) a vector comprising a promoter operably linked to the nucleic acid
CC encoding a polypeptide whose expression is inhibited by the antisense
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC polypeptide or its fragment whose expression is inhibited by the
CC antisense nucleic acid; (4) an antibody capable of specifically binding
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
CC proliferation or the activity of a gene in an operon required for
CC proliferation; (7) identifying a compound that influences the activity of
CC the gene product or that has an activity against a biological pathway
CC required for proliferation, or that inhibits cellular proliferation; (8)
CC identifying a gene required for cellular proliferation or the biological
CC pathway in which a proliferation-required gene or its gene product lies
CC or a gene on which the test compound that inhibits proliferation of an
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC compound's activity; (11) a culture comprising strains in which the gene
CC product is overexpressed or underexpressed; (12) determining the extent
CC to which each of the strains is present in a culture or collection of
CC strains; or (13) identifying the target of a compound that inhibits the
CC proliferation of an organism. The antisense nucleic acids are useful for
CC identifying proteins or screening for homologous nucleic acids required
CC for cellular proliferation to isolate candidate molecules for rational
CC drug discovery programs, or for screening homologous nucleic acids
CC required for proliferation in cells other than S. aureus, S. typhimurium,
CC K. pneumoniae or P. aeruginosa. The present sequence is one of the target
CC prokaryotic essential genes. Note: The sequence data for this patent did
CC not form part of the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 1044 BP; 159 A; 373 C; 334 G; 178 T; 0 U; 0 Other;

Query Match 66.7%; Score 16; DB 7; Length 1044;
Best Local Similarity 81.2%; Pred. No. 13;
Matches 13; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGCUGAAGGGCUUCA 16
Db ||||:|||||:|:|

812 CCGCTGAAGGGCTTCA 797

RESULT 12
AAZ89962/c
ID AAZ89962 standard; cDNA; 2278 BP.
XX
XX AAZ89962;
XX
XX 05-MAY-2000 (first entry)
XX
XX Corn ADA2 transcription co-activator nucleotide sequence.
XX
XX ADA2; transcription co-activator; adaptor; plant breeding; corn; ss;
XX transgenic plant.
XX
XX Zea mays.
XX
XX WO200003026-A2.
XX
XX 20-JAN-2000.
XX
XX

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PF 12-JUL-1999; 99WO-US015664.
XX
PR 13-JUL-1998; 98US-0092659P.
XX
XX (DUPO ) DU PONT DE NEMOURS & CO E I.
XX
PI Cahoon RE, Liu Z, Odell JT, Sakai H;
XX
XX WPI; 2000-160931/14.
DR P-PSDB; AAY78518.
XX
XX New isolated nucleic acid fragment encoding a transcription coactivator
PT in plants and seeds useful as a probe to isolate genes encoding
PT homologous proteins from other plant species, and as a primer.
XX
XX Claim 3; Page 29-30; 42pp; English.
XX
XX This sequence represents an ADA2 transcription adaptor/co-activator. In
CC yeast ADA2 functionally interacts with the acidic activation domain of
CC transcriptional activators. The invention relates to ADA2 nucleotide and
CC protein sequences, and also to a chimeric gene comprising of the ADA2
CC nucleotide sequence operably linked to a suitable regulatory sequence.
CC The ADA2 nucleotide sequence can be used as a DNA hybridization probe to
CC screen libraries from any desired plant and to isolate cDNAs and genes
CC encoding other ADA2 transcription adaptors, either as cDNAs or genomic
CC DNAs from the same or other plant species. The ADA2 nucleotide sequence
CC is also used as a primer to amplify longer nucleic acid fragments
CC encoding homologous genes from DNA or RNA. The ADA2 nucleotide and
CC peptide sequences are used in the immunological screening of cDNA
CC expression libraries. The nucleotide sequence is used to create
CC transgenic plants in which the protein is present at higher or lower
CC levels than normal or in cell types or developmental stages in which they
CC are not normally found. This would have the effect of altering the level
CC of transcription initiation in those cells. The ADA2 protein is used to
CC prepare antibodies which are useful for detecting them in situ in cells
CC or in vitro in cell extracts. All or a substantial portion of the ADA2
CC nucleotide sequence is used as probes for genetically and physically
CC mapping the genes that they are a part of, and as markers of traits
CC linked to those genes. Such information may be useful in plant breeding
CC in order to develop lines with desired phenotypes. In addition, they are
CC used to probe southern blots containing restriction endonuclease-treated
CC genomic DNAs of a set of individuals representing parent and progeny of a
CC defined genetic cross. Loss of function mutant phenotypes for the cDNA
CC clones identified by target gene disruption or by identifying specific
CC mutants for the genes contained in maize population carrying mutations in
CC all possible genes, are used for producing a plant containing a mutation
CC in the endogenous gene encoding ADA2. This mutant plant can then be used
CC to determine or confirm the natural function of ADA2
XX
XX SQ Sequence 2278 BP; 669 A; 451 C; 590 G; 561 T; 0 U; 7 Other;
Query Match 66.7%; Score 16; DB 3; Length 2278;
Best Local Similarity 68.8%; Pred. No. 13;
Matches 11; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 7 AAGGGCUCAUGUCC 22
Db 1289 AAGGGCTTCATGTTCC 1274

RESULT 13
AAZ56382/c
ID AAZ56382 standard; DNA; 2599 BP.
XX
XX AAZ56382;
XX
XX 17-MAR-2000 (first entry)
XX
XX Escherichia coli flagellin protein nucleotide sequence SEQ ID NO:52.
DE
XX Flagellin; fliC; antigen; detection; ds.
XX
XX Escherichia coli.
OS

PF 10-JUL-1999; 99WO-AU000385.
XX
PR 02-DEC-1999.
XX
XX 21-MAY-1999; 99WO-AU000385.
XX
PR 21-MAY-1998; 98AU-00003634.
XX
XX (UNSY ) UNIV SYDNEY.
XX
XX Reeves PR, Wang L;
XX
XX WPI; 2000-072598/06.
DR
XX
XX Novel nucleic acid molecule useful for the detection of flagellated
PT bacterial strains in food, feces, etc.
XX
XX Claim 3; Page 226-227; 245pp; English.
XX
XX AAZ56331 to AAZ56398 represent nucleic acid molecules (I) encoding all or
CC part of an Escherichia coli flagellin protein except a protein expressed
CC by E. coli H1, H7, H12 or H48 type strains. The present invention also
CC describes a method of detecting the presence of E. coli of a particular H
CC serotype in a sample, comprising specifically hybridising a nucleic acid,
CC preferably at least a pair, derived from a flagellating gene, specific
CC for a particular flagellin gene associated with the H serotype, to any
CC E. coli in the sample which contain the gene, and detecting any hybridised
CC molecules, identifying the presence of that serotype in the sample. (I)
CC are useful for: (1) detecting the presence of E. coli of H serotype in a
CC sample by hybridising at least one or a pair of (I) to any E. coli in the
CC sample and detecting the hybridised nucleic acid molecules; and (2) for
CC detecting the presence of both O and H-serotypes of E. coli by
CC hybridising at least one or a pair of (I) to any E. coli present in the
CC sample and detecting the hybridised nucleic acid molecules. (I) is
CC particularly useful for detecting the combination of O and H antigen.
CC Hybridised (I) when using at least one (I) is detected by southern blot
CC analysis and, when using a pair of (I), is detected by polymerase chain
CC reaction (PCR). AAZ56399 to AAZ56420 represent primers used in the
CC exemplification of the present invention
XX
XX SQ Sequence 2599 BP; 708 A; 651 C; 615 G; 625 T; 0 U; 0 Other;
Query Match 66.7%; Score 16; DB 3; Length 2599;
Best Local Similarity 62.5%; Pred. No. 13;
Matches 10; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 5 UGAGGGCUCAUGUU 20
Db 1072 TGAGGGCTTCATGTT 1057

RESULT 14
AAV36957
ID AAV36957 standard; cDNA; 3460 BP.
XX
XX AAV36957;
XX
XX 26-OCT-1998 (first entry)
XX
XX Nucleotide sequence of human ClqR gene.
DE
XX
XX Human; Clq receptor protein; ClqR; phagocytosis; complement;
KW immune system; inflammation; prophylactic; genetic immune deficiency;
KW HIV; cancer; chemotherapy; inhibition; vasculitis; sepsis; Fragment;
KW primer; probe; antibody; ss.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH 149..2107
FT CDS /*tag= a
FT /product= "ClqR gene product"

```

```

XX WO9822584-A1.
XX PD
XX 28-MAY-1998.
XX PF 12-NOV-1997; 97WO-US021205.
XX PR 18-NOV-1996; 96US-00751305.
XX PA (REGC ) UNIV CALIFORNIA.
XX PI Tenner AJ, Nepomuceno RR;
XX DR WPI; 1998-312470/27.
XX DR P-PSDB; AAW49879.
XX PT New complement C1q receptor - and methods for identifying modulators,
XX PT useful for controlling phagocytosis, e.g. to prevent infection or to
XX PT treat sepsis.
XX PS Claim 3; Fig 3A-3C; 99pp; English.
XX CC This is the nucleotide sequence of the novel human C1q receptor (C1qR)
XX CC gene, used in the method of the invention to identify modulators useful
XX CC for the control of phagocytosis. Delivering the C1qR nucleic acid to a
XX CC cell (in vivo, in vitro or ex vivo) alters the level of C1qR mRNA. C1qR
XX CC stimulates the complement component of the immune system, particularly
XX CC phagocytosis, without simultaneous increase in inflammation. C1qR
XX CC regulation is used for prophylactic treatment of subjects at risk of
XX CC infection (e.g. those with genetic immune deficiency, human immune
XX CC deficiency virus infection, undergoing cancer chemotherapy or high risk
XX CC surgery), also for treating cancer. Antisense or similar sequences are
XX CC used to inhibit phagocytosis or the complement component of immunity,
XX CC e.g. in cases of vasculitis or sepsis. Fragments of C1qR are useful as
XX CC primers and probes for detecting C1qR and related nucleic acids. C1qR
XX CC polypeptides and antibodies are all useful for treating disorders
XX CC involving the complement component or immune deficiencies
XX SQ Sequence 3460 BP; 764 A; 943 C; 996 G; 757 T; 0 U; 0 Other;

Query Match 66.7%; Score 16; DB 2; Length 3460;
Best Local Similarity 81.2%; Pred. No. 13;
Matches 13; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGCUGAGGGCUUCA 16
Db ||||:|||||:|
476 CCGCTGAGGGCTTCA 491

RESULT 15
AAZ34989
ID AAZ34989 standard; cDNA; 3460 BP.
XX AC AAZ34989;
XX DT
XX 28-FEB-2000 (first entry)
XX DE Human cell surface receptor C1qR cDNA.
XX C1qR; receptor; cell surface; transmembrane; glycoprotein; human;
XX KW host defence; infection; HIV; therapy; immunodeficiency; immunostimulant;
XX KW phagocytosis; signal transduction; ss.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX CDS 149..2107
FT /*tag= a
FT sig_peptide 149..211
FT /*tag= b
FT mat_peptide 212..2104
FT /*tag= b
XX

```

```

PN WO9955839-A1.
XX PD
XX 04-NOV-1999.
XX PF 29-APR-1999; 99WO-US009335.
XX PR 30-APR-1998; 98US-00071386.
XX PA (REGC ) UNIV CALIFORNIA.
XX PI Tenner AJ, Nepomuceno RR;
XX DR WPI; 2000-062021/05.
XX DR P-PSDB; AAY32345.
XX PT A new cell surface receptor protein used as a prophylactic for
XX PT individuals at risk from infection, e.g. HIV.
XX PS Claim 5; Fig 3; 49pp; English.
XX CC This is the nucleotide sequence of isolated cDNA coding for a novel human
XX CC cell surface transmembrane glycoprotein receptor designated C1qR (see
XX CC AAY32345). The cDNA was obtained from a U937 library by PCR using primers
XX CC based on tryptic peptides of C1qR. The receptor plays a role in
XX CC stimulating the classic complement component of the immune system,
XX CC specifically in stimulating phagocytosis in cells without a concomitant
XX CC increase in inflammation. A method of hybridisation based on the C1qR
XX CC nucleic acid sequence is provided, as well as methods for detecting novel
XX CC ligands for C1qR, including those which function as agonists or
XX CC antagonists. C1qR nucleic acid or recombinant protein can be used to
XX CC effect the role of the classical complement component of the immune
XX CC system. Transgenic animals may be created to aid in the study of the role
XX CC of C1qR during growth and metabolism and as a model for disease states
XX CC in which the normal level of C1qR is effected. The ability to regulate
XX CC the phagocytic capacity of myeloid cells via the regulation of cell
XX CC surface expression and function of C1qR will be valuable as a
XX CC prophylactic treatment of individuals at risk from infection,
XX CC particularly those with genetic immunodeficiencies, HIV infection, or
XX CC undergoing cancer chemotherapy or high risk surgery
XX SQ Sequence 3460 BP; 764 A; 943 C; 996 G; 757 T; 0 U; 0 Other;

Query Match 66.7%; Score 16; DB 3; Length 3460;
Best Local Similarity 81.2%; Pred. No. 13;
Matches 13; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGCUGAGGGCUUCA 16
Db ||||:|||||:|
476 CCGCTGAGGGCTTCA 491

Search completed: May 26, 2004, 16:52:25
Job time : 107.037 secs

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: May 26, 2004, 16:02:51 ; Search time 20.2274 Seconds  
(without alignments)  
658.454 Million cell updates/sec

Title: US-09-121-239-19  
Perfect score: 24  
Sequence: 1 CCGUGAAGGCUUACUUCAC 24

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 682709 seqs, 277475446 residues

Word size : 0  
Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents NA.\*  
1: /cgn2\_6/ptodata/2/ina/5A COMB.seq.\*  
2: /cgn2\_6/ptodata/2/ina/5B COMB.seq.\*  
3: /cgn2\_6/ptodata/2/ina/6A COMB.seq.\*  
4: /cgn2\_6/ptodata/2/ina/6B COMB.seq.\*  
5: /cgn2\_6/ptodata/2/ina/PTUS COMB.seq.\*  
6: /cgn2\_6/ptodata/2/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	16	66.7	306	4	US-09-252-991A-6328
C 2	16	66.7	897	4	US-09-252-991A-6056
C 3	16	66.7	1536	4	US-09-252-991A-6218
C 4	16	66.7	3460	2	US-08-751-305-1
C 5	15	62.5	23	1	US-08-363-233B-21
C 6	15	62.5	23	1	US-08-363-233B-22
C 7	15	62.5	33	3	US-08-793-408-9
C 8	15	62.5	33	3	US-08-793-408-11
C 9	15	62.5	33	3	US-09-139-762A-9
C 10	15	62.5	33	3	US-09-139-762A-11
C 11	15	62.5	47	3	US-08-448-446B-12
C 12	15	62.5	62	3	US-08-448-446B-1
C 13	15	62.5	80	1	US-08-152-621-7
C 14	15	62.5	80	1	US-08-306-691B-38
C 15	15	62.5	80	5	PCT-US92-05035-7
C 16	15	62.5	204	5	PCT-US93-06251-5
C 17	15	62.5	257	1	US-08-152-621-1
C 18	15	62.5	257	1	US-08-306-691B-36
C 19	15	62.5	257	5	PCT-US92-05035-1
C 20	15	62.5	1818	4	US-09-252-991A-3290
C 21	15	62.5	2115	4	US-09-252-991A-3388
C 22	15	62.5	3623	1	US-08-306-691B-35
C 23	15	62.5	30001	1	US-08-125-468-1
C 24	15	62.5	30001	2	US-08-474-933-1
C 25	14	58.3	23	1	US-08-152-621-34
C 26	14	58.3	23	1	US-08-363-233B-24
C 27	14	58.3	23	1	US-08-363-233B-25

C 28	14	58.3	23	5	PCT-US92-05035-34
C 29	14	58.3	25	4	US-09-168-947-31
C 30	14	58.3	26	1	US-08-152-621-29
C 31	14	58.3	26	1	US-08-152-621-33
C 32	14	58.3	26	1	US-08-306-691B-1
C 33	14	58.3	26	1	US-08-306-691B-2
C 34	14	58.3	26	3	US-09-341-955-1
C 35	14	58.3	26	4	US-09-779-881-1
C 36	14	58.3	26	5	PCT-US92-05035-29
C 37	14	58.3	26	5	PCT-US92-05035-33
C 38	14	58.3	26	5	PCT-US93-07541-12
C 39	14	58.3	26	5	PCT-US93-07541-25
C 40	14	58.3	42	2	US-08-768-177-3
C 41	14	58.3	42	3	US-08-991-675A-3
C 42	14	58.3	56	1	US-07-940-652-14
C 43	14	58.3	56	1	US-07-940-652-19
C 44	14	58.3	56	1	US-08-255-553-14
C 45	14	58.3	56	1	US-08-255-553-19

ALIGNMENTS

RESULT 1  
US-09-252-991A-6328/c  
; Sequence 6328, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 6328  
; LENGTH: 306  
; TYPE: DNA  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-6328

Query Match 66.7%; Score 16; DB 4; Length 306;  
Best Local Similarity 81.2%; Pred. No. 2.4;  
Matches 13; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGUGAAGGCUUCA 16  
| | | | | | | | | | | | | | | | | |  
Db 74 CCGCTGAAGGGCTTCA 59

RESULT 2  
US-09-252-991A-6056  
; Sequence 6056, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 6056  
; LENGTH: 897  
; TYPE: DNA

```
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-6056

Query Match          66.7%; Score 16; DB 4; Length 897;
Best Local Similarity 81.2%; Pred. No. 2.4;
Matches 13; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGCUGAAGGGCUUCA 16
    |||||:|||||:|
Db 19 CCGCTGAAGGGCTTCA 34

RESULT 3
US-09-252-991A-6218
; Sequence 6218, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 6218
; LENGTH: 1536
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-6218

Query Match          66.7%; Score 16; DB 4; Length 1536;
Best Local Similarity 81.2%; Pred. No. 2.4;
Matches 13; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGCUGAAGGGCUUCA 16
    |||||:|||||:|
Db 1319 CCGCTGAAGGGCTTCA 1334

RESULT 4
US-08-751-305-1
; Sequence 1, Application US/08751305
; Patent No. 5965439
; GENERAL INFORMATION:
; APPLICANT: Tenner et al., Andrea J.
; TITLE OF INVENTION: HOST DEFENSE ENHANCEMENT
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/751,305
; FILING DATE: 18-NOV-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Wetherell, Jr., John R.
; REGISTRATION NUMBER: 31,678
; REFERENCE/DOCKET NUMBER: 07306/012001
; TELEPHONE: 619/678-5070
```

```
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3460 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 149..2105
; US-08-751-305-1

Query Match          66.7%; Score 16; DB 2; Length 3460;
Best Local Similarity 81.2%; Pred. No. 2.3;
Matches 13; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGCUGAAGGGCUUCA 16
    |||||:|||||:|
Db 476 CCGCTGAAGGGCTTCA 491

RESULT 5
US-08-363-233B-21/c
; Sequence 21, Application US/08363233B
; Patent No. 5714383
; GENERAL INFORMATION:
; APPLICANT: Thompson, James D.
; TITLE OF INVENTION: METHOD AND REAGENT FOR TREATING CHRONIC
; MYELOGENOUS LEUKEMIA
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/363,233B
; FILING DATE: December 23, 1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION DATA: including application
; PRIOR APPLICATION DATA: described below: 2
; APPLICATION NUMBER: 07/882,822
; FILING DATE: May 14, 1992
; APPLICATION NUMBER: 08/193,922
; FILING DATE: February 7, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 209/165
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 23 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-363-233B-21

Query Match          62.5%; Score 15; DB 1; Length 23;
Best Local Similarity 80.0%; Pred. No. 9.1;
```

Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCGUGAAGGGCUUC 15  
||||:|||||:  
Db 18 CCGCTGAAGGGCTTC 4

## RESULT 6

US-08-363-233B-22/c  
; Sequence 22, Application US/08363233B  
; Patent No. 5714383

; GENERAL INFORMATION:

; APPLICANT: Thompson, James D.

; TITLE OF INVENTION: METHOD AND REAGENT FOR TREATING CHRONIC

; MYELOGENOUS LEUKEMIA

; NUMBER OF SEQUENCES: 39

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Lyon & Lyon

; STREET: 633 West Fifth Street

; CITY: Suite 4700

; STATE: Los Angeles

; COUNTRY: California

; ZIP: U.S.A.

; ZIP: 90071-2066

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

; MEDIUM TYPE: storage

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: IBM P.C. DOS 5.0

; SOFTWARE: FastSeq for Windows 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/363,233B

; FILING DATE: December 23, 1994

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; PRIOR APPLICATION DATA: including application

; PRIOR APPLICATION DATA: described below:

; APPLICATION NUMBER: 07/882,822

; FILING DATE: May 14, 1992

; APPLICATION NUMBER: 08/193,922

; FILING DATE: February 7, 1994

; ATTORNEY/AGENT INFORMATION:

; NAME: Warburg, Richard J.

; REGISTRATION NUMBER: 32,327

; REFERENCE/DOCKET NUMBER: 209/165

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (213) 489-1600

; TELEFAX: (213) 955-0440

; TELEX: 67-3510

; INFORMATION FOR SEQ ID NO: 22:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 23 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

US-08-363-233B-22

Query Match 62.5%; Score 15; DB 1; Length 23;

Best Local Similarity 80.0%; Pred. No. 9.1;

Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCGUGAAGGGCUUC 15  
||||:|||||:  
Db 17 CCGCTGAAGGGCTTC 3

## RESULT 7

US-08-793-408-9/c

; Sequence 9, Application US/08793408

; Patent No. 6007988

; GENERAL INFORMATION:

; APPLICANT: Choo, Yen

; APPLICANT: Klug, Aaron

; APPLICANT: Sanchez Garcia, Isidro  
; TITLE OF INVENTION: Improvements in or Relating to  
; Binding Proteins for Recognition of DNA  
; NUMBER OF SEQUENCES: 18  
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Pillsbury Madison & Sutro, L.L.P.

; STREET: 1100 New York Avenue, N.W.

; CITY: Washington

; STATE: D.C.

; COUNTRY: USA

; ZIP: 20005-3918

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Word Perfect

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/793,408

; FILING DATE:

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/GB95/01949

; FILING DATE: 17-AUG-1995

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: GB 9514698.1

; FILING DATE: 18-JUL-1995

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: GB 9422534.9

; FILING DATE: 08-NOV-1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: GB 9416880.4

; FILING DATE: 20-AUG-1994

; INFORMATION FOR SEQ ID NO: 9:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 33 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

US-08-793-408-9

Query Match 62.5%; Score 15; DB 3; Length 33;

Best Local Similarity 80.0%; Pred. No. 9.1;

Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCGUGAAGGGCUUC 15  
||||:|||||:  
Db 30 CCGCTGAAGGGCTTC 16

## RESULT 8

US-08-793-408-11/c

; Sequence 11, Application US/08793408

; Patent No. 6007988

; GENERAL INFORMATION:

; APPLICANT: Choo, Yen

; APPLICANT: Klug, Aaron

; APPLICANT: Sanchez Garcia, Isidro

; TITLE OF INVENTION: Improvements in or Relating to

; Binding Proteins for Recognition of DNA

; NUMBER OF SEQUENCES: 18

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Pillsbury Madison & Sutro, L.L.P.

; STREET: 1100 New York Avenue, N.W.

; CITY: Washington

; STATE: D.C.

; COUNTRY: USA

; ZIP: 20005-3918

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Word Perfect

; CURRENT APPLICATION DATA:

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/ APPLICATION NUMBER: US/08/793,408
/ FILING DATE:
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA: PCT/GB95/01949
/ FILING DATE: 17-AUG-1995
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: GB 9514698.1
/ FILING DATE: 18-JUL-1995
/ PRIOR APPLICATION DATA: GB 9422534.9
/ FILING DATE: 08-NOV-1994
/ APPLICATION NUMBER: GB 9416880.4
/ FILING DATE: 20-AUG-1994
/ INFORMATION FOR SEQ ID NO: 11:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 33 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ US-08-793-408-11

Query Match 62.5%; Score 15; DB 3; Length 33;
Best Local Similarity 80.0%; Pred. No. 9.1;
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGCTGAAGGGCTTC 15
Db 30 CCGCTGAAGGGCTTC 16

RESULT 9
US-09-139-762A-9/c
/ Sequence 9, Application US/09139762A
/ Patent No. 6013453
/ GENERAL INFORMATION:
/ APPLICANT: Choo, Yen
/ APPLICANT: Klug, Aaron
/ TITLE OF INVENTION: Improvements in or Relating to
/ TITLE OF INVENTION: Binding Proteins for Recognition of DNA
/ NUMBER OF SEQUENCES: 125
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Pillsbury Madison & Sutro, L.L.P.
/ STREET: 1100 New York Avenue, N.W.
/ CITY: Washington
/ STATE: D.C.
/ COUNTRY: USA
/ ZIP: 20005-3918
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Word Perfect
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/139,762A
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/793,408
/ FILING DATE: 02-JUN-1997
/ APPLICATION NUMBER: PCT/GB95/01949
/ FILING DATE: 17-AUG-1995
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: GB 9514698.1
/ FILING DATE: 18-JUL-1995
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: GB 9422534.9
/ FILING DATE: 08-NOV-1994
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: GB 9416880.4
/ FILING DATE: 20-AUG-1994
/ INFORMATION FOR SEQ ID NO: 11:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 33 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ US-09-139-762A-11

Query Match 62.5%; Score 15; DB 3; Length 33;
Best Local Similarity 80.0%; Pred. No. 9.1;
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGCTGAAGGGCTTC 15
Db 30 CCGCTGAAGGGCTTC 16

RESULT 9
US-09-139-762A-9/c
/ Sequence 9, Application US/09139762A
/ Patent No. 6013453
/ GENERAL INFORMATION:
/ APPLICANT: Choo, Yen
/ APPLICANT: Klug, Aaron
/ TITLE OF INVENTION: Improvements in or Relating to
/ TITLE OF INVENTION: Binding Proteins for Recognition of DNA
/ NUMBER OF SEQUENCES: 125
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Pillsbury Madison & Sutro, L.L.P.
/ STREET: 1100 New York Avenue, N.W.
/ CITY: Washington
/ STATE: D.C.
/ COUNTRY: USA
/ ZIP: 20005-3918
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Word Perfect
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/139,762A
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/793,408
/ FILING DATE: 02-JUN-1997
/ APPLICATION NUMBER: PCT/GB95/01949
/ FILING DATE: 17-AUG-1995
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: GB 9514698.1
/ FILING DATE: 18-JUL-1995
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: GB 9422534.9
/ FILING DATE: 08-NOV-1994
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: GB 9416880.4
/ FILING DATE: 20-AUG-1994
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/ INFORMATION FOR SEQ ID NO: 9:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 33 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ US-09-139-762A-9

Query Match 62.5%; Score 15; DB 3; Length 33;
Best Local Similarity 80.0%; Pred. No. 9.1;
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGCTGAAGGGCTTC 15
Db 30 CCGCTGAAGGGCTTC 16

RESULT 10
US-09-139-762A-11/c
/ Sequence 11, Application US/09139762A
/ Patent No. 6013453
/ GENERAL INFORMATION:
/ APPLICANT: Choo, Yen
/ APPLICANT: Klug, Aaron
/ TITLE OF INVENTION: Improvements in or Relating to
/ TITLE OF INVENTION: Binding Proteins for Recognition of DNA
/ NUMBER OF SEQUENCES: 125
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Pillsbury Madison & Sutro, L.L.P.
/ STREET: 1100 New York Avenue, N.W.
/ CITY: Washington
/ STATE: D.C.
/ COUNTRY: USA
/ ZIP: 20005-3918
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Word Perfect
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/139,762A
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/793,408
/ FILING DATE: 02-JUN-1997
/ APPLICATION NUMBER: PCT/GB95/01949
/ FILING DATE: 17-AUG-1995
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: GB 9514698.1
/ FILING DATE: 18-JUL-1995
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: GB 9422534.9
/ FILING DATE: 08-NOV-1994
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: GB 9416880.4
/ FILING DATE: 20-AUG-1994
/ INFORMATION FOR SEQ ID NO: 11:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 33 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ US-09-139-762A-11

Query Match 62.5%; Score 15; DB 3; Length 33;
Best Local Similarity 80.0%; Pred. No. 9.1;
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGCTGAAGGGCTTC 15
Db 30 CCGCTGAAGGGCTTC 16
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RESULT 11
US-08-448-446B-12/c
; Sequence 12, Application US/08448446B
; Patent No. 6080851
; GENERAL INFORMATION:
; APPLICANT: Pachuk et al.
; TITLE OF INVENTION: Compounds and Methods for the Treatment
; TITLE OF INVENTION: of Leukemias
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn
; ADDRESSEE: Kurtz Mackiewicz & No. 6080851Iris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/448,446B
; FILING DATE: July 10, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/989,852
; FILING DATE: December 4, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Doreen Yanko Trujillo
; REGISTRATION NUMBER: 35,719
; REFERENCE/DOCKET NUMBER: APOL-0020
; TELECOMMUNICATION INFORMATION: C
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 47
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; ANTI-SENSE:
; US-08-448-446B-12
Query Match 62.5%; Score 15; DB 3; Length 47;
Best Local Similarity 80.0%; Pred. No. 9.1;
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGCUGAAGGGCUUC 15
Db 30 CCGCTGAAGGGCTTC 16

RESULT 12
US-08-448-446B-1/c
; Sequence 1, Application US/08448446B
; Patent No. 6080851
; GENERAL INFORMATION:
; APPLICANT: Pachuk et al.
; TITLE OF INVENTION: Compounds and Methods for the Treatment
; TITLE OF INVENTION: of Leukemias
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn
; ADDRESSEE: Kurtz Mackiewicz & No. 6080851Iris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103

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; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/448,446B
; FILING DATE: July 10, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/989,852
; FILING DATE: December 4, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Doreen Yanko Trujillo
; REGISTRATION NUMBER: 35,719
; REFERENCE/DOCKET NUMBER: APOL-0020
; TELECOMMUNICATION INFORMATION: C
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 62
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; ANTI-SENSE: No
; US-08-448-446B-1
Query Match 62.5%; Score 15; DB 3; Length 62;
Best Local Similarity 80.0%; Pred. No. 9;
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGCUGAAGGGCUUC 15
Db 45 CCGCTGAAGGGCTTC 31

RESULT 13
US-08-152-621-7/c
; Sequence 7, Application US/08152621
; Patent No. 5652222
; GENERAL INFORMATION:
; APPLICANT: Calabretta, Bruno
; APPLICANT: Gewirtz, Alan M.
; TITLE OF INVENTION: Selective Inhibition of
; TITLE OF INVENTION: Leukemic Cell Proliferation by bcr-abl
; TITLE OF INVENTION: Antisense Oligonucleotides
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEIDEL, GONDA, LAVORGNA
; ADDRESSEE: & MONACO, P.C.
; STREET: 1800 Two Penn Center
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: U.S.A.
; ZIP: 19102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/152,621
; FILING DATE: No. 5652222ember 15, 1993
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/718,302
; FILING DATE: June 18, 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Monaco, Daniel A.
; REGISTRATION NUMBER: 30,480
; REFERENCE/DOCKET NUMBER: 6056-120 (CT.) 1
; TELECOMMUNICATION INFORMATION:

```

/ TELEPHONE: (215) 568-8383  
/ TELEFAX: (215) 568-5549  
/ TELEX: No. 5652222e  
/ INFORMATION FOR SEQ ID NO: 7:  
/ SEQUENCE CHARACTERISTICS:  
/ LENGTH: 80 Nucleotides  
/ TYPE: nucleic acid  
/ STRANDEDNESS: single stranded  
/ TOPOLOGY: linear  
US-08-152-621-7

Query Match 62.5%; Score 15; DB 1; Length 80;  
Best Local Similarity 80.0%; Pred. No. 9;  
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGCUGAAGGGCUUC 15  
Db 45 CCGCTGAAGGGCTTC 31

## RESULT 14

US-08-306-691B-38/c  
Sequence 38, Application US/08306691B

/ Patent No. 5734039

/ GENERAL INFORMATION:

/ APPLICANT: Calabretta, Bruno

/ APPLICANT: Skorski, Tomasz

/ TITLE OF INVENTION: ANTISENSE

/ TITLE OF INVENTION: OLIGONUCLEOTIDES TARGETING COOPERATING ONCOGENES

/ NUMBER OF SEQUENCES: 55

/ CORRESPONDENCE ADDRESS:

/ ADDRESSEE: Seigel, Gonda, Lavorgna & Monaco, P.C.

/ STREET: Two Penn Center, Suite 1800

/ CITY: Philadelphia

/ STATE: Pennsylvania

/ COUNTRY: U.S.A.

/ ZIP: 19102

/ COMPUTER READABLE FORM:

/ MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb

/ COMPUTER: IBM PS/2

/ OPERATING SYSTEM: MS-DOS

/ SOFTWARE: WordPerfect 5.1

/ CURRENT APPLICATION DATA:

/ APPLICATION NUMBER: US/08/306,691B

/ FILING DATE: September 15, 1994

/ CLASSIFICATION: 514

/ PRIOR APPLICATION DATA:

/ APPLICATION NUMBER:

/ FILING DATE:

/ ATTORNEY/AGENT INFORMATION:

/ NAME: Monaco, Daniel A.

/ REGISTRATION NUMBER: 30,480

/ REFERENCE/DOCKET NUMBER: 8321-8

/ TELECOMMUNICATION INFORMATION:

/ TELEPHONE: (215) 568-8383

/ TELEFAX: (215) 568-5549

/ TELEX: No. 5734039e

/ INFORMATION FOR SEQ ID NO: 38:

/ SEQUENCE CHARACTERISTICS:

/ LENGTH: 80 base pairs

/ TYPE: nucleic acid

/ STRANDEDNESS: single

/ TOPOLOGY: linear

US-08-306-691B-38

Query Match 62.5%; Score 15; DB 1; Length 80;  
Best Local Similarity 80.0%; Pred. No. 9;  
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGCUGAAGGGCUUC 15  
Db 45 CCGCTGAAGGGCTTC 31

## RESULT 15

PCT-US92-05035-7/c

/ Sequence 7, Application PC/TUS9205035

/ GENERAL INFORMATION:

/ APPLICANT: Calabretta, Bruno

/ APPLICANT: Gewirtz, Alan M.

/ TITLE OF INVENTION: Selective Inhibition of

/ TITLE OF INVENTION: Leukemic Cell Proliferation by bcr-abl

/ TITLE OF INVENTION: Antisense Oligonucleotides

/ NUMBER OF SEQUENCES: 34

/ CORRESPONDENCE ADDRESS:

/ ADDRESSEE: Temple University - Of The Common-

/ ADDRESSEE: wealth System of Higher Education

/ STREET: 406 University Services Building

/ CITY: Philadelphia

/ STATE: Pennsylvania

/ COUNTRY: U.S.A.

/ ZIP: 19122

/ COMPUTER READABLE FORM:

/ MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb

/ COMPUTER: IBM PS/2

/ OPERATING SYSTEM: MS-DOS

/ SOFTWARE: WordPerfect 5.1

/ CURRENT APPLICATION DATA:

/ APPLICATION NUMBER: PCT/US92/05035

/ FILING DATE: 19920615

/ CLASSIFICATION: 514

/ PRIOR APPLICATION DATA:

/ APPLICATION NUMBER: 07/718,302

/ FILING DATE: June 18, 1991

/ PRIOR APPLICATION DATA:

/ APPLICATION NUMBER: 07/869,911

/ FILING DATE: April 14, 1991

/ ATTORNEY/AGENT INFORMATION:

/ NAME: Monaco, Daniel A.

/ REGISTRATION NUMBER: 30,480

/ REFERENCE/DOCKET NUMBER: 6056-120 (CIP) 1

/ TELECOMMUNICATION INFORMATION:

/ TELEPHONE: (215) 568-8383

/ TELEFAX: (215) 568-5549

/ TELEX: None

/ INFORMATION FOR SEQ ID NO: 7:

/ SEQUENCE CHARACTERISTICS:

/ LENGTH: 80 Nucleotides

/ TYPE: NUCLEIC ACID

/ STRANDEDNESS: single stranded

/ TOPOLOGY: linear

PCT-US92-05035-7

Query Match 62.5%; Score 15; DB 5; Length 80;  
Best Local Similarity 80.0%; Pred. No. 9;  
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGCUGAAGGGCUUC 15  
Db 45 CCGCTGAAGGGCTTC 31

Search completed: May 27, 2004, 02:25:15  
Job time : 20.2274 secs



GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: May 27, 2004, 11:30:47 ; Search time 126.301 Seconds  
(without alignments)  
864.392 Million cell updates/sec

Title: US-09-121-239-19

Perfect score: 24

Sequence: 1 CCGUGAAGGCUCAUGUCCAC 24

Scoring table: OLIGO\_NUC

Gapop 60.0 , Gapext 60.0

Searched: 2960401 seqs, 2274450654 residues

Word size : 0

Total number of hits satisfying chosen parameters: 5920802

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published Applications NA:\*

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- 3: /cgn2\_6/ptodata/2/pubpna/US06\_PUBCOMB.seq:\*
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- 9: /cgn2\_6/ptodata/2/pubpna/US09A\_PUBCOMB.seq:\*
- 10: /cgn2\_6/ptodata/2/pubpna/US09B\_PUBCOMB.seq:\*
- 11: /cgn2\_6/ptodata/2/pubpna/US09C\_PUBCOMB.seq:\*
- 12: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq:\*
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- 14: /cgn2\_6/ptodata/2/pubpna/US10B\_PUBCOMB.seq:\*
- 15: /cgn2\_6/ptodata/2/pubpna/US10C\_PUBCOMB.seq:\*
- 16: /cgn2\_6/ptodata/2/pubpna/US10C\_PUBCOMB.seq:\*
- 17: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq:\*
- 18: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq:\*
- 19: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Length	DB ID	Description
C 1	24	100.0	3450	16 US-10-457-954-5
C 2	18	75.0	34125	9 US-09-782-378A-25
C 3	16	66.7	65	10 US-09-908-975-27688
C 4	16	66.7	310	15 US-10-029-386-26614
C 5	16	66.7	555	15 US-10-029-386-12914
C 6	16	66.7	1044	9 US-09-815-242-7861
C 7	16	66.7	1044	13 US-10-282-122A-30374
C 8	16	66.7	1424	13 US-10-425-114-523
C 9	16	66.7	1951	15 US-10-029-386-22997
C 10	16	66.7	6699	13 US-10-211-462-130
C 11	16	66.7	6699	15 US-10-021-660-15
C 12	16	66.7	85076	16 US-10-085-117-97
C 13	16	66.7	126413	13 US-10-087-192-1831
C 14	15	62.5	24	13 US-10-382-634-21

C	15	62.5	24	15	US-10-349-320-20	Sequence 20, Appl
	16	62.5	205	9	US-09-867-701-10433	Sequence 10433, A
	17	62.5	436	9	US-09-960-352-5213	Sequence 5213, Ap
	18	62.5	489	13	US-10-424-599-43483	Sequence 43483, A
C	19	62.5	491	13	US-10-424-599-7082	Sequence 7082, Ap
	20	62.5	499	13	US-10-027-632-85551	Sequence 85551, A
	21	62.5	499	16	US-10-027-632-85551	Sequence 85551, A
	22	62.5	729	13	US-10-107-431-100	Sequence 100, App
C	23	62.5	773	13	US-10-027-632-133705	Sequence 133705,
	24	62.5	773	16	US-10-027-632-133705	Sequence 133705,
	25	62.5	1133	13	US-10-425-114-4855	Sequence 4855, Ap
	26	62.5	1163	13	US-10-027-632-118039	Sequence 118039,
	27	62.5	1163	13	US-10-027-632-118040	Sequence 118040,
	28	62.5	1163	16	US-10-027-632-118039	Sequence 118039,
	29	62.5	1163	16	US-10-027-632-118040	Sequence 118040,
C	30	62.5	1590	16	US-10-369-493-27261	Sequence 27261, A
	31	62.5	1749	13	US-10-282-122A-25460	Sequence 25460, A
C	32	62.5	1765	13	US-10-424-599-103532	Sequence 103532,
	33	62.5	1806	9	US-09-815-242-4015	Sequence 4015, Ap
	34	62.5	1806	13	US-10-282-122A-7373	Sequence 7373, Ap
	35	62.5	2482	13	US-10-363-616-49	Sequence 49, Appl
C	36	62.5	3393	15	US-10-263-480-1	Sequence 1, Appl
	37	62.5	3606	16	US-10-214-529-6	Sequence 6, Appl
C	38	62.5	3840	15	US-10-204-041-3	Sequence 3, Appl
	39	62.5	5527	9	US-09-880-107-3710	Sequence 3710, Ap
C	40	62.5	5744	16	US-10-439-703-5	Sequence 5, Appl
	41	62.5	38734	10	US-09-373-658-30	Sequence 30, Appl
	42	62.5	38734	11	US-09-989-687-30	Sequence 30, Appl
	43	62.5	45055	13	US-10-107-431-277	Sequence 277, Appl
C	44	62.5	84539	9	US-09-962-436-36	Sequence 36, Appl
	45	62.5	212231	13	US-10-087-192-1126	Sequence 1126, Ap

ALIGNMENTS

RESULT 1

US-10-457-954-5/c  
; Sequence 5, Application US/10457954  
; Publication No. US20040005623A1  
; GENERAL INFORMATION:  
; APPLICANT: Longley, B. Jack  
; TITLE OF INVENTION: Method of determining tumor sensitivities to therapeutic drugs  
; FILE REFERENCE: 960296.98890  
; CURRENT APPLICATION NUMBER: US/10/457,954  
; CURRENT FILING DATE: 2003-06-10  
; PRIOR APPLICATION NUMBER: 60/387,370  
; PRIOR FILING DATE: 2002-06-10  
; PRIOR APPLICATION NUMBER: 60/387,406  
; PRIOR FILING DATE: 2002-06-10  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 5  
; LENGTH: 3450  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(3447)  
; FEATURE:  
; NAME/KEY: misc\_structure  
; LOCATION: (730)..(765)  
; OTHER INFORMATION: encode  
; OTHER INFORMATION: pocket  
; FEATURE:  
; NAME/KEY: misc\_structure  
; LOCATION: (931)..(1077)  
; OTHER INFORMATION: encode  
; OTHER INFORMATION: pocket  
; FEATURE:  
; NAME/KEY: misc\_structure  
; LOCATION: (1141)..(1206)  
; OTHER INFORMATION: encode

amino acids 244-255 for forming the sides of the enzymatic  
amino acids 311-359 for forming the sides of the enzymatic  
amino acids 381-402 for forming the enzymatic pocket's

OTHER INFORMATION: activation loop  
US-10-457-954-5

Query Match 100.0%; Score 24; DB 16; Length 3450;  
Best Local Similarity 75.0%; Pred. No. 0.00011;  
Matches 18; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGCUAAGGGCUCAUGUCCAC 24  
DB 150 CCGCTGAAGGCTTCATGTTCCAC 127

RESULT 2

US-09-782-378A-25  
Sequence 25, Application US/09782378A  
Patent No. US20020102731A1  
GENERAL INFORMATION:  
APPLICANT: Hearing, Patrick  
APPLICANT: Bahou, Wadie  
APPLICANT: Sandalon, Ziv  
APPLICANT: Gnatenko, Dmitri  
TITLE OF INVENTION: Adenoviral Vectors  
FILE REFERENCE: STONYB-04970  
CURRENT APPLICATION NUMBER: US/09/782,378A  
CURRENT FILING DATE: 2001-02-12  
PRIOR APPLICATION NUMBER: 60/237,747  
PRIOR FILING DATE: 2000-10-02  
NUMBER OF SEQ ID NOS: 27  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 25  
LENGTH: 34125  
TYPE: DNA  
ORGANISM: Human adenovirus type 12  
US-09-782-378A-25

Query Match 75.0%; Score 18; DB 9; Length 34125;  
Best Local Similarity 66.7%; Pred. No. 0.41;  
Matches 12; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 5 UGNAGGGCUCAUGUCC 22  
DB 3998 TGAAGGCTTCATGTTCC 4015

RESULT 3

US-09-908-975-27688/c  
Sequence 27688, Application US/09908975  
Publication No. US20030165843A1  
GENERAL INFORMATION:  
APPLICANT: SHOSHAN, Avi  
APPLICANT: WASSERMAN, Alon  
APPLICANT: MINTZ, Eli  
APPLICANT: MINTZ, Liat  
APPLICANT: FAIGLER, Simchon  
TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICING  
FILE REFERENCE: 36688-0005  
CURRENT APPLICATION NUMBER: US/09/908,975  
CURRENT FILING DATE: 2001-07-20  
PRIOR APPLICATION NUMBER: US 60/287,724  
PRIOR FILING DATE: 2001-05-02  
PRIOR APPLICATION NUMBER: US 60/221,607  
PRIOR FILING DATE: 2000-07-28  
NUMBER OF SEQ ID NOS: 32337  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 27688  
LENGTH: 65  
TYPE: DNA  
ORGANISM: Mus musculus  
US-09-908-975-27688

Query Match 66.7%; Score 16; DB 10; Length 65;  
Best Local Similarity 68.8%; Pred. No. 7.9;

Matches 11; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 9 GGGCUCAUGUCCAC 24  
DB 22 GGGCTTCATGTTCCAC 7

RESULT 4

US-10-029-386-26614/c  
Sequence 26614, Application US/10029386  
Publication No. US20030194704A1  
GENERAL INFORMATION:  
APPLICANT: Penn, Sharron G.  
APPLICANT: Rank, David R.  
APPLICANT: Hanzel, David K.  
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR GENOTYPING  
FILE REFERENCE: AEOMICA-X-2  
CURRENT APPLICATION NUMBER: US/10/029,386  
CURRENT FILING DATE: 2001-12-20  
NUMBER OF SEQ ID NOS: 34288  
SOFTWARE: Anomax Sequence Listing Engine vers. 1.1  
SEQ ID NO 26614  
LENGTH: 310  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: MAP TO CHR20.3  
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.2  
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 3.5  
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.5  
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.9  
OTHER INFORMATION: SWISSPROT HIT: P07204, EVALUE 2.00e-08  
OTHER INFORMATION: NT HIT: g112742414, EVALUE 0.00e+00  
OTHER INFORMATION: EST\_HUMAN HIT: BI907890.1, EVALUE 0.00e+00  
US-10-029-386-26614

Query Match 66.7%; Score 16; DB 15; Length 310;  
Best Local Similarity 81.2%; Pred. No. 7.5;  
Matches 13; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGCUAAGGGCUCA 16  
DB 62 CCGCTGAAGGCTTCA 47

RESULT 5

US-10-029-386-12914/c  
Sequence 12914, Application US/10029386  
Publication No. US20030194704A1  
GENERAL INFORMATION:  
APPLICANT: Penn, Sharron G.  
APPLICANT: Rank, David R.  
APPLICANT: Hanzel, David K.  
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR GENOTYPING  
FILE REFERENCE: AEOMICA-X-2  
CURRENT APPLICATION NUMBER: US/10/029,386  
CURRENT FILING DATE: 2001-12-20  
NUMBER OF SEQ ID NOS: 34288  
SOFTWARE: Anomax Sequence Listing Engine vers. 1.1  
SEQ ID NO 12914  
LENGTH: 555  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: MAP TO CHR20.3  
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.2  
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 3.5  
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.5  
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.9  
OTHER INFORMATION: SWISSPROT HIT: P07204, EVALUE 4.00e-08  
OTHER INFORMATION: NT HIT: g112742414, EVALUE 0.00e+00

OTHER INFORMATION: EST\_HUMAN HIT: BI907890.1, EVALUATE 0.00e+00  
US-10-029-386-12914

Query Match 66.7%; Score 16; DB 15; Length 555;  
Best Local Similarity 81.2%; Pred. No. 7.3;  
Matches 13; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGCUGAAGGGCUUCA 16  
||||:|||||:|  
DB 90 CCGCTGAAGGGCTTCA 75

## RESULT 6

US-09-815-242-7861/c  
Sequence 7861, Application US/09815242  
Patent No. US20020061569A1  
GENERAL INFORMATION:  
APPLICANT: Haselbeck, Robert  
APPLICANT: Ohlsen, Kari L.  
APPLICANT: Zyskind, Judith W.  
APPLICANT: Wall, Daniel  
APPLICANT: Trawick, John D.  
APPLICANT: Carr, Grant J.  
APPLICANT: Yamamoto, Robert T.  
APPLICANT: Xu, H. Howard

TITLE OF INVENTION: Identification of Essential Genes in  
FILE REFERENCE: ELITRA.011A

CURRENT APPLICATION NUMBER: US/09/815,242

CURRENT FILING DATE: 2001-03-21  
PRIOR APPLICATION NUMBER: 60/191,078  
PRIOR FILING DATE: 2000-03-21  
PRIOR APPLICATION NUMBER: 60/206,848  
PRIOR FILING DATE: 2000-05-23  
PRIOR APPLICATION NUMBER: 60/207,727  
PRIOR FILING DATE: 2000-05-26  
PRIOR APPLICATION NUMBER: 60/242,578  
PRIOR FILING DATE: 2000-10-23  
PRIOR APPLICATION NUMBER: 60/253,625  
PRIOR FILING DATE: 2000-11-27  
PRIOR APPLICATION NUMBER: 60/257,931  
PRIOR FILING DATE: 2000-12-22  
PRIOR APPLICATION NUMBER: 60/267,636  
PRIOR FILING DATE: 2001-02-09  
PRIOR APPLICATION NUMBER: 60/269,308  
PRIOR FILING DATE: 2001-02-16  
NUMBER OF SEQ ID NOS: 14110

SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 7861

LENGTH: 1044

TYPE: DNA

ORGANISM: Pseudomonas aeruginosa

FEATURE:

NAME/KEY: CDS

LOCATION: (1)...(1044)

US-09-815-242-7861

Query Match 66.7%; Score 16; DB 9; Length 1044;  
Best Local Similarity 81.2%; Pred. No. 7.2;  
Matches 13; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGCUGAAGGGCUUCA 16  
||||:|||||:|  
DB 812 CCGCTGAAGGGCTTCA 797

## RESULT 7

US-10-282-122A-30374/c  
Sequence 30374, Application US/10282122A  
Publication No. US20040029129A1

GENERAL INFORMATION:

APPLICANT: Wang, Liangsu

APPLICANT: Zamudio, Carlos

APPLICANT: Malone, Cheryl

APPLICANT: Haselbeck, Robert

APPLICANT: Ohlsen, Kari  
APPLICANT: Zyskind, Judith  
APPLICANT: Wall, Daniel  
APPLICANT: Trawick, John  
APPLICANT: Carr, Grant  
APPLICANT: Yamamoto, Robert  
APPLICANT: Forsyth, R.  
APPLICANT: Xu, H.  
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms  
FILE REFERENCE: ELITRA.034A

CURRENT APPLICATION NUMBER: US/10/282,122A

CURRENT FILING DATE: 2003-02-20

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR FILING DATE: 2000-03-21

PRIOR APPLICATION NUMBER: 60/206,848

PRIOR FILING DATE: 2000-05-23

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: 60/230,335

PRIOR FILING DATE: 2000-09-06

PRIOR APPLICATION NUMBER: 60/230,347

PRIOR FILING DATE: 2000-09-09

PRIOR APPLICATION NUMBER: 60/242,578

PRIOR FILING DATE: 2000-10-23

PRIOR APPLICATION NUMBER: 60/253,625

PRIOR FILING DATE: 2000-11-27

PRIOR APPLICATION NUMBER: 60/257,931

PRIOR FILING DATE: 2000-12-22

PRIOR APPLICATION NUMBER: 60/267,636

PRIOR FILING DATE: 2001-02-09

PRIOR APPLICATION NUMBER: 60/269,308

PRIOR FILING DATE: 2001-02-16

Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 78614

SOFTWARE: PatentIn version 3.1

SEQ ID NO 30374

LENGTH: 1044

TYPE: DNA

ORGANISM: Pseudomonas aeruginosa

US-10-282-122A-30374

Query Match 66.7%; Score 16; DB 13; Length 1044;  
Best Local Similarity 81.2%; Pred. No. 7.2;  
Matches 13; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGCUGAAGGGCUUCA 16

||||:|||||:|

DB 812 CCGCTGAAGGGCTTCA 797

## RESULT 8

US-10-425-114-523/c

Sequence 523, Application US/10425114

Publication No. US20040034888A1

GENERAL INFORMATION:

APPLICANT: Liu, Jingdong

APPLICANT: Zhou, Yihua

APPLICANT: Kovalic, David K.

APPLICANT: Screen, Steven E.

APPLICANT: Tabaska, Jack E.

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
File Reference: 38-21(53313)B

CURRENT APPLICATION NUMBER: US/10/425,114

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 73128

SEQ ID NO 523

LENGTH: 1424

TYPE: DNA

ORGANISM: Zea mays

FEATURE:

OTHER INFORMATION: Clone ID: 700076886\_FLI

US-10-425-114-523

Query Match 66.7%; Score 16; DB 13; Length 1424;  
Best Local Similarity 68.8%; Pred. No. 7.1;  
Matches 11; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 7 AAGGCGUUCGUAUCC 22  
|||||:||||:|:|:  
Db 481 AAGGCGTTCATGTCC 466

RESULT 9

US-10-029-386-22997  
; Sequence 22997, Application US/10029386  
; Publication No. US20030194704A1  
; GENERAL INFORMATION:  
; APPLICANT: Penn, Sharon G.  
; APPLICANT: Rank, David R.  
; APPLICANT: Hanzel, David K.  
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
; TITLE OF INVENTION: EXPRESSION ANALYSIS TWO  
; FILE REFERENCE: AEOMICA-X-2  
; CURRENT APPLICATION NUMBER: US/10/029,386  
; CURRENT FILING DATE: 2001-12-20  
; NUMBER OF SEQ ID NOS: 34288  
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1  
; SEQ ID NO 22997  
; LENGTH: 1951  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: MAP TO AL118508.6  
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.4  
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.83  
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.3  
; OTHER INFORMATION: SWISSPROT HIT: O73775, EVALUE 1.00e-39  
; OTHER INFORMATION: NT HIT: G112742414, EVALUE 0.00e+00  
; OTHER INFORMATION: EST\_HUMAN HIT: B1907890.1, EVALUE 0.00e+00  
US-10-029-386-22997

Query Match 66.7%; Score 16; DB 15; Length 1951;  
Best Local Similarity 81.2%; Pred. No. 7;  
Matches 13; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGCUGAAGGCGUCCA 16  
|||||:|||||:|:|:  
Db 328 CCGCTGAAGGGCTTCA 343

RESULT 10

US-10-211-462-130  
; Sequence 130, Application US/10211462  
; Publication No. US20040033495A1  
; GENERAL INFORMATION:  
; APPLICANT: Murray, Richard  
; APPLICANT: Glynn, Richard  
; APPLICANT: Watson, Susan R.  
; APPLICANT: Aziz, Natasha  
; APPLICANT: Eos Biotechnology, Inc.  
; TITLE OF INVENTION: Methods of Diagnosis of Angiogenesis, Compositions and  
; TITLE OF INVENTION: Methods of Screening for Angiogenesis Modulators  
; FILE REFERENCE: 018501-006200US  
; CURRENT APPLICATION NUMBER: US/10/211,462  
; CURRENT FILING DATE: 2003-02-13  
; PRIOR APPLICATION NUMBER: US 09/784,356  
; PRIOR FILING DATE: 2001-02-14  
; PRIOR APPLICATION NUMBER: US 09/791,390  
; PRIOR FILING DATE: 2001-02-22  
; PRIOR APPLICATION NUMBER: US 60/310,025  
; PRIOR FILING DATE: 2001-08-03  
; PRIOR APPLICATION NUMBER: US 60/334,244  
; PRIOR FILING DATE: 2001-11-29  
; NUMBER OF SEQ ID NOS: 230

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 130  
; LENGTH: 6699  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-211-462-130

Query Match 66.7%; Score 16; DB 13; Length 6699;  
Best Local Similarity 81.2%; Pred. No. 6.7;  
Matches 13; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGCUGAAGGCGUCCA 16  
|||||:|||||:|:|:  
Db 476 CCGCTGAAGGGCTTCA 491

RESULT 11

US-10-021-660-15  
; Sequence 15, Application US/10021660  
; Publication No. US20030152926A1  
; GENERAL INFORMATION:  
; APPLICANT: Murray, Richard  
; APPLICANT: Glynn, Richard  
; APPLICANT: Watson, Susan R.  
; APPLICANT: Eos Biotechnology, Inc.  
; TITLE OF INVENTION: No. US20030152926A1 Methods of Diagnosis of Angiogenesis,  
; TITLE OF INVENTION: Compositions and Methods of Screening for Angiogenesis  
; TITLE OF INVENTION: Modulators  
; FILE REFERENCE: 018501-0007100US  
; CURRENT APPLICATION NUMBER: US/10/021,660  
; CURRENT FILING DATE: 2001-12-06  
; PRIOR APPLICATION NUMBER: US/09/784,356  
; PRIOR FILING DATE: 2001-02-14  
; PRIOR APPLICATION NUMBER: US 09/637,977  
; PRIOR FILING DATE: 2000-08-11  
; NUMBER OF SEQ ID NOS: 135  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 15  
; LENGTH: 6699  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-021-660-15

Query Match 66.7%; Score 16; DB 15; Length 6699;  
Best Local Similarity 81.2%; Pred. No. 6.7;  
Matches 13; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGCUGAAGGCGUCCA 16  
|||||:|||||:|:|:  
Db 476 CCGCTGAAGGGCTTCA 491

RESULT 12

US-10-085-117-97/c  
; Sequence 97, Application US/10085117  
; Publication No. US20030232334A1  
; GENERAL INFORMATION:  
; APPLICANT: Morris, David W.  
; APPLICANT: Engelhard, Eric K.  
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER  
; FILE REFERENCE: 529452000121  
; CURRENT APPLICATION NUMBER: US/10/085,117  
; CURRENT FILING DATE: 2002-02-27  
; PRIOR APPLICATION NUMBER: US 09/798,586  
; PRIOR FILING DATE: 2001-03-02  
; NUMBER OF SEQ ID NOS: 361  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 97  
; LENGTH: 85076  
; TYPE: DNA  
; ORGANISM: Mus musculus  
; FEATURE:  
; NAME/KEY: variation

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; LOCATION: (1)....(85076)
; OTHER INFORMATION: n = any nucleotide
US-10-085-117-97

Query Match
Best Local Similarity 66.7%; Score 16; DB 16; Length 85076;
Matches 12; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 3 GCUGAAGGCGUUCVAVG 18
Db 30797 GCTGAAGGCTTCATG 30782

RESULT 13
US-10-087-192-1831
; Sequence 1831, Application US/10087192
; Publication No. US20020182586A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Engelhard, Eric K.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
; FILE REFERENCE: 529452000122
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US/10/087,192
; PRIOR FILING DATE: 2000-12-22
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: US 09/798,586
; NUMBER OF SEQ ID NOS: 2059
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1831
; LENGTH: 126413
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)....(126413)
; OTHER INFORMATION: n = A,T,C or G
US-10-087-192-1831

Query Match
Best Local Similarity 66.7%; Score 16; DB 13; Length 126413;
Matches 11; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 9 GGGCUUCVAVGUCAC 24
Db 101481 GGGCTTCATGTTCCAC 101496

RESULT 14
US-10-382-634-21/c
; Sequence 21, Application US/10382634
; Publication No. US20040038921A1
; GENERAL INFORMATION:
; APPLICANT: Kreutzer, Roalnd
; TITLE OF INVENTION: Composition and Method for Inhibiting Expression of a Target Gene
; FILE REFERENCE: 20200/2062
; CURRENT APPLICATION NUMBER: US/10/382,634
; CURRENT FILING DATE: 2003-03-07
; PRIOR APPLICATION NUMBER: DE 101 55 280.7
; PRIOR FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: DE 101 58 411.3
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: DE 101 60 151.4
; PRIOR FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: DE 102 30 996.5
; PRIOR FILING DATE: 2002-07-09
; PRIOR APPLICATION NUMBER: PCT/EP02/00152
; PRIOR FILING DATE: 2002-01-09
; PRIOR APPLICATION NUMBER: PCT/EP02/00151
; PRIOR FILING DATE: 2002-01-09
; PRIOR APPLICATION NUMBER: PCT/EP02/11971
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; PRIOR FILING DATE: 2002-10-25
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 21
; LENGTH: 24
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: PRIMER
US-10-382-634-21

Query Match
Best Local Similarity 62.5%; Score 15; DB 13; Length 24;
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGCUGAAGGCGUUC 15
Db 23 CCGCTGAAGGCGCTTC 9

RESULT 15
US-10-349-320-20/c
; Sequence 20, Application US/10349320
; Publication No. US20030190654A1
; GENERAL INFORMATION:
; APPLICANT: Heidenreich, Olaf
; TITLE OF INVENTION: DOUBLE-STRANDED RNA (dsRNA) AND METHOD OF USE
; FILE REFERENCE: 20200/2112
; CURRENT APPLICATION NUMBER: US/10/349,320
; CURRENT FILING DATE: 2003-01-22
; PRIOR APPLICATION NUMBER: DE 102 02 419.7
; PRIOR FILING DATE: 2002-01-22
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Tagman probe
US-10-349-320-20

Query Match
Best Local Similarity 62.5%; Score 15; DB 15; Length 24;
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGCUGAAGGCGUUC 15
Db 23 CCGCTGAAGGCGCTTC 9

Search completed: May 27, 2004, 14:58:31
Job time : 126.301 secs
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GenCore version 5.1.1.6  
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OM nucleic - nucleic search, using sw model

Run on: May 26, 2004, 15:22:41 ; Search time 847.385 Seconds

(without alignments)  
845.770 Million cell updates/sec

Title: US-09-121-239-19

Perfect score: 24

Sequence: 1 CGCGAAGGCGUUCAGUUCAC 24

Scoring table: OLIGO\_NUC

Gapop 60.0 , Gapext 60.0

Searched: 27513289 seqs, 14931090276 residues

Word size : 0

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

EST:

1: em\_estba.\*

2: em\_esthum.\*

3: em\_estin.\*

4: em\_estmu.\*

5: em\_estov.\*

6: em\_estpl.\*

7: em\_estro.\*

8: em\_htc.\*

9: gb\_est1.\*

10: gb\_est2.\*

11: gb\_htc.\*

12: gb\_est3.\*

13: gb\_est4.\*

14: gb\_est5.\*

15: em\_estfun.\*

16: em\_estom.\*

17: em\_gss\_hum.\*

18: em\_gss\_inv.\*

19: em\_gss\_pln.\*

20: em\_gss\_vrt.\*

21: em\_gss\_fun.\*

22: em\_gss\_mam.\*

23: em\_gss\_mus.\*

24: em\_gss\_pro.\*

25: em\_gss\_rod.\*

26: em\_gss\_phg.\*

27: em\_gss\_vrl.\*

28: gb\_gsl.\*

29: gb\_gss2.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	24	100.0	404	14	H81820	H81820 ys68e09.r1
C 2	24	100.0	421	12	BM832613	BM832613 K-EST0107
C 3	24	100.0	544	9	AL707819	AL707819 DKFZp686L
4	24	100.0	781	13	BX097261	BX097261 BX097261

5	18	75.0	525	14	CD848190	CD848190 DH0AC002Z
c	18	75.0	546	13	BU019091	BU019091 QHE20D24.
6	18	75.0	573	13	BY243155	BY243155 BY243155
c	18	75.0	1110	12	BM917206	BM917206 AGENCOURT
9	17	70.8	303	14	CD588643	CD588643 RK047A3H0
10	17	70.8	317	14	CD585274	CD585274 RK030A2C0
11	17	70.8	323	14	CD591703	CD591703 RK065A4G0
12	17	70.8	324	14	CD601328	CD601328 RK132A1C1
13	17	70.8	330	14	CD601373	CD601373 RK132A2C1
14	17	70.8	330	14	CD602150	CD602150 RK140A2F0
15	17	70.8	496	14	CD603852	CD603852 RZ150A3E0
16	17	70.8	500	14	CD585675	CD585675 RK032A1F0
17	17	70.8	514	12	BQ617441	BQ617441 fab04C07.
c	17	70.8	705	13	BQ617441	BQ617441 fab04C07.
18	17	70.8	925	10	BF120890	BF120890 601757493
c	16	66.7	157	10	AM386252	AM386252 CM4-PT001
c	21	66.7	191	10	AW420212	AW420212 fj88g07.Y
c	22	66.7	235	9	AI035445	AI035445 ub47a08.r
c	23	66.7	256	9	AA881130	AA881130 v206g05.r
c	24	66.7	281	12	BG985652	BG985652 ba02a03.u
25	16	66.7	288	10	BB009502	BB009502 BB009502
26	16	66.7	322	14	CD166258	CD166258 MML-0002P
c	27	66.7	324	10	BB838010	BB838010 BB838010
28	16	66.7	325	10	BF148232	BF148232 ux49f03.x
29	16	66.7	335	10	BF318395	BF318395 ux11e01.x
30	16	66.7	339	12	BM211354	BM211354 C0804F12-
c	31	66.7	342	13	BY139003	BY139003 BY139003
c	32	66.7	344	10	BB869806	BB869806 BB869806
33	16	66.7	347	12	BM211586	BM211586 C0808G06-
c	34	66.7	348	13	BY175856	BY175856 BY175856
c	35	66.7	354	13	BY310701	BY310701 BY310701
c	36	66.7	356	9	AA268399	AA268399 va41h09.r
c	37	66.7	359	13	BY020770	BY020770 BY020770
c	38	66.7	361	28	AQ037986	AQ037986 CIT-HSP-2
c	39	66.7	362	28	AQ040284	AQ040284 CIT-HSP-2
40	16	66.7	363	12	BM195340	BM195340 C0308E04-
c	41	66.7	363	13	BY304103	BY304103 BY304103
c	42	66.7	364	9	AA119050	AA119050 mp62h06.r
c	43	66.7	373	13	BY319051	BY319051 BY319051
c	44	66.7	377	13	BX636769	BX636769 BX636769
45	16	66.7	378	14	CD538683	CD538683 B0205E11-

ALIGNMENTS

RESULT 1	H81820	H81820	404 bp	mRNA	linear	EST 09-NOV-1995
LOCUS	ys68e09.r1	Soares retina N2b4HR	Homo sapiens	cDNA clone		
DEFINITION	IMAGE:219976.5	similar to gb:M14752	PROTO-ONCOGENE	TYROSINE-PROTEIN KINASE ABL (HUMAN)		mRNA sequence.
ACCESSION	H81820					
VERSION	H81820.1	GI:1059909				
KEYWORDS	EST.					
SOURCE	Homo sapiens	(human)				
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
REFERENCE	1	(bases 1 to 404)				
AUTHORS	Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevasakis, E., Waterston, R., Williamson, A., Wohldmann, P., and Wilson, R.					
TITLE	The WashU-Merck EST Project					
JOURNAL	Unpublished (1995)					
COMMENT	Contact: Wilson RK Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: est@watson.wustl.edu					





```

ORIGIN
Query Match      100.0%; Score 24; DB 9; Length 544;
Best Local Similarity 75.0%; Pred. No. 0.004;
Matches 18; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGUGAAGGCUCAUGUCCAC 24
    |||:|||||:|||||:|||||
DB 524 CCGCTGAAGGCTTCATGTTCCAC 501

RESULT 4
LOCUS BX097261
DEFINITION BX097261 Soares retina N2b4HR Homo sapiens cDNA clone
ACCESSION BX097261
VERSION 1
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE 1 (bases 1 to 781)
JOURNAL Ebert, L., Heil, O., Hennig, S., Neubert, P., Partsch, E., Peters, M.,
COMMENT Radelof, U., Schneider, D. and Korn, B.
Human Unigeneset - RZPD3
Unpublished (2003)
Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
RZPD; IMAGp998C17436.
RZPDLIB; I.M.A.G.E. cDNA Clone Collection;
http://www.rzpd.de/CloneCards/cgi-
bin/showLib.pl.cgi?response?libno=972 Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 101
Fax: +49 30 32639 111
www.rzpd.de
This clone is available royalty-free from RZPD;
contact RZPD (clone@rzpd.de) for further information. Seq primer:
M13r, Primer sequence: TTTCACAGGAACAGCATATGAC.
FEATURES
source
1..781
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGp998C17436 ; IMAGE:219976"
/sex="male"
/tissue_type="retina"
/dev_stage="55 year old"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares retina N2b4HR"
/noted="Organ: eye; Vector: pT7T3D (Pharmacia) with a
modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(GT) primer [5',
TGTTCACATCTGAGTGGAGCGCGCGCTTTTCTTTTCTTTT 3']."
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT7T3 vector
(Pharmacia). The retinas were obtained from a 55 year old
Caucasian and total cellular poly(A)+ RNA was extracted 6
hrs after their removal. The retina RNA was kindly
provided by Roderick R. McInnes M.D. Ph.D. from the
University of Toronto. Library constructed by Bento
Soares and M.Fatima Bonaldo.
ORIGIN
Query Match      100.0%; Score 24; DB 13; Length 781;
Best Local Similarity 75.0%; Pred. No. 0.0045;

ORIGIN
Query Match      75.0%; Score 18; DB 14; Length 525;
Best Local Similarity 72.2%; Pred. No. 10;
Matches 13; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 7 AAGGCUCAUGUCCAC 24
    |||:|||||:|||||:|||||
DB 211 AAGGCTTCATGTTCCAC 228

RESULT 6
LOCUS BU019091/c
DEFINITION QHE20D24.yg.ab1 QH EFGHJ sunflower RHA280 Helianthus annuus cDNA
ACCESSION BU019091
VERSION 1
KEYWORDS EST.
SOURCE Helianthus annuus (common sunflower)
ORGANISM Helianthus annuus
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Lai, Z., Church, S., Jackson, L. and Bradford, K.
Lettuce and Sunflower ESTs from the Compositae Genome Project
TITLE

ORIGIN
Query Match      75.0%; Score 18; DB 14; Length 525;
Best Local Similarity 72.2%; Pred. No. 10;
Matches 13; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGUGAAGGCUCAUGUCCAC 24
    |||:|||||:|||||:|||||
DB 91 CCGCTGAAGGCTTCATGTTCCAC 114

RESULT 5
LOCUS CD848190
DEFINITION DH0AC002ZH02FM1 HaDevR2 Helianthus annuus cDNA clone HaDevR2002H02,
ACCESSION CD848190
VERSION 1
KEYWORDS EST.
SOURCE Helianthus annuus (common sunflower)
ORGANISM Helianthus annuus
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
JOURNAL asterids; campanulids; Asterales; Asteraceae; Asteroideae;
COMMENT Heliantheae; Helianthus.
1 (bases 1 to 525)
Genoplante.
Genoplante, a major partnership french program in plant genomics
Unpublished (2003)
Contact: Genoplante
Genoplante
93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplante' (http://www.genoplante.com
and http://genoplante-info.infobiogen.fr).
FEATURES
source
1..525
/organism="Helianthus annuus"
/mol_type="mRNA"
/cultivar="pssc8"
/db_xref="taxon:4232"
/clone="HaDevR2002H02"
/tissue_type="terminal bud"
/clone_lib="HaDevR2"

```

http://compgenomics.ucdavis.edu/  
 Unpublished (2002)  
 Contact: Alexander Kozik [R.W.Michelmore]  
 Department of Vegetable Crops, R.W.Michelmore Lab  
 University of California at Davis (UCD)  
 Aemundson Hall, UCD, Davis, CA 95616, USA  
 Tel: 1-(530)-742-1742  
 Fax: 1-(530)-752-9659  
 Email: akozik@ucdavis.edu [michelmore@vegmail.ucdavis.edu]  
 singleton, see http://cgpdb.ucdavis.edu/ for details.  
 Plate: QHE20 row: D column: 24.

**TITLE**  
 Analysis of the mouse transcriptome based on functional annotation  
 of 60,770 full-length cDNAs

**JOURNAL**  
 MEDLINE  
 PUBMED  
 COMMENT

**FEATURES**  
 source  
 1. .546  
 /organism="Heliathus annuus"  
 /mol\_type="mRNA"  
 /cultivar="RHA280"  
 /db\_xref="taxon:4232"  
 /clone="QHE20D24"  
 /lab\_host="E.coli"  
 /clone\_lib="QH EFGHJ sunflower RHA280"  
 /note="Vector: pBRCN2ASf1AB; The library was constructed from 11 different sources of RNA from a single genotype. Separate cDNAs were generated using primers that incorporated unique 5' and 3' tags to distinguish each source of RNA. cDNAs were then pooled, size-fractionated, directionally cloned into a custom medium-copy vector and transformations made with four size classes to minimize size bias. Details of each source of RNA and library construction can be obtained at http://cgpdb.ucdavis.edu/  
 TAG TISSUE=roots environmental stress  
 TAG LIB=QH EFGHJ sunflower RHA280  
 TAG\_SEQ=ATTCGCGGG"

**ORIGIN**  
 Query Match 75.0%; Score 18; DB 13; Length 546;  
 Best Local Similarity 72.2%; Pred. No. 10;  
 Matches 13; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 7 AACGGGUCAUGUCCAC 24  
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 Db 309 AAGGCTTCATGTTCCAC 292

**RESULT 7**  
 BY243155  
 LOCUS  
 DEFINITION  
 BY243155 RIKEN full-length enriched, visual cortex Mus musculus  
 cDNA clone K230039L14 5', mRNA sequence.  
 ACCESSION  
 VERSION  
 BY243155.1 GI:26424667  
 KEYWORDS  
 EST.  
 SOURCE  
 Mus musculus (house mouse)  
 ORGANISM  
 Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 573)  
 Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I.,  
 Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A.,  
 Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C.,  
 Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H.,  
 Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V.,  
 Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A.,  
 Fletcher,C.P., Forrest,A., Frazer,K.S., Gaasterland,T.,  
 Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S.,  
 Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A.,  
 Kawai,H., Kawasawa,Y., Kedzierzki,R.M., King,B.L., Konagaya,A.,  
 Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R.,  
 Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T.,  
 Numata,K., Okido,T., Pavan,W.J., Perlea,G., Pesole,G.,  
 Petrovsky,N., Fillat,R., Pontius,J.U., Qi,D., Ramachandran,S.,  
 Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M.,  
 Sandelin,A., Schneider,C., Sempie,C.A., Setou,M., Shimada,K.,

Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M.,  
 Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y.,  
 Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I.,  
 Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P.,  
 Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M.,  
 Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K.,  
 Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y.,  
 Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K.,  
 Shinagawa,A., Yagunishi,A., Yoshino,M., Waterston,R., Lander,E.S.,  
 Rogers,J., Birney,E. and Hayashizaki,Y.  
 Analysis of the mouse transcriptome based on functional annotation  
 of 60,770 full-length cDNAs  
 Nature 420, 563-573 (2002)  
 12466851  
 Contact: Yoshihide Hayashizaki  
 Laboratory for Genome Exploration Research Group, RIKEN Genomic  
 Sciences Center (GSC), Yokohama Institute  
 The Institute of Physical and Chemical Research (RIKEN)  
 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan  
 Tel: 81-45-503-9222  
 Fax: 81-45-503-9216  
 Email: genome-res@gsr.riken.go.jp,  
 URL:http://genome.gsc.riken.go.jp/  
 Aizawa,K., Akimura,T., Arakawa,T., Itoh,M., Kawai,J., Konno,H.,  
 Hirozane,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H.,  
 Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R.,  
 Ohno,M., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K.,  
 Shiraki,T., Tagami,M., Waki,K., Watanabe,A., Muramatsu,M. and  
 Hayashizaki,Y. Direct Submission  
 Computational Analysis of Full-Length Mouse cDNAs Compared with  
 Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)  
 Normalization and subtraction of cap-trapper-selected cDNAs to  
 prepare full-length cDNA libraries for rapid discovery of new  
 genes. Genome Res. 10 (10), 1617-1630 (2000)  
 RIKEN integrated sequence analysis (RISA) system-384-format  
 sequencing pipeline with 384 multipipillary sequencer. Genome Res.  
 10 (11), 1757-1771 (2000)  
 Computer-based methods for the mouse full-length cDNA  
 encyclopedia: real-time sequence clustering for construction of a  
 nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)  
 cDNA library was prepared and sequenced in Mouse Genome  
 Encyclopedia Project of Genome Exploration Research Group in Riken  
 Genomic Sciences Center and Genome Science Laboratory in RIKEN.  
 Division of Experimental Animal Research in Riken contributed to  
 prepare mouse tissues.  
 Tissues were provided by Michela Fagioli and Takao K. Hensch (  
 Laboratory for Neuronal Circuit Development Brain Science Institute  
 RIKEN 2-1 Hiroosawa,Wako-shi,Saitama 351-0198 Japan ) whose  
 assistance we gratefully acknowledge. Please visit our web site  
 (http://genome.gsc.riken.go.jp) for further details.

**FEATURES**  
 Location/Qualifiers  
 1. .573  
 /organism="Mus musculus"  
 /mol\_type="mRNA"  
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 /db\_xref="taxon:10090"  
 /clone="K230039L14"  
 /tissue\_type="visual cortex"  
 /clone\_lib="RIKEN full-length enriched, visual cortex"

**ORIGIN**  
 Query Match 75.0%; Score 18; DB 13; Length 573;  
 Best Local Similarity 77.8%; Pred. No. 11;  
 Matches 14; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGCGUAGAGGCTTCAUG 18  
 |||||:||||:|||||  
 Db 462 CCGCTGAGGCTTCATG 479

**RESULT 8**  
 BM917206/c

```

LOCUS       BM917206               1110 bp    mRNA    linear    EST 12-MAR-2002
DEFINITION  AGENCOURT_6702147 NIH_MGC_106 Homo sapiens cDNA clone IMAGE:5483703
            5', mRNA sequence.
ACCESSION   BM917206
VERSION     BM917206.1 GI:19367585
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 1110)
AUTHORS     NIH-MGC http://mgc.nci.nih.gov/
TITLE       National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL     Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgabs@mail.nih.gov
            Tissue Procurement: Dr. Daniel McVicar, DBS/NCI
            cDNA Library Preparation: Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LCM2011 row: m column: 16
            High quality sequence stop: 651.

FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5483703"
                     /tissue_type="natural killer cells, cell line"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH MGC 106"
                     /note="Organ: blood; Vector: pOTB7; Site 1: XhoI; Site 2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GCACAGAG(G). Library constructed by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life Technologies). Note: this is a
                     NIH_MGC Library."

ORIGIN
Query Match       75.0%; Score 18; DB 12; Length 1110;
Best Local Similarity 66.7%; Pred. No. 13;
Matches 12; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY  3  GCUGAAGGCGUUCAGUU 20
    ||:|||||:||||:|
DB   823  GCTGAAGGCGTTCATGTT 806

RESULT 9
CD588643
LOCUS       CD588643               303 bp    mRNA    linear    EST 16-JUN-2003
DEFINITION  RK047A3H04.T3 Zebrafish Kidney Marrow cDNA library Danio rerio cDNA
            clone RK047A3H04 5', mRNA sequence.
ACCESSION   CD588643
VERSION     CD588643.1 GI:31769995
KEYWORDS    EST.
SOURCE      Danio rerio (zebrafish)
  ORGANISM  Danio rerio
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
            Cypriniformes; Cyprinidae; Danio.
REFERENCE   1 (bases 1 to 303)
AUTHORS     Song,H.D., Wu,X.Y., Sun,X.J., Zhou,Y., Liu,T.X., Zhang,G.W.,
            Sheng,Y., Chen,Y., Ruan,Z., Jiang,C.L., Fan,H.Y., Look,A.T.,
            Zou,L.I. and Chen,Z.
TITLE       Gene Expression Profiling in the Zebrafish Kidney Marrow Tissue
JOURNAL     Unpublished (2003)
COMMENT     Contact: Chen Z.

QY  3  GCUGAAGGCGUUCAGUU 20
    ||:|||||:||||:|
DB   823  GCTGAAGGCGTTCATGTT 806

FEATURES             Location/Qualifiers
     source           1..317
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                     /mol_type="mRNA"
                     /db_xref="taxon:7955"
                     /clone="RK047A3H04"
                     /dev_stage="mature"
                     /clone_lib="Zebrafish Kidney Marrow cDNA library"
                     /note="Organ: kidney; Vector: pBS-CMV; Site 1: XhoI;
                     Site 2: EcoRI; Total RNA was extracted from the kidney
                     tissues of mature zebrafish. The poly (A) + RNA fraction
                     was separated from total RNA by oligo (dT) cellulose
                     chromatography. Library was initially constructed in the
                     lambdaZAP Express vector (Stratagene) and in vivo excised
                     into pBS-CMV vector."

ORIGIN
Query Match       70.8%; Score 17; DB 14; Length 303;
Best Local Similarity 64.7%; Pred. No. 32;
Matches 11; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY  4  CUGAAGGCGUUCAGUU 20
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DB   111  CTGAAGGCGTTCATGTT 127

RESULT 10
CD585274
LOCUS       CD585274               317 bp    mRNA    linear    EST 16-JUN-2003
DEFINITION  RK030A2C01.T3 Zebrafish Kidney Marrow cDNA library Danio rerio cDNA
            clone RK030A2C01 5', mRNA sequence.
ACCESSION   CD585274
VERSION     CD585274.1 GI:31766016
KEYWORDS    EST.
SOURCE      Danio rerio (zebrafish)
  ORGANISM  Danio rerio
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
            Cypriniformes; Cyprinidae; Danio.
REFERENCE   1 (bases 1 to 317)
AUTHORS     Song,H.D., Wu,X.Y., Sun,X.J., Zhou,Y., Liu,T.X., Zhang,G.W.,
            Sheng,Y., Chen,Y., Ruan,Z., Jiang,C.L., Fan,H.Y., Look,A.T.,
            Zou,L.I. and Chen,Z.
TITLE       Gene Expression Profiling in the Zebrafish Kidney Marrow Tissue
JOURNAL     Unpublished (2003)
COMMENT     Contact: Chen Z.

QY  4  CUGAAGGCGUUCAGUU 20
    |:|||||:||||:|
DB   111  CTGAAGGCGTTCATGTT 127

FEATURES             Location/Qualifiers
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                     /db_xref="taxon:7955"
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                     /dev_stage="mature"
                     /clone_lib="Zebrafish Kidney Marrow cDNA library"
                     /note="Organ: kidney; Vector: pBS-CMV; Site 1: XhoI;
                     Site 2: EcoRI; Total RNA was extracted from the kidney
                     tissues of mature zebrafish. The poly (A) + RNA fraction
                     was separated from total RNA by oligo (dT) cellulose
                     chromatography. Library was initially constructed in the
                     lambdaZAP Express vector (Stratagene) and in vivo excised
                     into pBS-CMV vector."

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State Key Lab for Medical Genomics
Shanghai Institute of Hematology, Ruijin Hospital Affiliated to
Shanghai Second Medical University
197 Rui Jin Road II, Shanghai 200025, P. R. China
Tel: 86-21-64740490
Fax: 86-21-64743206
Email: zchen@stn.sh.cn
Seq primer: T3.

FEATURES             Location/Qualifiers
     source           1..303
                     /organism="Danio rerio"
                     /mol_type="mRNA"
                     /db_xref="taxon:7955"
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                     /dev_stage="mature"
                     /clone_lib="Zebrafish Kidney Marrow cDNA library"
                     /note="Organ: kidney; Vector: pBS-CMV; Site 1: XhoI;
                     Site 2: EcoRI; Total RNA was extracted from the kidney
                     tissues of mature zebrafish. The poly (A) + RNA fraction
                     was separated from total RNA by oligo (dT) cellulose
                     chromatography. Library was initially constructed in the
                     lambdaZAP Express vector (Stratagene) and in vivo excised
                     into pBS-CMV vector."

ORIGIN
Query Match       70.8%; Score 17; DB 14; Length 303;
Best Local Similarity 64.7%; Pred. No. 32;
Matches 11; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY  4  CUGAAGGCGUUCAGUU 20
    |:|||||:||||:|
DB   111  CTGAAGGCGTTCATGTT 127

RESULT 10
CD585274
LOCUS       CD585274               317 bp    mRNA    linear    EST 16-JUN-2003
DEFINITION  RK030A2C01.T3 Zebrafish Kidney Marrow cDNA library Danio rerio cDNA
            clone RK030A2C01 5', mRNA sequence.
ACCESSION   CD585274
VERSION     CD585274.1 GI:31766016
KEYWORDS    EST.
SOURCE      Danio rerio (zebrafish)
  ORGANISM  Danio rerio
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
            Cypriniformes; Cyprinidae; Danio.
REFERENCE   1 (bases 1 to 317)
AUTHORS     Song,H.D., Wu,X.Y., Sun,X.J., Zhou,Y., Liu,T.X., Zhang,G.W.,
            Sheng,Y., Chen,Y., Ruan,Z., Jiang,C.L., Fan,H.Y., Look,A.T.,
            Zou,L.I. and Chen,Z.
TITLE       Gene Expression Profiling in the Zebrafish Kidney Marrow Tissue
JOURNAL     Unpublished (2003)
COMMENT     Contact: Chen Z.

QY  4  CUGAAGGCGUUCAGUU 20
    |:|||||:||||:|
DB   111  CTGAAGGCGTTCATGTT 127

FEATURES             Location/Qualifiers
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                     /clone="RK030A2C01"
                     /dev_stage="mature"
                     /clone_lib="Zebrafish Kidney Marrow cDNA library"
                     /note="Organ: kidney; Vector: pBS-CMV; Site 1: XhoI;
                     Site 2: EcoRI; Total RNA was extracted from the kidney
                     tissues of mature zebrafish. The poly (A) + RNA fraction
                     was separated from total RNA by oligo (dT) cellulose
                     chromatography. Library was initially constructed in the
                     lambdaZAP Express vector (Stratagene) and in vivo excised
                     into pBS-CMV vector."

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was separated from total RNA by oligo (dT) cellulose chromatography. Library was initially constructed in the lambdaZAP Express vector (Stratagene) and in vivo excised into pBS-CMV vector."

## ORIGIN

Query Match 70.8%; Score 17; DB 14; Length 317;  
Best Local Similarity 64.7%; Pred. No. 32;  
Matches 11; Conservative 6; Mismatches 0; Indels 0; Gaps 0;  
  
QY 4 CUGAAGGCGUUCAGUU 20  
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Db 123 CTGAAGGCTTCATGTT 139

## RESULT 11

CD591703  
LOCUS  
DEFINITION 323 bp mRNA linear EST 16-JUN-2003  
clone RK065A4G05.T3 Zebrafish Kidney Marrow cDNA library Danio rerio cDNA  
clone RK065A4G05 5', mRNA sequence.

CD591703  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

Danio rerio (zebrafish)  
State Key Lab for Medical Genomics  
Shanghai Institute of Hematology, Ruijin Hospital Affiliated to  
Shanghai Second Medical University

REFERENCE  
AUTHORS  
Actinopterygii; Neopterygii; Teleostei; Osteiophysi;  
Cypriniformes; Cyprinidae; Danio.

1 (bases 1 to 323)  
Song,H.D., Wu,X.Y., Sun,X.J., Zhou,Y., Liu,T.X., Zhang,G.W.,  
Sheng,Y., Chen,Y., Ruan,Z., Jiang,C.L., Fan,H.Y., Look,A.T.,  
Zou,L.I. and Chen,Z.  
Gene Expression Profiling in the Zebrafish Kidney Marrow Tissue  
Unpublished (2003)  
Contact: Chen Z.

State Key Lab for Medical Genomics  
Shanghai Institute of Hematology, Ruijin Hospital Affiliated to  
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197 Rui Jin Road II, Shanghai 200025, P. R. China  
Tel: 86-21-64740490  
Fax: 86-21-64743206  
Email: zchen@stn.sh.cn  
Seq primer: T3.

## FEATURES

## source

1..323  
/organism="Danio rerio"  
/mol\_type="mRNA"  
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/clone="RK065A4G05"  
/dev\_stage="mature"  
/clone\_lib="Zebrafish Kidney Marrow cDNA library"  
/note="Organ: kidney; Vector: pBS-CMV; Site 1: XhoI;  
Site 2: EcoRI; Total RNA was extracted from the kidney  
tissues of mature zebrafish. The poly (A)+ RNA fraction  
was separated from total RNA by oligo (dT) cellulose  
chromatography. Library was initially constructed in the  
lambdaZAP Express vector (Stratagene) and in vivo excised  
into pBS-CMV vector."

## ORIGIN

Query Match 70.8%; Score 17; DB 14; Length 323;  
Best Local Similarity 64.7%; Pred. No. 32;  
Matches 11; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 4 CUGAAGGCGUUCAGUU 20  
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Db 120 CTGAAGGCTTCATGTT 136

## RESULT 12

CD601328  
LOCUS  
DEFINITION 324 bp mRNA linear EST 16-JUN-2003  
clone RK132A1C12.T3 Zebrafish Kidney Marrow cDNA library Danio rerio cDNA

clone RK132A1C12 5', mRNA sequence.

CD601328  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

Danio rerio (zebrafish)  
State Key Lab for Medical Genomics  
Shanghai Institute of Hematology, Ruijin Hospital Affiliated to  
Shanghai Second Medical University

REFERENCE  
AUTHORS  
Actinopterygii; Neopterygii; Teleostei; Osteiophysi;  
Cypriniformes; Cyprinidae; Danio.

1 (bases 1 to 324)  
Song,H.D., Wu,X.Y., Sun,X.J., Zhou,Y., Liu,T.X., Zhang,G.W.,  
Sheng,Y., Chen,Y., Ruan,Z., Jiang,C.L., Fan,H.Y., Look,A.T.,  
Zou,L.I. and Chen,Z.  
Gene Expression Profiling in the Zebrafish Kidney Marrow Tissue  
Unpublished (2003)  
Contact: Chen Z.

State Key Lab for Medical Genomics  
Shanghai Institute of Hematology, Ruijin Hospital Affiliated to  
Shanghai Second Medical University  
197 Rui Jin Road II, Shanghai 200025, P. R. China  
Tel: 86-21-64740490  
Fax: 86-21-64743206  
Email: zchen@stn.sh.cn  
Seq primer: T3.

## FEATURES

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1..324  
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/clone\_lib="Zebrafish Kidney Marrow cDNA library"  
/note="Organ: kidney; Vector: pBS-CMV; Site 1: XhoI;  
Site 2: EcoRI; Total RNA was extracted from the kidney  
tissues of mature zebrafish. The poly (A)+ RNA fraction  
was separated from total RNA by oligo (dT) cellulose  
chromatography. Library was initially constructed in the  
lambdaZAP Express vector (Stratagene) and in vivo excised  
into pBS-CMV vector."

## ORIGIN

Query Match 70.8%; Score 17; DB 14; Length 324;  
Best Local Similarity 64.7%; Pred. No. 33;  
Matches 11; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 4 CUGAAGGCGUUCAGUU 20  
|:|||||:|:|:|:  
Db 111 CTGAAGGCTTCATGTT 127

## RESULT 13

## CD601373

LOCUS  
DEFINITION 330 bp mRNA linear EST 16-JUN-2003  
clone RK132A2C11.T3 Zebrafish Kidney Marrow cDNA library Danio rerio cDNA  
clone RK132A2C11 5', mRNA sequence.

CD601373  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

Danio rerio (zebrafish)  
State Key Lab for Medical Genomics  
Shanghai Institute of Hematology, Ruijin Hospital Affiliated to  
Shanghai Second Medical University

REFERENCE  
AUTHORS  
Actinopterygii; Neopterygii; Teleostei; Osteiophysi;  
Cypriniformes; Cyprinidae; Danio.

1 (bases 1 to 330)  
Song,H.D., Wu,X.Y., Sun,X.J., Zhou,Y., Liu,T.X., Zhang,G.W.,  
Sheng,Y., Chen,Y., Ruan,Z., Jiang,C.L., Fan,H.Y., Look,A.T.,  
Zou,L.I. and Chen,Z.  
Gene Expression Profiling in the Zebrafish Kidney Marrow Tissue  
Unpublished (2003)  
Contact: Chen Z.

State Key Lab for Medical Genomics  
Shanghai Institute of Hematology, Ruijin Hospital Affiliated to  
Shanghai Second Medical University

197 Rui Jin Road II, Shanghai 200025, P. R. China  
 Tel: 86-21-64740490  
 Fax: 86-21-64743206  
 Email: zchen@stn.sh.cn  
 Seq primer: T3.

# FEATURES

Location/Qualifiers  
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 /mol\_type="mRNA"  
 /db\_xref="taxon:7955"  
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 /clone\_lib="Zebrafish Kidney Marrow cDNA library"  
 /note="Organ: kidney; Vector: pBS-CMV; Site: 1: XhoI;  
 Site 2: EcoRI; Total RNA was extracted from the kidney  
 tissues of mature zebrafish. The poly (A)+ RNA fraction  
 was separated from total RNA by oligo (dT) cellulose  
 chromatography. Library was initially constructed in the  
 lambdaZAP Express vector (Stratagene) and in vivo excised  
 into pBS-CMV vector."

## ORIGIN

Query Match 70.8%; Score 17; DB 14; Length 330;  
 Best Local Similarity 64.7%; Pred. No. 33;  
 Matches 11; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 4 CUGAAGGGCUCAUGUU 20  
 |:|||||:|:|:|:  
 Db 111 CTGAAGGCTTCATGTT 127

## RESULT 14

CD602150  
 LOCUS  
 DEFINITION  
 CD602150 330 bp mRNA linear EST 16-JUN-2003  
 clone RK140A2F04 T3 Zebrafish Kidney Marrow cDNA library Danio rerio cDNA  
 clone RK140A2F04 5', mRNA sequence.

ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 EST.  
 CD602150.1 GI:31783502

ORGANISM  
 Danio rerio (zebrafish)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Actinopterygii; Neopterygii; Teleostei; Ostariophysi;  
 Cypriniformes; Cyprinidae; Danio.

## REFERENCE

AUTHORS  
 Song, H.D., Wu, X.Y., Sun, X.J., Zhou, Y., Liu, T.X., Zhang, G.W.,  
 Sheng, Y., Chen, Y., Ruan, Z., Jiang, C.L., Fan, H.Y., Look, A.T.,  
 Zou, L.I., and Chen, Z.

TITLE  
 JOURNAL  
 COMMENT  
 Gene Expression Profiling in the Zebrafish Kidney Marrow Tissue  
 Unpublished (2003)  
 Contact: Chen Z.

State Key Lab for Medical Genomics  
 Shanghai Institute of Hematology, Ruijin Hospital Affiliated to  
 Shanghai Second Medical University  
 197 Rui Jin Road II, Shanghai 200025, P. R. China  
 Tel: 86-21-64740490  
 Fax: 86-21-64743206  
 Email: zchen@stn.sh.cn  
 Seq primer: T3.

# FEATURES

Location/Qualifiers  
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 Site 2: EcoRI; Total RNA was extracted from the kidney  
 tissues of mature zebrafish. The poly (A)+ RNA fraction  
 was separated from total RNA by oligo (dT) cellulose  
 chromatography. Library was initially constructed in the  
 lambdaZAP Express vector (Stratagene) and in vivo excised

ORIGIN  
 into pBS-CMV vector."

Query Match 70.8%; Score 17; DB 14; Length 330;  
 Best Local Similarity 64.7%; Pred. No. 33;  
 Matches 11; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 4 CUGAAGGGCUCAUGUU 20  
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 Db 123 CTGAAGGCTTCATGTT 139

## RESULT 15

CD603852  
 LOCUS  
 DEFINITION  
 CD603852 496 bp mRNA linear EST 16-JUN-2003  
 clone RZ150A3E05 T3 Zebrafish Kidney Marrow cDNA library Danio rerio cDNA  
 clone RZ150A3E05 5', mRNA sequence.

ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 EST.  
 CD603852.1 GI:31785204

ORGANISM  
 Danio rerio (zebrafish)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Actinopterygii; Neopterygii; Teleostei; Ostariophysi;  
 Cypriniformes; Cyprinidae; Danio.

## REFERENCE

AUTHORS  
 1 (bases 1 to 496)  
 Song, H.D., Wu, X.Y., Sun, X.J., Zhou, Y., Liu, T.X., Zhang, G.W.,  
 Sheng, Y., Chen, Y., Ruan, Z., Jiang, C.L., Fan, H.Y., Look, A.T.,  
 Zou, L.I., and Chen, Z.

## TITLE

JOURNAL  
 COMMENT  
 Gene Expression Profiling in the Zebrafish Kidney Marrow Tissue  
 Unpublished (2003)  
 Contact: Chen Z.  
 State Key Lab for Medical Genomics  
 Shanghai Institute of Hematology, Ruijin Hospital Affiliated to  
 Shanghai Second Medical University  
 197 Rui Jin Road II, Shanghai 200025, P. R. China  
 Tel: 86-21-64740490  
 Fax: 86-21-64743206  
 Email: zchen@stn.sh.cn  
 Seq primer: T3.

## FEATURES

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 Site 2: EcoRI; Total RNA was extracted from the kidney  
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 was separated from total RNA by oligo (dT) cellulose  
 chromatography. Library was initially constructed in the  
 lambdaZAP Express vector (Stratagene) and in vivo excised  
 into pBS-CMV vector."

## ORIGIN

Query Match 70.8%; Score 17; DB 14; Length 496;  
 Best Local Similarity 64.7%; Pred. No. 37;  
 Matches 11; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

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 Db 180 CTGAAGGCTTCATGTT 196

Search completed: May 26, 2004, 22:44:34  
 Job time : 847.385 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 26, 2004, 16:00:31 ; Search time 1149.26 Seconds  
(without alignments)  
2036.547 Million cell updates/sec

Title: US-09-121-239-2

Perfect score: 54

Sequence: 1 UAAUUAUACGACUCACUA.....CCUGAGGCGUCAAAGUCAGA 54

Scoring table:

OLIGO NUC

Gapop 60.0 , Gapext 60.0

Searched: 3470272 seqs, 21671516995 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

GenEmbl.\*

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3: gb\_in.\*

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5: gb\_ov.\*

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14: gb\_vi.\*

15: em\_ba.\*

16: em\_fun.\*

17: em\_hum.\*

18: em\_in.\*

19: em\_mu.\*

20: em\_om.\*

21: em\_or.\*

22: em\_ov.\*

23: em\_pat.\*

24: em\_ph.\*

25: em\_pl.\*

26: em\_ro.\*

27: em\_sts.\*

28: em\_un.\*

29: em\_vi.\*

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31: em\_hcg\_inv.\*

32: em\_hcg\_other.\*

33: em\_hcg\_mus.\*

34: em\_hcg\_pln.\*

35: em\_hcg\_rtd.\*

36: em\_hcg\_nam.\*

37: em\_hcg\_vrt.\*

38: em\_sy.\*

39: em\_hugo\_hum.\*

40: em\_hugo\_mus.\*

41: em\_hugo\_other.\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	54	100.0	54	6	BD222523	BD222523 Methods f
2	54	100.0	54	6	BD222524	BD222524 Methods f
3	54	100.0	54	6	BD222525	BD222525 Methods f
4	54	100.0	54	6	BD222526	BD222526 Methods f
5	49	90.7	50	6	AR352057	AR352057 Sequence
6	32	59.3	54	6	BD236957	BD236957 Nucleic a
7	32	59.3	54	6	AR307443	AR307443 Sequence
8	30	55.6	49	6	BD236963	BD236963 Nucleic a
9	30	55.6	49	6	AR307449	AR307449 Sequence
10	30	55.6	50	6	BD236956	BD236956 Nucleic a
11	30	55.6	50	6	AR307442	AR307442 Sequence
12	30	55.6	52	6	BD236968	BD236968 Nucleic a
13	30	55.6	52	6	AR307454	AR307454 Sequence
14	29	53.7	37	6	I25071	I25071 Sequence 5
15	29	53.7	45	6	AX575411	AX575411 Sequence
16	29	53.7	50	6	AR102985	AR102985 Sequence
17	29	53.7	51	6	AR344851	AR344851 Sequence
18	29	53.7	51	6	AX397806	AX397806 Sequence
19	29	53.7	52	6	BD236961	BD236961 Nucleic a
20	29	53.7	52	6	BD236967	BD236967 Nucleic a
21	29	53.7	52	6	AR307447	AR307447 Sequence
22	29	53.7	52	6	AR307453	AR307453 Sequence
23	29	53.7	54	6	BD236955	BD236955 Nucleic a
24	29	53.7	54	6	BD236974	BD236974 Nucleic a
25	29	53.7	54	6	AR307441	AR307441 Sequence
26	29	53.7	54	6	AR307460	AR307460 Sequence
27	29	53.7	55	6	BD236972	BD236972 Nucleic a
28	29	53.7	55	6	AR307458	AR307458 Sequence
29	29	53.7	60	6	I25073	I25073 Sequence 7
30	29	53.7	79	6	I25069	I25069 Sequence 3
31	29	53.7	180	6	I25067	I25067 Sequence 1
32	29	53.7	586	6	AX701716	AX701716 Sequence
33	29	53.7	1440	6	AX701737	AX701737 Sequence
34	29	53.7	2073	12	CU002284	CU002284 Cloning vec
35	29	53.7	6306	6	AX286493	AX286493 Sequence
36	29	53.7	7201	6	AX800664	AX800664 Sequence
37	29	53.7	7231	6	AX806466	AX806466 Sequence
38	29	53.7	7297	6	AX806467	AX806467 Sequence
39	29	53.7	7429	6	AX839727	AX839727 Sequence
40	29	53.7	7456	6	AX806465	AX806465 Sequence
41	28	51.9	28	6	BD236969	BD236969 Nucleic a
42	28	51.9	28	6	AR307455	AR307455 Sequence
43	28	51.9	30	6	AR369578	AR369578 Sequence
44	28	51.9	30	6	AR404157	AR404157 Sequence
45	28	51.9	33	6	AR344815	AR344815 Sequence

ALIGNMENTS

RESULT 1  
BD222523  
LOCUS BD222523 54 bp DNA linear PAT 17-JUL-2003  
DEFINITION Methods for detecting and measuring spliced nucleic acids.  
ACCESSION BD222523  
VERSION BD222523.1 GI:33032293  
KEYWORDS JP 2002521037-A/1.  
SOURCE synthetic construct  
ORGANISM artificial sequences.  
REFERENCE 1 (bases 1 to 54)  
AUTHORS Harvey, R.C. and Eastman, P.S.  
TITLE Methods for detecting and measuring spliced nucleic acids  
JOURNAL Patent: JP 2002521037-A 1 16-JUL-2002;  
GEN PROBE INC

```
COMMENT OS Artificial Sequence
PN JP 2002521037-A/1
PD 16-JUL-2002
PF 23-JUL-1999 JP 2000561364
PR 23-JUL-1998 US 09/121239
PT RICHARD C HARVEY, PAUL S EASTMAN
PC C12Q1/68, C12N15/09, C12N15/00
CC Description of Artificial Sequence: Synthetic promoter primer
CC promoter sequence at residues 1-27
FH Key Location/Qualifiers
FT source 1..54
/organism='Artificial Sequence'.

FEATURES
source
1..54
/organism="synthetic construct"
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/db_xref="taxon:32630"

ORIGIN
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Best Local Similarity 79.6%; Pred. No. 1.1e-20; Indels 0; Gaps 0;
Matches 43; Conservative 11; Mismatches 0;

QY 1 UAAUUUAUACGACUCACUAUAGGGAGAGCUCAGACCCUGAGGCUCUAAAGUCAGA 54
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Db 1 TAAATTATACGACTCACTATAGGGAGACTCAGACCCCTGAGGCTCAAGTCAGA 54

RESULT 2
BD222524
LOCUS 54 bp RNA linear PAT 17-JUL-2003
DEFINITION Methods for detecting and measuring spliced nucleic acids.
ACCESSION BD222524
VERSION BD222524.1 GI:33032294
KEYWORDS JP 2002521037-A/2.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 54)
HARVEY,R.C. and EASTMAN,P.S.
METHODS FOR DETECTING AND MEASURING SPLICED NUCLEIC ACIDS
TITLE Patent: JP 2002521037-A 2 16-JUL-2002;
JOURNAL GEN PROBE INC
COMMENT OS Artificial Sequence
PN JP 2002521037-A/2
PD 16-JUL-2002
PF 23-JUL-1999 JP 2000561364
PR 23-JUL-1998 US 09/121239
PT RICHARD C HARVEY, PAUL S EASTMAN
PC C12Q1/68, C12N15/09, C12N15/00
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FH Key Location/Qualifiers
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/organism='Artificial Sequence'.

FEATURES
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ORIGIN
Query Match 100.0%; Score 54; DB 6; Length 54;
Best Local Similarity 79.6%; Pred. No. 1.1e-20; Indels 0; Gaps 0;
Matches 43; Conservative 11; Mismatches 0;

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Db 1 TAAATTATACGACTCACTATAGGGAGACTCAGACCCCTGAGGCTCAAGTCAGA 54

RESULT 3
BD222525/c
LOCUS 54 bp DNA linear PAT 17-JUL-2003
DEFINITION Methods for detecting and measuring spliced nucleic acids.
ACCESSION BD222525
VERSION BD222525.1 GI:33032295
KEYWORDS JP 2002521037-A/3.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 54)
HARVEY,R.C. and EASTMAN,P.S.
METHODS FOR DETECTING AND MEASURING SPLICED NUCLEIC ACIDS
TITLE Patent: JP 2002521037-A 3 16-JUL-2002;
JOURNAL GEN PROBE INC
COMMENT OS Artificial Sequence
PN JP 2002521037-A/3
PD 16-JUL-2002
PF 23-JUL-1999 JP 2000561364
PR 23-JUL-1998 US 09/121239
PT RICHARD C HARVEY, PAUL S EASTMAN
PC C12Q1/68, C12N15/09, C12N15/00
CC Description of Artificial Sequence: Reverse complement of SEQ ID NO:1
FH Key Location/Qualifiers
FT source 1..54
/organism='Artificial Sequence'.

FEATURES
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/db_xref="taxon:32630"

ORIGIN
Query Match 100.0%; Score 54; DB 6; Length 54;
Best Local Similarity 79.6%; Pred. No. 1.1e-20; Indels 0; Gaps 0;
Matches 43; Conservative 11; Mismatches 0;

QY 1 UAAUUUAUACGACUCACUAUAGGGAGAGCUCAGACCCUGAGGCUCUAAAGUCAGA 54
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Db 54 TAAATTATACGACTCACTATAGGGAGACTCAGACCCCTGAGGCTCAAGTCAGA 1

RESULT 4.
BD222526/c
LOCUS 54 bp RNA linear PAT 17-JUL-2003
DEFINITION Methods for detecting and measuring spliced nucleic acids.
ACCESSION BD222526
VERSION BD222526.1 GI:33032296
KEYWORDS JP 2002521037-A/4.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 54)
HARVEY,R.C. and EASTMAN,P.S.
METHODS FOR DETECTING AND MEASURING SPLICED NUCLEIC ACIDS
TITLE Patent: JP 2002521037-A 4 16-JUL-2002;
JOURNAL GEN PROBE INC
COMMENT OS Artificial Sequence
PN JP 2002521037-A/4
PD 16-JUL-2002
PF 23-JUL-1999 JP 2000561364
PR 23-JUL-1998 US 09/121239
PT RICHARD C HARVEY, PAUL S EASTMAN
PC C12Q1/68, C12N15/09, C12N15/00
CC Description of Artificial Sequence: RNA version of SEQ ID NO:3
FH Key Location/Qualifiers
FT source 1..54
/organism='Artificial Sequence'.

FEATURES
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1..54
/organism="synthetic construct"
/mol_type="genomic RNA"
/db_xref="taxon:32630"

ORIGIN
Query Match 100.0%; Score 54; DB 6; Length 54;
Best Local Similarity 79.6%; Pred. No. 1.1e-20; Indels 0; Gaps 0;
Matches 43; Conservative 11; Mismatches 0;

QY 1 UAAUUUAUACGACUCACUAUAGGGAGAGCUCAGACCCUGAGGCUCUAAAGUCAGA 54
:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 1 TAAATTATACGACTCACTATAGGGAGACTCAGACCCCTGAGGCTCAAGTCAGA 54
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## ORIGIN

Query Match 55.6%; Score 30; DB 6; Length 49;  
Best Local Similarity 73.3%; Pred. No. 1.5e-06;  
Matches 22; Conservative 8; Mismatches 0; Indels 0; Gaps 0;

QY 1 UAAAUUUAUACGACUCACUUAUAGGGAGACU 30  
:||||:||||:||||:||||:||||:||||:  
DB 1 TAAATTAAATACGACTCACTATAGGGAGACT 30

RESULT 9  
AR307449  
LOCUS AR307449 49 bp DNA linear PAT 12-JUN-2003  
DEFINITION Sequence 38 from patent US 6551778.  
ACCESSION AR307449  
VERSION AR307449.1 GI:31697988  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 49)  
AUTHORS Harvey,R.C. and Clark,T.J. Jr.  
TITLE Nucleic acid sequences for detecting genetic markers for cancer in a biological sample  
JOURNAL Patent: US 6551778-A 38 22-APR-2003;  
FEATURES Location/Qualifiers  
source 1..49  
/organism="unknown"  
/mol\_type="genomic DNA"

ORIGIN

Query Match 55.6%; Score 30; DB 6; Length 49;  
Best Local Similarity 73.3%; Pred. No. 1.5e-06;  
Matches 22; Conservative 8; Mismatches 0; Indels 0; Gaps 0;

QY 1 UAAAUUUAUACGACUCACUUAUAGGGAGACU 30  
:||||:||||:||||:||||:||||:||||:  
DB 1 TAAATTAAATACGACTCACTATAGGGAGACT 30

RESULT 10  
BD236956  
LOCUS BD236956 50 bp DNA linear PAT 17-JUL-2003  
DEFINITION Nucleic acid sequence for detecting genetic marker for cancer in biological samples.  
ACCESSION BD236956  
VERSION BD236956.1 GI:33046726  
KEYWORDS JP 2002535014-A/31.  
SOURCE synthetic construct  
ORGANISM artificial sequences.  
REFERENCE 1 (bases 1 to 50)  
AUTHORS Harvey,R.C. and Jr,T.J.C.  
TITLE Nucleic acid sequence for detecting genetic marker for cancer in biological samples  
JOURNAL Patent: JP 2002535014-A 31 22-OCT-2002;  
COMMENT GEN PROBE INC  
OS Artificial Sequence  
PN JP 2002535014-A/31  
PD 22-OCT-2002  
PF 28-JAN-2000 JP 2000596180  
PR 28-JAN-1999 US 60/117640  
PI RICHARD C HARVEY, THOMAS J CLARK JR  
PC C12N15/09.C12Q1/68.C12N15/00  
CC Description of Artificial Sequence: synthetic construct FH  
Key Description of Artificial Sequence: synthetic construct FH  
FT promoter Location/Qualifiers  
source 1..50  
/organism="synthetic construct"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"

ORIGIN

Query Match 55.6%; Score 30; DB 6; Length 50;  
Best Local Similarity 73.3%; Pred. No. 1.5e-06;  
Matches 22; Conservative 8; Mismatches 0; Indels 0; Gaps 0;

QY 1 UAAAUUUAUACGACUCACUUAUAGGGAGACU 30  
:||||:||||:||||:||||:||||:||||:  
DB 1 TAAATTAAATACGACTCACTATAGGGAGACT 30

RESULT 11  
AR307442  
LOCUS AR307442 50 bp DNA linear PAT 12-JUN-2003  
DEFINITION Sequence 31 from patent US 6551778.  
ACCESSION AR307442  
VERSION AR307442.1 GI:31697981  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 50)  
AUTHORS Harvey,R.C. and Clark,T.J. Jr.  
TITLE Nucleic acid sequences for detecting genetic markers for cancer in a biological sample  
JOURNAL Patent: US 6551778-A 31 22-APR-2003;  
FEATURES Location/Qualifiers  
source 1..50  
/organism="unknown"  
/mol\_type="genomic DNA"

ORIGIN

Query Match 55.6%; Score 30; DB 6; Length 50;  
Best Local Similarity 73.3%; Pred. No. 1.5e-06;  
Matches 22; Conservative 8; Mismatches 0; Indels 0; Gaps 0;

QY 1 UAAAUUUAUACGACUCACUUAUAGGGAGACU 30  
:||||:||||:||||:||||:||||:||||:  
DB 1 TAAATTAAATACGACTCACTATAGGGAGACT 30

RESULT 12  
BD236968  
LOCUS BD236968 52 bp DNA linear PAT 17-JUL-2003  
DEFINITION Nucleic acid sequence for detecting genetic marker for cancer in biological samples.  
ACCESSION BD236968  
VERSION BD236968.1 GI:33046738  
KEYWORDS JP 2002535014-A/43.  
SOURCE synthetic construct  
ORGANISM artificial sequences.  
REFERENCE 1 (bases 1 to 52)  
AUTHORS Harvey,R.C. and Jr,T.J.C.  
TITLE Nucleic acid sequence for detecting genetic marker for cancer in biological samples  
JOURNAL Patent: JP 2002535014-A 43 22-OCT-2002;  
COMMENT GEN PROBE INC  
OS Artificial Sequence  
PN JP 2002535014-A/43  
PD 22-OCT-2002  
PF 28-JAN-2000 JP 2000596180  
PR 28-JAN-1999 US 60/117640  
PI RICHARD C HARVEY, THOMAS J CLARK JR  
PC C12N15/09.C12Q1/68.C12N15/00  
CC Description of Artificial Sequence: synthetic construct FH  
Key Description of Artificial Sequence: synthetic construct FH  
FT promoter Location/Qualifiers  
source 1..52  
/organism="synthetic construct"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"

ORIGIN

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Query Match      55.6%; Score 30; DB 6; Length 52;
Best Local Similarity 73.3%; Pred. No. 1.5e-06;
Matches 22; Conservative 8; Mismatches 0; Indels 0; Gaps 0;

QY 1 UAAUUAUACGACUCACUUAUAGGGAGACU 30
   :|||:|||||:|||||:|||||:|||||:
Db 1 TAAATTATACGACTCACTATAGGGAGACT 30

RESULT 13
LOCUS AR307454 52 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 43 from patent US 6551778.
ACCESSION AR307454
VERSION AR307454.1 GI:31697993
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 52)
AUTHORS Harvey,R.C. and Clark,T.J. Jr.
TITLE Nucleic acid sequences for detecting genetic markers for cancer in
a biological sample
JOURNAL Patent: US 6551778-A 43 22-APR-2003;
FEATURES Location/Qualifiers
   source
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     /mol_type="genomic DNA"

ORIGIN
Query Match      55.6%; Score 30; DB 6; Length 52;
Best Local Similarity 73.3%; Pred. No. 1.5e-06;
Matches 22; Conservative 8; Mismatches 0; Indels 0; Gaps 0;

QY 1 UAAUUAUACGACUCACUUAUAGGGAGACU 30
   :|||:|||||:|||||:|||||:|||||:
Db 1 TAAATTATACGACTCACTATAGGGAGACT 30

RESULT 14
LOCUS I25071 37 bp DNA linear PAT 07-OCT-1996
DEFINITION Sequence 5 from patent US 5547862.
ACCESSION I25071
VERSION I25071.1 GI:1604941
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 37)
AUTHORS Meador,J., McElroy,H.E., Herrmann,M.L. and Winkler,M.
TITLE Vectors containing multiple promoters in the same orientation
JOURNAL Patent: US 5547862-A 5 20-AUG-1996;
FEATURES Location/Qualifiers
   source
     1..37
     /organism="unknown"
     /mol_type="unassigned DNA"

ORIGIN
Query Match      53.7%; Score 29; DB 6; Length 37;
Best Local Similarity 75.9%; Pred. No. 6.3e-06;
Matches 22; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 3 AAUUAUACGACUCACUUAUAGGGAGACUC 31
   |||:|||||:|||||:|||||:|||||:
Db 1 AATTATACGACTCACTATAGGGAGACTC 29

RESULT 15
LOCUS AX575411 45 bp DNA linear PAT 07-JAN-2003
DEFINITION Sequence 4 from Patent WO02068635.
ACCESSION AX575411
```

```
VERSION AX575411.1 GI:27552050
KEYWORDS synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Billy,E., Filipowicz,W. and Mueller,U.
TITLE Methods of inhibiting expression of a target gene in mammalian
cells
JOURNAL Patent: WO 02068635-A 4 06-SEP-2002;
Novartis Forschungsinstitut Zueigniederlassung (CH)
FEATURES Location/Qualifiers
   source
     1..45
     /organism="synthetic construct"
     /mol_type="unassigned DNA"
     /db_xref="taxon:32630"
     /note="oligonucleotide"

ORIGIN
Query Match      53.7%; Score 29; DB 6; Length 45;
Best Local Similarity 75.9%; Pred. No. 6.1e-06;
Matches 22; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 5 UUAUACGACUCACUUAUAGGGAGACUCAG 33
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Db 1 TTAATACGACTCACTATAGGGAGACTCAG 29

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: May 26, 2004, 14:55:11 ; Search time 240.833 Seconds  
(without alignments)  
952.539 Million cell updates/sec

Title: US-09-121-239-2  
Perfect score: 54  
Sequence: 1 UAAUUAUACGACUCACUA.....CCUGAGGCUCAAGUCAGCA 54

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 3373863 seqs, 2124099041 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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5: Geneseqn2001bs.\*  
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7: Geneseqn2003as.\*  
8: Geneseqn2003bs.\*  
9: Geneseqn2003cs.\*  
10: Geneseqn2004s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	54	100.0	54	3 AAZ60843	Aaz60843 Oligonucleotide
2	54	100.0	54	3 AAZ60841	Aaz60841 Oligonucleotide
3	54	100.0	54	3 AAZ60840	Aaz60840 Oligonucleotide
4	54	100.0	54	3 AAZ60842	Aaz60842 Oligonucleotide
5	49	90.7	50	2 AAZ60826	Aaz60826 CML chrom
6	49	90.7	50	2 AAZ60827	Aaz60827 CML-2 chr
7	49	90.7	50	2 AAZ60828	Aaz60828 CML-2 chr
8	49	90.7	50	2 AAZ60829	Aaz60829 CML-2 chr
9	49	90.7	50	2 AAZ60830	Aaz60830 CML chrom
10	49	90.7	50	2 AAZ60831	Aaz60831 CML chrom
11	32	59.3	54	3 AAZ60867	Aaz60867 Human pro
12	30	55.6	49	3 AAZ60868	Aaz60868 Human pro
13	30	55.6	49	3 AAZ60869	Aaz60869 Human pro
14	30	55.6	49	3 AAZ60870	Aaz60870 Human pro
15	29	53.7	45	6 AAZ60871	Aaz60871 Human pro
16	29	53.7	50	2 AAZ60872	Aaz60872 LacZ RNA
17	29	53.7	51	6 AAZ60873	Aaz60873 T7 gene 1
18	29	53.7	51	6 AAZ60874	Aaz60874 HIV-1 rev
19	29	53.7	52	3 AAZ60875	Aaz60875 HIV-1 pol
20	29	53.7	52	3 AAZ60876	Aaz60876 Human pro
21	29	53.7	52	3 AAZ60877	Aaz60877 Human pro
22	29	53.7	54	3 AAZ60878	Aaz60878 Human pro
23	29	53.7	55	3 AAZ60879	Aaz60879 Human pro

24	29	53.7	180	2	AAT41733	Promoter
25	29	53.7	1442	7	ABZ70392	Abz70392 AutoFluor
26	29	53.7	6306	6	ABA03923	Abao3923 Human NHP
27	29	53.7	7201	8	ACF05731	Acf05731 Plasmid p
28	29	53.7	7231	8	ACF06299	Acf06299 Plasmid p
29	29	53.7	7297	8	ACF06300	Acf06300 SigptdIPA
30	29	53.7	7429	8	ACF05558	Acf05558 Plasmid p
31	29	53.7	7456	8	ACF06298	Acf06298 Plasmid p
32	28	51.9	28	3	AA76212	Aaa76212 Human pro
33	28	51.9	30	2	AAT95233	Aat95233 Macaque s
34	28	51.9	33	4	AAD11020	Aad11020 Bacteriop
35	28	51.9	33	4	AAD11286	Aad11286 Bacteriop
36	28	51.9	33	6	ABK53104	Abk53104 T7 promot
37	28	51.9	33	6	ABK93905	Abk93905 Human imm
38	28	51.9	33	6	AAI45466	Aai45466 Bacteriop
39	28	51.9	35	2	AAV05796	Aav05796 Primer fo
40	28	51.9	35	2	AAV05794	Aav05794 Primer fo
41	28	51.9	35	6	AAL50495	Aal50495 3-frame H
42	28	51.9	35	8	ADA24416	Ada24416 His-tag v
43	28	51.9	36	4	AAC64735	Aac64735 Human pro
44	28	51.9	36	6	ABQ81381	Abq81381 Human pro
45	28	51.9	36	9	ADB71188	Adb71188 Human pro

## ALIGNMENTS

RESULT 1  
AAZ60843/c  
ID AAZ60843 standard; RNA; 54 BP.  
XX  
AC AAZ60843;  
XX  
DT 16-MAY-2000 (first entry)  
XX  
DE Oligonucleotide used to detect bcr b3-abl fusion transcripts.  
XX  
KW Fusion transcript; translocation; bcr b3 region; abl gene;  
KW amplification assay; detection assay; medical diagnosis;  
KW clinical monitoring; chimeric RNA; fusion RNA; condition marker;  
KW disease marker; cancer; leukemia; ss.  
XX  
OS Synthetic.  
XX  
PN WO200005418-A1.  
XX  
PD 03-FEB-2000.  
XX  
PF 23-JUL-1999; 99WO-US016832.  
XX  
XX 23-JUL-1999; 98US-00121239.  
XX (GENP-) GEN-PROBE INC.  
XX  
PI Harvey RC, Eastman PS;  
XX  
DR WPI; 2000-182730/16.  
XX  
PT Novel methods for preparing RNA from biological samples, used for the  
XX detection and measurement of nucleic acids and fusion nucleic acids.  
XX  
XX Claim 19; Page 40; 49pp; English.  
XX  
CC Oligonucleotides AAZ60840-62 and AAZ60865-66 are used in the method of  
CC the invention to detect fusion transcripts produced from a translocation  
CC between the bcr b3 region and the abl gene. The specification describes a  
CC method for detecting a fusion nucleic acid (particularly chimeric mRNA  
CC species), in a biological sample. The method comprises contacting a  
CC sample of fusion nucleic acid with primers, amplifying the hybridized  
CC fusion nucleic acid, and detecting the target hybrid. The method is used  
CC for the sample and rapid preparation of RNA from a biological sample,  
CC particularly from the cytoplasm of eukaryotic cells, which is suitable  
CC for use in an amplification and detection assay. The methods are used for



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Db      54  TAAATTAAATAGACTACTACTATAGGAGACTCAGACCCCTGAGGCTCAAAGTCAGA 1

RESULT 5
AAQ86626
ID      AAQ86626 standard; DNA; 50 BP.
XX      AC      AAQ86626;
XX      XX
XX      25-MAR-2003 (revised)
XX      15-NOV-1995 (first entry)
XX      XX
DE      CML chromosomal translocation minus strand primer.
XX      XX
XX      Primer; autocatalytic; target; CML; translocation; ss.
XX      XX
XX      Synthetic.
XX      XX
XX      US5399491-A.
XX      XX
XX      21-MAR-1995.
XX      XX
XX      19-MAR-1992; 92US-00855732.
XX      XX
XX      11-JUL-1989; 89US-00379501.
XX      10-JUL-1990; 90US-00550837.
XX      XX
XX      (GENP-) GEN-PROBE INC.
XX      XX
XX      Fultz TJ, Kacian DL;
XX      XX
XX      WPI; 1995-130686/17.
XX      XX
XX      Amplification of nucleic acid targets - using a reverse transcriptase
XX      with RNase H activity and a RNA polymerase at constant temp.
XX      XX
XX      Disclosure; Col 9; 58pp; English.
XX      XX
XX      AAQ86626-28 are primers and a probe for the CML chromosomal
XX      translocation. They are used to produce autocatalytic oligonucleotides
XX      which require no change in the experimental conditions i.e constant
XX      temperature, pH and ionic strength. These sequences are useful in
XX      generating multiple copies of specific nucleic acid target sequences.
XX      (Updated on 25-MAR-2003 to correct PF field.)
XX      XX
XX      Sequence 50 BP; 17 A; 12 C; 11 G; 10 T; 0 U; 0 Other;

Query Match      90.7%; Score 49; DB 2; Length 50;
Best Local Similarity 79.6%; Pred. No. 8.8e-17;
Matches 39; Conservative 10; Mismatches 0; Indels 0; Gaps 0;

Qy      3  AAUUAUACGACUCACUAUAGGGAGACUCAGACCCUGAGGCUCUCAAAGUC 51
         ||:::||:::||:::||:::||:::||:::||:::||:::||:::||::||
Db      2  AATTATACGACTCACTATATAGGAGACTCAGACCCCTGAGGCTCAAAGTC 50

RESULT 6
AAT15571
ID      AAT15571 standard; DNA; 50 BP.
XX      AC      AAT15571;
XX      XX
XX      25-MAR-2003 (revised)
XX      17-JUL-1996 (first entry)
XX      XX
DE      CML-2 chromosomal translocation major breakpoint t(9;22) (-) primer.
XX      XX
XX      CML-2 chromosomal translocation major breakpoint; t(9; 22); primer;
XX      auto-catalytic; synthesis; RNA target sequence; assay; detection;
XX      quantification; ss.
XX      XX
XX      Synthetic.
XX      XX

```

PN US5480784-A.  
 XX  
 PD 02-JAN-1996.  
 XX  
 PF 10-JUL-1990; 90US-00550837.  
 XX  
 PR 11-JUL-1989; 89US-00379501.  
 XX  
 PA (GENP-) GEN-PROBE INC.  
 XX  
 PI Fultz TJ, Kacian DL;  
 XX  
 DR WPI; 1996-068248/07.  
 XX  
 PT Auto-catalytic synthesis of multiple copies of an RNA target sequence -  
 PT uses cooperative action of a DNA and RNA polymerase in presence of RNase  
 PT H, useful for detection of target sequence e.g. in clinical or  
 PT environmental sample.  
 XX  
 PS Example; Col 9-10; 51pp; English.  
 XX  
 CC The present sequence is a primer for the CML-2 chromosomal translocation  
 CC major breakpoint t(9;22), which was used to demonstrate an improved  
 CC method for synthesising multiple copies of a RNA target sequence. The  
 CC method comprises combining the target with a primer which hybridises to  
 CC the 3'-terminal portion of the target, a promoter primer which hybridises  
 CC with a portion of the DNA primer extension prod., reverse transcriptase,  
 CC RNase H and transcriptase. It can be used as a component of an assay to  
 CC detect and/or quantitate specific target sequences in clinical,  
 CC environmental or forensic samples. It also has the advantages of being  
 CC autocatalytic, using the cooperative action of a DNA polymerase, e.g. a  
 CC reverse transcriptase and avoids repetitive manipulations of reaction  
 CC conditions, e.g. temp., ionic strength and pH. (Updated on 25-MAR-2003 to  
 CC correct PF field.)  
 XX  
 SQ Sequence 50 BP; 17 A; 12 C; 11 G; 10 T; 0 U; 0 Other;  
 Query Match 90.7%; Score 49; DB 2; Length 50;  
 Best Local Similarity 79.6%; Pred. No. 8.8e-17;  
 Matches 39; Conservative 10; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 AAUUAUACGACUCACUUAUAGGAGACUCAGACCCUGAGGCUCAAGUC 51  
 Db 2 AATTAATACGACTCACTATAGGAGACTCAGACCCCTGAGGCTCAAGTC 50  
 RESULT 7  
 AAT42417  
 ID AAT42417 standard; DNA; 50 BP.  
 AC AAT42417;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 28-APR-1997 (first entry)  
 XX  
 DE CML chromosomal translocation primer #1.  
 XX  
 KW HIV; probe; primer; amplify; polymerase chain reaction; microorganism;  
 KW BCL-2; PCR; hepatitis B virus; HBV; CML; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN EP731175-A2.  
 XX  
 PD 11-SEP-1996.  
 XX  
 PF 10-JUL-1990; 96EP-00101621.  
 XX  
 PR 11-JUL-1989; 89US-00379501.  
 PR 10-JUL-1990; 90EP-00307503.  
 XX  
 PA (GENP-) GEN-PROBE INC.  
 XX

PI Mcdonough S;  
 XX  
 DR WPI; 1996-403995/41.  
 XX  
 PT Detection of HIV nucleic acids in samples - using new specific oligo-  
 PT nucleotide(s) for the amplification and detection of target sequences.  
 XX  
 PS Disclosure; Page 8; 66pp; English.  
 XX  
 CC AAT42417-T42419 represent primers and a probe for the CML chromosomal  
 CC translocation t(9;22). These sequences can be used in modified versions  
 CC of the kits of the invention. The kits of the invention, are for  
 CC detecting the presence of HIV nucleic acid sequences in a sample. The  
 CC kits comprise two amplification primers (such as AAT40182 and AAT40183),  
 CC and a probe (such as AAT42404) for detection of the amplified sequence.  
 CC By using these sequences, the amplification of HIV nucleic acid sequences  
 CC is improved. The kits can also be used for the detection of other  
 CC microorganisms, by using different probe sequences. Other sequences that  
 CC can be detected using this method include those from HBV (using the  
 CC sequences shown in AAT42410-T42412), and BCL-2 (using AAT42413-T42416).  
 CC The samples can be clinical, environmental or forensic samples, and the  
 CC method produces large amounts of the target sequence for a variety of  
 CC uses. The method can also be used to produce multiple copies of a target  
 CC sequence for use in cloning, and sequencing, and to produce probes for  
 CC the target sequence. (Updated on 25-MAR-2003 to correct PF field.)  
 CC (Updated on 25-MAR-2003 to correct PR field.)  
 XX  
 SQ Sequence 50 BP; 17 A; 12 C; 11 G; 10 T; 0 U; 0 Other;  
 Query Match 90.7%; Score 49; DB 2; Length 50;  
 Best Local Similarity 79.6%; Pred. No. 8.8e-17;  
 Matches 39; Conservative 10; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 AAUUAUACGACUCACUUAUAGGAGACUCAGACCCUGAGGCUCAAGUC 51  
 Db 2 AATTAATACGACTCACTATAGGAGACTCAGACCCCTGAGGCTCAAGTC 50  
 RESULT 8  
 AAV66349  
 ID AAV66349 standard; DNA; 50 BP.  
 AC AAV66349;  
 XX  
 DT 06-JAN-1999 (first entry)  
 XX  
 DE CML-2 chromosomal translocation t(9;22) primer.  
 XX  
 KW CML-2 chromosomal translocation t(9;22); block splice template;  
 KW autocatalytic RNA amplification; primer; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN US5824518-A.  
 XX  
 PD 20-OCT-1998.  
 XX  
 PF 06-JUN-1995; 95US-00469067.  
 XX  
 PR 11-JUL-1989; 89US-00379501.  
 PR 10-JUL-1990; 90US-00550837.  
 XX  
 PA (GENP-) GEN-PROBE INC.  
 XX  
 PI Fultz TJ, Kacian DL;  
 XX  
 DR WPI; 1998-582557/49.  
 XX  
 PT Block splice template useful for amplification of nucleic acids -  
 PT comprises two nucleic acid regions, the first region located 3' of the  
 PT second region and blocked at its 3' terminus to inhibit primer extension  
 PT by a DNA polymerase.  
 XX



PS Example 15; Col 9; 51pp; English.

AA AAV6349-50 represent CML-2 chromosomal translocation t(9;22) primers,  
 CC for the (+) and (-) strands respectively. The primers are used to  
 CC exemplify the insertion, together with probe AAV6351. The specification  
 CC describes methods of synthesising multiple copies of a target nucleic  
 CC acid sequence autocatalytically under conditions of substantially  
 CC constant temperature, ionic strength and pH are provided in which  
 CC multiple RNA copies of the target sequence autocatalytically generate  
 CC additional copies. The target sequence is a block splice template which  
 CC comprises two nucleic acid regions. The first region is located 3' of the  
 CC second region and is blocked at its 3' terminus to inhibit primer  
 CC extension by a DNA polymerase, and the second region comprises a promoter  
 CC sequence recognised by an RNA polymerase. The methods are used to amplify  
 CC nucleic acids, especially RNA, for analysis, cloning or probe production  
 XX  
 XX Sequence 50 BP; 17 A; 12 C; 11 G; 10 T; 0 U; 0 Other;

Query Match	90.7%	Score 49	DB 2	Length 50
Best Local Similarity	79.6%	Pred. No. 8.8e-17		
Matches 39	Conservative 10	Mismatches 0	Indels 0	Gaps 0

Qy		3	AUUUAUACGACUCACUAAGGGAGACUCAGACCCUGAGGCCUCAAAAGUC	51
	:   :		:   :	
	:   :		:   :	
	:   :		:   :	
	:   :		:   :	
	:   :		:   :	
Dd		2	AATTAATACGACTCACTAATAGGGAGACTCAGACCCCTGAGGCTCAAAGTC	50

RESULT 9  
AAX23191

XX  
ID  
AAX:

AC AAX23191;  
YY

DT 11-JUN-1999 (first entry)

DE CML chromo

KW Autocatalytic amplification



CC markers for prostate and breast cancer, and PCR primers and probes which  
 CC are able to detect and quantify these markers. Prostate specific antigen  
 CC (PSA), prostate-specific membrane antigen (PSMA) and glandular kallikrein  
 CC -2 (hk2) have all been linked to prostate and breast cancers, and the  
 CC primers and probes of the invention are able to detect the abnormal  
 CC presence of mRNA expressed by their coding sequences in tissues other  
 CC than the prostate. This enables the presence of cancer to be perceived  
 CC and aids in the detection of metastases

XX  
 SQ Sequence 50 BP; 16 A; 11 C; 11 G; 12 T; 0 U; 0 Other;

Query Match 55.6%; Score 30; DB 3; Length 50;  
 Best Local Similarity 73.3%; Pred. No. 1.5e-06;  
 Matches 22; Conservative 8; Mismatches 0; Indels 0; Gaps 0;

QY 1 UAAUUAUACGACUCACUUAUAGGGAGACU 30  
 :||||:||||:||||:||||:||||:||||:  
 Db 1 TAAATTAATACGACTCACTATAGGGAGACT 30

RESULT 14  
 AAA76211  
 ID AAA76211 standard; DNA; 52 BP.  
 XX  
 AC AAA76211;  
 XX  
 DT 25-JAN-2001 (first entry)  
 XX  
 DE Human prostate specific antigen PCR primer SEQ ID NO: 40.  
 XX  
 KW Prostate specific antigen; PSA; prostate-specific membrane antigen; PSMA;  
 KW glandular kallikrein-2; hk2; prostate cancer; breast cancer; probe;  
 KW PCR primer; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200044940-A2.  
 XX  
 PD 03-AUG-2000.  
 XX  
 PF 28-JAN-2000; 2000WO-US002270.  
 XX  
 PR 28-JAN-1999; 99US-0117640P.  
 XX  
 PA (GENP-) GEN-PROBE INC.  
 XX  
 PI Harvey RC, Clark TJ;  
 XX  
 WPI; 2000-505986/45.  
 XX  
 DR Detecting prostate-specific antigen (PSA), prostate specific membrane  
 PT antigen (PSMA) or human kallikrein 2 (hk2) nucleic acids in samples using  
 PT probe molecules, useful for the diagnosis of prostate and breast cancers.  
 XX  
 PS Claim 1; Page 13; 77pp; English.

CC The present invention is concerned with the detection of nucleic acid  
 CC markers for prostate and breast cancer, and PCR primers and probes which  
 CC are able to detect and quantify these markers. Prostate specific antigen  
 CC (PSA), prostate-specific membrane antigen (PSMA) and glandular kallikrein  
 CC -2 (hk2) have all been linked to prostate and breast cancers, and the  
 CC primers and probes of the invention are able to detect the abnormal  
 CC presence of mRNA expressed by their coding sequences in tissues other  
 CC than the prostate. This enables the presence of cancer to be perceived  
 CC and aids in the detection of metastases

XX  
 SQ Sequence 52 BP; 17 A; 11 C; 11 G; 13 T; 0 U; 0 Other;

Query Match 55.6%; Score 30; DB 3; Length 52;  
 Best Local Similarity 73.3%; Pred. No. 1.5e-06;  
 Matches 22; Conservative 8; Mismatches 0; Indels 0; Gaps 0;

QY 1 UAAUUAUACGACUCACUUAUAGGGAGACU 30

Db 1 TAAATTAATACGACTCACTATAGGGAGACT 30  
 :||||:||||:||||:||||:||||:||||:  
 RESULT 15  
 ASZ59191  
 ID ASZ59191 standard; DNA; 45 BP.  
 XX  
 AC ASZ59191;  
 XX  
 DT 15-MAY-2003 (first entry)  
 XX  
 DE LacZ RNA generating primer.  
 XX  
 KW LacZ; gene expression; gene function; pharmaceutical; PCR; primer; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200268635-A2.  
 XX  
 PD 06-SEP-2002.  
 XX  
 PF 27-FEB-2002; 2002WO-EP002098.  
 XX  
 PR 28-FEB-2001; 2001GB-00004948.  
 XX  
 PA (NOVS ) NOVARTIS FORSCHUNGSSTIFTUNG ZWEIGNIEDERL.  
 XX  
 PI Billy E, Filipowicz W, Mueller U;  
 XX  
 WPI; 2002-706992/76.  
 XX  
 DR Inhibiting expression of a target gene, useful for identifying gene  
 PT function in an organism, comprises exposing a mammalian cell to a  
 PT partially double-stranded ribonucleic acid with at least 60% sequence  
 PT identity to a target gene.  
 XX  
 PS Example 1; Page 16; 31pp; English.

CC The invention relates to inhibiting expression of a target gene. The  
 CC method involves exposing a renewable, mammalian cell to a partially  
 CC double-stranded ribonucleic acid and with at least 60% sequence identity  
 CC to a target gene. The method is useful for identifying gene function in  
 CC an organism, in determining potential targets for pharmaceuticals,  
 CC understanding normal and pathological events associated with development,  
 CC and determining signal pathways responsible for post-natal development/  
 CC aging. The method may also be used to allow the inhibition of essential  
 CC genes which may be required for cell or organism viability at particular  
 CC stages of development or cellular compartments, and to allow addition or  
 CC expression of RNA at specific times of development and locations in the  
 CC organism without introducing permanent mutations into the target genome.  
 CC The present sequence represents a PCR primer for generating a lacZ RNA,  
 CC used in the preparation of dsRNA

XX  
 SQ Sequence 45 BP; 15 A; 10 C; 10 G; 10 T; 0 U; 0 Other;

Query Match 53.7%; Score 29; DB 6; Length 45;  
 Best Local Similarity 75.9%; Pred. No. 5.3e-06;  
 Matches 22; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 5 UUAUACGACUCACUUAUAGGGAGACUCAG 33  
 :||||:||||:||||:||||:||||:||||:  
 Db 1 TTAATACGACTCACTATAGGGAGACTCAG 29

Search completed: May 26, 2004, 16:52:13  
 Job time : 240.833 secs

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Result No.	Score	Query		Length	DB	ID	Description
		Match	\$				
1	49	90.7	50	4	US-09-168-947-45	Sequence 45, Appl	
2	32	59.3	54	4	US-09-493-491-29	Sequence 29, Appl	
3	32	59.3	54	4	US-09-493-491A-32	Sequence 32, Appl	
4	30	55.6	49	4	US-09-493-491-35	Sequence 35, Appl	
5	30	55.6	49	4	US-09-493-491A-38	Sequence 38, Appl	
6	30	55.6	50	4	US-09-493-491-28	Sequence 28, Appl	
7	30	55.6	50	4	US-09-493-491A-31	Sequence 31, Appl	
8	30	55.6	52	4	US-09-493-491-40	Sequence 40, Appl	
9	30	55.6	52	4	US-09-493-491A-43	Sequence 43, Appl	
10	29	53.7	37	1	US-08-099-867-5	Sequence 5, Appl	
11	29	53.7	50	3	US-08-972-799A-25	Sequence 25, Appl	
12	29	53.7	50	3	US-09-506-282-25	Sequence 25, Appl	
13	29	53.7	50	5	PCF-US95-03339-25	Sequence 25, Appl	
14	29	53.7	51	4	US-09-944-036-40	Sequence 40, Appl	
15	29	53.7	52	4	US-09-493-491-33	Sequence 33, Appl	
16	29	53.7	52	4	US-09-493-491-39	Sequence 39, Appl	
17	29	53.7	52	4	US-09-493-491A-36	Sequence 36, Appl	
18	29	53.7	52	4	US-09-493-491A-42	Sequence 42, Appl	
19	29	53.7	54	4	US-09-493-491-27	Sequence 27, Appl	
20	29	53.7	54	4	US-09-493-491-49	Sequence 49, Appl	
21	29	53.7	54	4	US-09-493-491A-30	Sequence 30, Appl	
22	29	53.7	54	4	US-09-493-491A-49	Sequence 49, Appl	
23	29	53.7	55	4	US-09-493-491-47	Sequence 47, Appl	
24	29	53.7	60	1	US-09-493-491A-47	Sequence 47, Appl	
25	29	53.7	60	1	US-08-099-867-7	Sequence 7, Appl	
26	29	53.7	79	1	US-08-099-867-3	Sequence 3, Appl	
27	29	53.7	180	1	US-08-099-867-1	Sequence 1, Appl	

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 29

; LENGTH: 54

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: synthetic

; OTHER INFORMATION: construct

US-09-493-491-29

Query Match

Best Local Similarity 59.3%; Score 32; DB 4; Length 54;

Matches 24; Conservative 8; Mismatches 0; Indels 0; Gaps 0;

QY 1 UAAAUUAUACGACUCACUUAAGGGAGACUCA 32

Db 1 TAAATTAATACGACTCACTATAGGGAGACTCA 32

RESULT 3

US-09-493-491A-32

; Sequence 32, Application US/09493491A

; Patent No. 6551778

; GENERAL INFORMATION:

; APPLICANT: HARVEY, Richard, C.

; APPLICANT: CLARK, JR., Thomas, J.

; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FOR DETECTING GENETIC MARKERS

; TITLE OF INVENTION: FOR CANCER IN A BIOLOGICAL SAMPLE

; FILE REFERENCE: GP097-02.UT

; CURRENT APPLICATION NUMBER: US/09/493,491A

; PRIOR FILING DATE: 2000-01-28

; PRIOR APPLICATION NUMBER: 60/117,640 US

; PRIOR FILING DATE: 1999-01-28

; NUMBER OF SEQ ID NOS: 50

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 32

; LENGTH: 54

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: synthetic

; OTHER INFORMATION: construct

; NAME/KEY: promoter

; LOCATION: (1)..(28)

US-09-493-491A-32

Query Match

Best Local Similarity 59.3%; Score 32; DB 4; Length 54;

Matches 24; Conservative 8; Mismatches 0; Indels 0; Gaps 0;

QY 1 UAAAUUAUACGACUCACUUAAGGGAGACUCA 32

Db 1 TAAATTAATACGACTCACTATAGGGAGACTCA 32

RESULT 4

US-09-493-491-35

; Sequence 35, Application US/09493491

; Patent No. 6391556

; GENERAL INFORMATION:

; APPLICANT: HARVEY, Richard, C.

; APPLICANT: CLARK, JR., Thomas, J.

; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FOR DETECTING GENETIC MARKERS

; TITLE OF INVENTION: FOR CANCER IN A BIOLOGICAL SAMPLE

; FILE REFERENCE: GP097-02.UT

; CURRENT APPLICATION NUMBER: US/09/493,491

; PRIOR FILING DATE: 2000-01-28

; PRIOR APPLICATION NUMBER: 60/117,640 US

; PRIOR FILING DATE: 1999-01-28

; NUMBER OF SEQ ID NOS: 50

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 35

; LENGTH: 49

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: synthetic

; OTHER INFORMATION: construct

US-09-493-491-35

Query Match

Best Local Similarity 55.6%; Score 30; DB 4; Length 49;

Matches 22; Conservative 8; Mismatches 0; Indels 0; Gaps 0;

QY 1 UAAAUUAUACGACUCACUUAAGGGAGACU 30

Db 1 TAAATTAATACGACTCACTATAGGGAGACT 30

RESULT 5

US-09-493-491A-38

; Sequence 38, Application US/09493491A

; Patent No. 6551778

; GENERAL INFORMATION:

; APPLICANT: HARVEY, Richard, C.

; APPLICANT: CLARK, JR., Thomas, J.

; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FOR DETECTING GENETIC MARKERS

; TITLE OF INVENTION: FOR CANCER IN A BIOLOGICAL SAMPLE

; FILE REFERENCE: GP097-02.UT

; CURRENT APPLICATION NUMBER: US/09/493,491A

; PRIOR FILING DATE: 2000-01-28

; PRIOR APPLICATION NUMBER: 60/117,640 US

; PRIOR FILING DATE: 1999-01-28

; NUMBER OF SEQ ID NOS: 50

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 38

; LENGTH: 49

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: synthetic

; OTHER INFORMATION: construct

; NAME/KEY: promoter

; LOCATION: (1)..(28)

US-09-493-491A-38

Query Match

Best Local Similarity 55.6%; Score 30; DB 4; Length 49;

Matches 22; Conservative 8; Mismatches 0; Indels 0; Gaps 0;

QY 1 UAAAUUAUACGACUCACUUAAGGGAGACU 30

Db 1 TAAATTAATACGACTCACTATAGGGAGACT 30

RESULT 6

US-09-493-491-28

; Sequence 28, Application US/09493491

; Patent No. 6391556

; GENERAL INFORMATION:

; APPLICANT: HARVEY, Richard, C.

; APPLICANT: CLARK, JR., Thomas, J.

; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FOR DETECTING GENETIC MARKERS

; TITLE OF INVENTION: FOR CANCER IN A BIOLOGICAL SAMPLE

; FILE REFERENCE: GP097-02.UT

; CURRENT APPLICATION NUMBER: US/09/493,491

; PRIOR FILING DATE: 2000-01-28

; PRIOR APPLICATION NUMBER: 60/117,640 US

; PRIOR FILING DATE: 1999-01-28

; NUMBER OF SEQ ID NOS: 50

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 28

; LENGTH: 50

; TYPE: DNA

ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: synthetic  
OTHER INFORMATION: construct  
US-09-493-491-28

Query Match 55.6%; Score 30; DB 4; Length 50;  
Best Local Similarity 73.3%; Pred. No. 1.2e-07;  
Matches 22; Conservative 8; Mismatches 0; Indels 0; Gaps 0;

QY 1 UAAAUUAUACGACUCACUUAUAGGGAGACU 30  
:||||:||||:||||:||||:||||:||||:  
Db 1 TAAATTATACGACTCACTATAGGGAGACT 30

## RESULT 7

US-09-493-491A-31  
Sequence 31, Application US/09493491A  
Patent No. 6551778  
GENERAL INFORMATION:  
APPLICANT: HARVEY, Richard, C.  
APPLICANT: CLARK, JR., Thomas, J.  
TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FOR DETECTING GENETIC MARKERS  
FILE REFERENCE: GP097-02.UT  
CURRENT APPLICATION NUMBER: US/09/493,491A  
CURRENT FILING DATE: 2000-01-28  
PRIOR APPLICATION NUMBER: 60/117,640 US  
PRIOR FILING DATE: 1999-01-28  
NUMBER OF SEQ ID NOS: 50  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 31  
LENGTH: 50  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: synthetic  
OTHER INFORMATION: construct  
FEATURE:  
NAME/KEY: promoter  
LOCATION: (1)..(28)  
US-09-493-491A-31

Query Match 55.6%; Score 30; DB 4; Length 50;  
Best Local Similarity 73.3%; Pred. No. 1.2e-07;  
Matches 22; Conservative 8; Mismatches 0; Indels 0; Gaps 0;

QY 1 UAAAUUAUACGACUCACUUAUAGGGAGACU 30  
:||||:||||:||||:||||:||||:||||:  
Db 1 TAAATTATACGACTCACTATAGGGAGACT 30

## RESULT 8

US-09-493-491-40  
Sequence 40, Application US/09493491  
Patent No. 6391556  
GENERAL INFORMATION:  
APPLICANT: HARVEY, Richard, C.  
APPLICANT: CLARK, JR., Thomas, J.  
TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FOR DETECTING GENETIC MARKERS  
FILE REFERENCE: GP097-02.UT  
CURRENT APPLICATION NUMBER: US/09/493,491  
CURRENT FILING DATE: 2000-01-28  
EARLIER APPLICATION NUMBER: 60/117,640 US  
EARLIER FILING DATE: 1999-01-28  
NUMBER OF SEQ ID NOS: 50  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 40  
LENGTH: 52  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: synthetic  
OTHER INFORMATION: construct  
US-09-493-491-40

Query Match 55.6%; Score 30; DB 4; Length 52;  
Best Local Similarity 73.3%; Pred. No. 1.2e-07;  
Matches 22; Conservative 8; Mismatches 0; Indels 0; Gaps 0;

QY 1 UAAAUUAUACGACUCACUUAUAGGGAGACU 30  
:||||:||||:||||:||||:||||:||||:  
Db 1 TAAATTATACGACTCACTATAGGGAGACT 30

## RESULT 9

US-09-493-491A-43  
Sequence 43, Application US/09493491A  
Patent No. 6551778  
GENERAL INFORMATION:  
APPLICANT: HARVEY, Richard, C.  
APPLICANT: CLARK, JR., Thomas, J.  
TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FOR DETECTING GENETIC MARKERS  
FILE REFERENCE: GP097-02.UT  
CURRENT APPLICATION NUMBER: US/09/493,491A  
CURRENT FILING DATE: 2000-01-28  
PRIOR APPLICATION NUMBER: 60/117,640 US  
PRIOR FILING DATE: 1999-01-28  
NUMBER OF SEQ ID NOS: 50  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 43  
LENGTH: 52  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: synthetic  
OTHER INFORMATION: construct  
FEATURE:  
NAME/KEY: promoter  
LOCATION: (1)..(28)  
US-09-493-491A-43

Query Match 55.6%; Score 30; DB 4; Length 52;  
Best Local Similarity 73.3%; Pred. No. 1.2e-07;  
Matches 22; Conservative 8; Mismatches 0; Indels 0; Gaps 0;

QY 1 UAAAUUAUACGACUCACUUAUAGGGAGACU 30  
:||||:||||:||||:||||:||||:||||:  
Db 1 TAAATTATACGACTCACTATAGGGAGACT 30

## RESULT 10

US-08-099-867-5  
Sequence 5, Application US/08099867  
Patent No. 5547062  
GENERAL INFORMATION:  
APPLICANT: James Meador  
APPLICANT: Hoyt E. McElroy  
APPLICANT: Michelle L. Herrmann  
APPLICANT: Matthew Winkler  
TITLE OF INVENTION: Vectors Containing Multiple Promoters  
TITLE OF INVENTION: in the Same Orientation  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESS: Arnold, White & Durkee  
STREET: P.O. Box 4433  
CITY: Houston  
STATE: Texas  
COUNTRY: USA  
ZIP: 77210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy Disk  
COMPUTER: IBM PC Compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

```
; SOFTWARE: ASCII-DOS
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/099,867
; FILING DATE: 19930729
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: David L. Parker
; REGISTRATION NUMBER: 32,165
; REFERENCE/DOCKET NUMBER: AMBI:009/PAR
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 320-7200
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 37 base pairs
; TYPE: nucleic acids
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-099-867-5

Query Match      53.7%; Score 29; DB 1; Length 37;
Best Local Similarity 75.9%; Pred. No. 4.1e-07;
Matches 22; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY      3 AAUUAUACGACUCACUUAAGGAGACUC 31
      ||:|||||:|||||:|||||:|||||:|
Db      1 AATTATAGCACTCACTATAGGAGACTC 29

RESULT 11
US-08-972-799A-25
; Sequence 25, Application US/08972799A
; Patent No. 6087133
; GENERAL INFORMATION:
; APPLICANT: Dattagupta, Nanibhushan
; APPLICANT: Stull, Paul Douglas
; APPLICANT: Spingola, Marc
; APPLICANT: Kacian, Daniel Louis
; TITLE OF INVENTION: ISOTHERMAL STRAND
; TITLE OF INVENTION: DISPLACEMENT NUCLEIC
; TITLE OF INVENTION: ACID AMPLIFICATION
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Gen-Probe Incorporated
; STREET: 9880 Campus Point Drive
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: 27
; FILING DATE:
; CLASSIFICATION:
; ADDRESSEE: Gen-Probe Incorporated
; STREET: 9880 Campus Point Drive
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/972,799A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA: including application
; PRIOR APPLICATION DATA: described below:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Fisher, Carlos
; REGISTRATION NUMBER: 36,510
; REFERENCE/DOCKET NUMBER: GP94/001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-2807
; TELEFAX: (619) 452-5848
; INFORMATION FOR SEQ ID NO: 25:
; none
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; SEQUENCE CHARACTERISTICS:
; LENGTH: 50
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-972-799A-25

Query Match      53.7%; Score 29; DB 3; Length 50;
Best Local Similarity 75.9%; Pred. No. 4.1e-07;
Matches 22; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY      2 AAUUAUACGACUCACUUAAGGAGACU 30
      ||:|||||:|||||:|||||:|||||:|
Db      2 AAATTAATAGCACTCACTATAGGAGACT 30

RESULT 12
US-09-506-282-25
; Sequence 25, Application US/09506282
; Patent No. 6214587
; GENERAL INFORMATION:
; APPLICANT: Dattagupta, Nanibhushan
; APPLICANT: Stull, Paul Douglas
; APPLICANT: Spingola, Marc
; APPLICANT: Kacian, Daniel Louis
; TITLE OF INVENTION: ISOTHERMAL STRAND DISPLACEMENT NUCLEIC
; TITLE OF INVENTION: ACID AMPLIFICATION
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Gen-Probe Incorporated
; STREET: 9880 Campus Point Drive
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/506,282
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/215,081
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Fisher, Carlos A.
; REGISTRATION NUMBER: 36,510
; REFERENCE/DOCKET NUMBER: GP94/001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-2807
; TELEFAX: (619) 452-5848
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 50
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-506-282-25

Query Match      53.7%; Score 29; DB 3; Length 50;
Best Local Similarity 75.9%; Pred. No. 4.1e-07;
Matches 22; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY      2 AAUUAUACGACUCACUUAAGGAGACU 30
      ||:|||||:|||||:|||||:|||||:|
Db      2 AAATTAATAGCACTCACTATAGGAGACT 30

RESULT 13
```



```

Query Match      53.7%; Score 29; DB 4; Length 51;
Best Local Similarity 75.9%; Pred. No. 4.3e-07;
Matches 22; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY      2  AAAUUAUACGACUCACUAUAGGGAGACU 30
Db      1  AAATTAATACGACTCACTATAGGGAGACT 29

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: May 27, 2004, 11:30:47 ; Search time 284.177 Seconds  
(without alignments)  
864.392 Million cell updates/sec

Title: US-09-121-239-2  
Perfect score: 54  
Sequence: 1 UAAUUAUACGACUCACUA.....CCUGAGGCUCAAAGUCAGA 54

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 2960401 seqs, 2274450654 residues

Word size : 0

Total number of hits satisfying chosen parameters: 5920802

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

- 1: /cgn2\_6/prodata/2/pubpna/US07\_PUBCOMB.seq\*
- 2: /cgn2\_6/prodata/2/pubpna/PCT\_NEW\_PUB.seq\*
- 3: /cgn2\_6/prodata/2/pubpna/US06\_NEW\_PUB.seq\*
- 4: /cgn2\_6/prodata/2/pubpna/US06\_PUBCOMB.seq\*
- 5: /cgn2\_6/prodata/2/pubpna/US07\_NEW\_PUB.seq\*
- 6: /cgn2\_6/prodata/2/pubpna/PCTUS\_PUBCOMB.seq\*
- 7: /cgn2\_6/prodata/2/pubpna/US08\_NEW\_PUB.seq\*
- 8: /cgn2\_6/prodata/2/pubpna/US08\_PUBCOMB.seq\*
- 9: /cgn2\_6/prodata/2/pubpna/US09A\_PUBCOMB.seq\*
- 10: /cgn2\_6/prodata/2/pubpna/US09B\_PUBCOMB.seq\*
- 11: /cgn2\_6/prodata/2/pubpna/US09C\_PUBCOMB.seq\*
- 12: /cgn2\_6/prodata/2/pubpna/US09\_NEW\_PUB.seq\*
- 13: /cgn2\_6/prodata/2/pubpna/US09\_NEW\_PUB.seq2\*
- 14: /cgn2\_6/prodata/2/pubpna/US10A\_PUBCOMB.seq\*
- 15: /cgn2\_6/prodata/2/pubpna/US10B\_PUBCOMB.seq\*
- 16: /cgn2\_6/prodata/2/pubpna/US10C\_PUBCOMB.seq\*
- 17: /cgn2\_6/prodata/2/pubpna/US10\_NEW\_PUB.seq\*
- 18: /cgn2\_6/prodata/2/pubpna/US60\_NEW\_PUB.seq\*
- 19: /cgn2\_6/prodata/2/pubpna/US60\_PUBCOMB.seq\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	49	90.7	50	15	US-10-244-490-45
2	32	59.3	54	15	US-10-273-707-32
3	30	55.6	49	15	US-10-273-707-38
4	30	55.6	50	15	US-10-273-707-31
5	30	55.6	52	15	US-10-273-707-43
6	29	53.7	51	9	US-09-944-036-40
7	29	53.7	51	16	US-10-425-975-40
8	29	53.7	52	15	US-10-273-707-36
9	29	53.7	52	15	US-10-273-707-42
10	29	53.7	54	15	US-10-273-707-30
11	29	53.7	54	15	US-10-273-707-49
12	29	53.7	55	15	US-10-273-707-47
13	29	53.7	6306	13	US-09-833-782-3
14	28	51.9	28	15	US-10-273-707-44

15	28	51.9	30	9	US-09-876-527-29	Sequence 29, Appl
16	28	51.9	30	15	US-10-134-089-29	Sequence 29, Appl
17	28	51.9	33	9	US-09-738-972-10	Sequence 10, Appl
18	28	51.9	33	9	US-09-944-036-4	Sequence 4, Appl
19	28	51.9	33	10	US-09-738-274-36	Sequence 36, Appl
20	28	51.9	33	14	US-10-001-407-29	Sequence 29, Appl
21	28	51.9	33	16	US-10-425-975-4	Sequence 4, Appl
22	28	51.9	35	9	US-09-202-972-15	Sequence 15, Appl
23	28	51.9	35	9	US-09-202-972-17	Sequence 17, Appl
24	28	51.9	35	10	US-09-897-776A-14	Sequence 14, Appl
25	28	51.9	35	10	US-09-897-776A-19	Sequence 19, Appl
26	28	51.9	36	13	US-03-803-810-7	Sequence 7, Appl
27	28	51.9	36	15	US-10-298-330-7	Sequence 7, Appl
28	28	51.9	37	9	US-09-944-036-2	Sequence 2, Appl
29	28	51.9	37	16	US-10-425-975-2	Sequence 2, Appl
30	28	51.9	39	12	US-10-651-563-9	Sequence 9, Appl
31	28	51.9	41	9	US-09-953-321-15	Sequence 15, Appl
32	28	51.9	49	15	US-10-273-707-37	Sequence 37, Appl
33	28	51.9	49	15	US-10-273-707-39	Sequence 39, Appl
34	28	51.9	50	15	US-10-273-707-40	Sequence 40, Appl
35	28	51.9	51	9	US-09-944-036-41	Sequence 41, Appl
36	28	51.9	51	15	US-10-273-707-41	Sequence 41, Appl
37	28	51.9	51	16	US-10-425-975-41	Sequence 41, Appl
38	28	51.9	52	9	US-09-944-036-39	Sequence 39, Appl
39	28	51.9	52	9	US-09-944-036-43	Sequence 43, Appl
40	28	51.9	52	10	US-09-738-274-12	Sequence 12, Appl
41	28	51.9	52	16	US-10-425-975-39	Sequence 39, Appl
42	28	51.9	52	16	US-10-425-975-43	Sequence 43, Appl
43	28	51.9	53	9	US-09-944-036-34	Sequence 34, Appl
44	28	51.9	53	9	US-09-944-036-35	Sequence 35, Appl
45	28	51.9	53	9	US-09-944-036-36	Sequence 36, Appl

## ALIGNMENTS

### RESULT 1

US-10-244-490-45  
; Sequence 45, Application US/10244490  
; Publication No. US20030152916A1  
; GENERAL INFORMATION:  
; APPLICANT: VACIAN, DANIEL L.  
; APPLICANT: FULTZ, TIMOTHY J.  
; APPLICANT: MCDONOUGH, SHERROL H.  
; TITLE OF INVENTION: DETECTION OF HIV  
; FILE REFERENCE: 218/130  
; CURRENT APPLICATION NUMBER: US/10/244,490  
; PRIOR FILING DATE: 2002-09-16  
; PRIOR APPLICATION NUMBER: US/09/168,947  
; PRIOR FILING DATE: 1998-10-08  
; PRIOR APPLICATION NUMBER: 08/469,067  
; PRIOR FILING DATE: 1995-06-06  
; PRIOR APPLICATION NUMBER: 07/550,837  
; PRIOR FILING DATE: 1990-07-10  
; NUMBER OF SEQ ID NOS: 46  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 45  
; LENGTH: 50  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthesized nucleic acid molecule  
US-10-244-490-45

Query Match 90.7%; Score 49; DB 15; Length 50;  
Best Local Similarity 79.6%; Pred. No. 3.4e-18;  
Matches 39; Conservative 10; Mismatches 0; Indels 0; Gaps 0;  
QY 3 AAUUAUACGACUCACUAUAGGAGACUCAGACCCUGGCUCAAAGUC 51  
DB 2 AATTAAACGACTACTATAGGAGACTCAGACCTGAGCTCAAAGTC 50

```
RESULT 2
US-10-273-707-32
; Sequence 32, Application US/10273707
; Publication No. US20030104448A1
; GENERAL INFORMATION:
; APPLICANT: HARVEY, Richard, C.
; APPLICANT: CLARK, JR., Thomas, J.
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FOR DETECTING GENETIC MARKERS
; TITLE OF INVENTION: FOR CANCER IN A BIOLOGICAL SAMPLE
; FILE REFERENCE: GP097-03.DVI
; CURRENT APPLICATION NUMBER: US/10/273,707
; CURRENT FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: 09/493,491
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/117,640 US
; PRIOR FILING DATE: 1999-01-28
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 32
; LENGTH: 54
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: construct
; NAME/KEY: promoter
; LOCATION: (1)..(28)
US-10-273-707-32

Query Match          59.3%; Score 32; DB 15; Length 54;
Best Local Similarity 75.0%; Pred. No. 2e-08;
Matches 24; Conservative 8; Mismatches 0; Indels 0; Gaps 0;

QY 1 UAAUUUAUACGACUCACUUAUAGGGAGACUCA 32
    :|||:|||||:|||||:|||||:|||||:
Db 1 TAAATTAAATACGACTCACTATAGGAGACTCA 32

RESULT 3
US-10-273-707-38
; Sequence 38, Application US/10273707
; Publication No. US20030104448A1
; GENERAL INFORMATION:
; APPLICANT: HARVEY, Richard, C.
; APPLICANT: CLARK, JR., Thomas, J.
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FOR DETECTING GENETIC MARKERS
; TITLE OF INVENTION: FOR CANCER IN A BIOLOGICAL SAMPLE
; FILE REFERENCE: GP097-03.DVI
; CURRENT APPLICATION NUMBER: US/10/273,707
; CURRENT FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: 09/493,491
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/117,640 US
; PRIOR FILING DATE: 1999-01-28
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 38
; LENGTH: 49
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: construct
; NAME/KEY: promoter
; LOCATION: (1)..(28)
US-10-273-707-38

Query Match          55.6%; Score 30; DB 15; Length 49;
Best Local Similarity 73.3%; Pred. No. 2.8e-07;
Matches 22; Conservative 8; Mismatches 0; Indels 0; Gaps 0;

QY 1 UAAUUUAUACGACUCACUUAUAGGGAGACUCA 32
    :|||:|||||:|||||:|||||:|||||:
Db 1 TAAATTAAATACGACTCACTATAGGAGACTCA 32

RESULT 4
US-10-273-707-31
; Sequence 31, Application US/10273707
; Publication No. US20030104448A1
; GENERAL INFORMATION:
; APPLICANT: HARVEY, Richard, C.
; APPLICANT: CLARK, JR., Thomas, J.
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FOR DETECTING GENETIC MARKERS
; TITLE OF INVENTION: FOR CANCER IN A BIOLOGICAL SAMPLE
; FILE REFERENCE: GP097-03.DVI
; CURRENT APPLICATION NUMBER: US/10/273,707
; CURRENT FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: 09/493,491
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/117,640 US
; PRIOR FILING DATE: 1999-01-28
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 31
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: construct
; NAME/KEY: promoter
; LOCATION: (1)..(28)
US-10-273-707-31

Query Match          55.6%; Score 30; DB 15; Length 50;
Best Local Similarity 73.3%; Pred. No. 2.8e-07;
Matches 22; Conservative 8; Mismatches 0; Indels 0; Gaps 0;

QY 1 UAAUUUAUACGACUCACUUAUAGGGAGACUC 30
    :|||:|||||:|||||:|||||:|||||:
Db 1 TAAATTAAATACGACTCACTATAGGAGACT 30

RESULT 5
US-10-273-707-43
; Sequence 43, Application US/10273707
; Publication No. US20030104448A1
; GENERAL INFORMATION:
; APPLICANT: HARVEY, Richard, C.
; APPLICANT: CLARK, JR., Thomas, J.
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FOR DETECTING GENETIC MARKERS
; TITLE OF INVENTION: FOR CANCER IN A BIOLOGICAL SAMPLE
; FILE REFERENCE: GP097-03.DVI
; CURRENT APPLICATION NUMBER: US/10/273,707
; CURRENT FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: 09/493,491
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/117,640 US
; PRIOR FILING DATE: 1999-01-28
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 43
; LENGTH: 52
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: construct
; NAME/KEY: promoter
; LOCATION: (1)..(28)
US-10-273-707-43

Query Match          55.6%; Score 30; DB 15; Length 49;
Best Local Similarity 73.3%; Pred. No. 2.8e-07;
Matches 22; Conservative 8; Mismatches 0; Indels 0; Gaps 0;
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QY 1 UAAUUUAUACGACUCACUUAUAGGGAGACUC 30
    :|||:|||||:|||||:|||||:|||||:
Db 1 TAAATTAAATACGACTCACTATAGGAGACT 30

RESULT 4
US-10-273-707-31
; Sequence 31, Application US/10273707
; Publication No. US20030104448A1
; GENERAL INFORMATION:
; APPLICANT: HARVEY, Richard, C.
; APPLICANT: CLARK, JR., Thomas, J.
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FOR DETECTING GENETIC MARKERS
; TITLE OF INVENTION: FOR CANCER IN A BIOLOGICAL SAMPLE
; FILE REFERENCE: GP097-03.DVI
; CURRENT APPLICATION NUMBER: US/10/273,707
; CURRENT FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: 09/493,491
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/117,640 US
; PRIOR FILING DATE: 1999-01-28
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 31
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: construct
; NAME/KEY: promoter
; LOCATION: (1)..(28)
US-10-273-707-31

Query Match          55.6%; Score 30; DB 15; Length 50;
Best Local Similarity 73.3%; Pred. No. 2.8e-07;
Matches 22; Conservative 8; Mismatches 0; Indels 0; Gaps 0;

QY 1 UAAUUUAUACGACUCACUUAUAGGGAGACUC 30
    :|||:|||||:|||||:|||||:|||||:
Db 1 TAAATTAAATACGACTCACTATAGGAGACT 30

RESULT 5
US-10-273-707-43
; Sequence 43, Application US/10273707
; Publication No. US20030104448A1
; GENERAL INFORMATION:
; APPLICANT: HARVEY, Richard, C.
; APPLICANT: CLARK, JR., Thomas, J.
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FOR DETECTING GENETIC MARKERS
; TITLE OF INVENTION: FOR CANCER IN A BIOLOGICAL SAMPLE
; FILE REFERENCE: GP097-03.DVI
; CURRENT APPLICATION NUMBER: US/10/273,707
; CURRENT FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: 09/493,491
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/117,640 US
; PRIOR FILING DATE: 1999-01-28
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 43
; LENGTH: 52
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: construct
; NAME/KEY: promoter
; LOCATION: (1)..(28)
US-10-273-707-43

Query Match          55.6%; Score 30; DB 15; Length 49;
Best Local Similarity 73.3%; Pred. No. 2.8e-07;
Matches 22; Conservative 8; Mismatches 0; Indels 0; Gaps 0;
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Query Match      55.6%; Score 30; DB 15; Length 52;
Best Local Similarity 73.3%; Pred. No. 2.8e-07;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 UAAUUUAUACGACUCACUUAAGGGAGACU 30
   :||||:||||:||||:||||:||||:||||:
Db 1 TAAATTAATACGACTCACTATAGGAGACT 30

RESULT 6
US-09-944-036-40
; Sequence 40, Application US/09944036
; Patent No. US2002005095A1
; GENERAL INFORMATION:
; APPLICANT: YANG, Yeasing Y.
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: BABOLA, Odile
; APPLICANT: TRAN, Nathalie
; APPLICANT: VERNET, Guy
; TITLE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF
; FILE REFERENCE: GP114-02.UT
; CURRENT APPLICATION NUMBER: US/09/944,036
; CURRENT FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/229,790
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 40
; TYPE: DNA
; LENGTH: 51
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Oligonucleotide primer for Reverse Transcriptase
; NAME/KEY: promoter
; LOCATION: (1)..(29)
US-09-944-036-40

Query Match      53.7%; Score 29; DB 9; Length 51;
Best Local Similarity 75.9%; Pred. No. 1.1e-06;
Matches 22; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 2 AAUUUAUACGACUCACUUAAGGGAGACU 30
   :||||:||||:||||:||||:||||:
Db 1 AAATTAATACGACTCACTATAGGAGACT 29

RESULT 7
US-10-425-975-40
; Sequence 40, Application US/10425975
; Publication No. US2003022857A1
; GENERAL INFORMATION:
; APPLICANT: YANG, Yeasing Y.
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: BABOLA, Odile
; APPLICANT: TRAN, Nathalie
; APPLICANT: VERNET, Guy
; TITLE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF
; FILE REFERENCE: GP114-02.UT
; CURRENT APPLICATION NUMBER: US/10/425,975
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US/09/944,036
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/229,790
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 40
; LENGTH: 51
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; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Oligonucleotide primer for Reverse Transcriptase
; OTHER INFORMATION: target sequence
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (1)..(29)
US-10-425-975-40

Query Match      53.7%; Score 29; DB 16; Length 51;
Best Local Similarity 75.9%; Pred. No. 1.1e-06;
Matches 22; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 2 AAUUUAUACGACUCACUUAAGGGAGACU 30
   :||||:||||:||||:||||:||||:
Db 1 AAATTAATACGACTCACTATAGGAGACT 29

RESULT 8
US-10-273-707-36
; Sequence 36, Application US/10273707
; Publication No. US20030104448A1
; GENERAL INFORMATION:
; APPLICANT: HARVEY, Richard, C.
; APPLICANT: CLARK, JR., Thomas, J.
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FOR DETECTING GENETIC MARKERS
; FILE REFERENCE: GP097-03.DV1
; CURRENT APPLICATION NUMBER: US/10/273,707
; CURRENT FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: 09/493,491
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/117,640 US
; PRIOR FILING DATE: 1999-01-28
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 36
; LENGTH: 52
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: construct
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (1)..(28)
US-10-273-707-36

Query Match      53.7%; Score 29; DB 15; Length 52;
Best Local Similarity 75.9%; Pred. No. 1.1e-06;
Matches 22; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 UAAUUUAUACGACUCACUUAAGGGAGAC 29
   :||||:||||:||||:||||:||||:
Db 1 TAAATTAATACGACTCACTATAGGAGAC 29

RESULT 9
US-10-273-707-42
; Sequence 42, Application US/10273707
; Publication No. US20030104448A1
; GENERAL INFORMATION:
; APPLICANT: HARVEY, Richard, C.
; APPLICANT: CLARK, JR., Thomas, J.
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FOR DETECTING GENETIC MARKERS
; FILE REFERENCE: GP097-03.DV1
; CURRENT APPLICATION NUMBER: US/10/273,707
; CURRENT FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: 09/493,491
; PRIOR FILING DATE: 2000-01-28
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; FILE REFERENCE: GP097-03.DV1
; CURRENT APPLICATION NUMBER: US/10/273,707
; PRIOR FILING DATE: 1999-01-28
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 42
; LENGTH: 52
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; NAME/KEY: promoter
; LOCATION: (1)..(28)
US-10-273-707-42

Query Match          53.7%; Score 29; DB 15; Length 52;
Best Local Similarity 75.9%; Pred. No. 1.1e-06;
Matches 22; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 UAAUUUAUACGACUCACUUAAGGGAGAC 29
Db 1 TAAATTAATACGACTCACTATAGGGAGAC 29

RESULT 10
US-10-273-707-30
; Sequence 30, Application US/10273707
; Publication No. US20030104448A1
; GENERAL INFORMATION:
; APPLICANT: HARVEY, Richard, C.
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FOR DETECTING GENETIC MARKERS
; FILE REFERENCE: GP097-03.DV1
; CURRENT APPLICATION NUMBER: US/10/273,707
; PRIOR FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: 09/493,491
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/117,640 US
; PRIOR FILING DATE: 1999-01-28
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 54
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; NAME/KEY: promoter
; LOCATION: (1)..(28)
US-10-273-707-30

Query Match          53.7%; Score 29; DB 15; Length 54;
Best Local Similarity 75.9%; Pred. No. 1.1e-06;
Matches 22; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 UAAUUUAUACGACUCACUUAAGGGAGAC 29
Db 1 TAAATTAATACGACTCACTATAGGGAGAC 29

RESULT 11
US-10-273-707-49
; Sequence 49, Application US/10273707
; Publication No. US20030104448A1
; GENERAL INFORMATION:
; APPLICANT: HARVEY, Richard, C.
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FOR DETECTING GENETIC MARKERS
; FILE REFERENCE: GP097-03.DV1
; CURRENT APPLICATION NUMBER: US/10/273,707
; PRIOR FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: 09/493,491
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/117,640 US
; PRIOR FILING DATE: 1999-01-28
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 49
; LENGTH: 54
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; NAME/KEY: promoter
; LOCATION: (1)..(28)
US-10-273-707-49

Query Match          53.7%; Score 29; DB 15; Length 54;
Best Local Similarity 75.9%; Pred. No. 1.1e-06;
Matches 22; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 UAAUUUAUACGACUCACUUAAGGGAGAC 29
Db 1 TAAATTAATACGACTCACTATAGGGAGAC 29

RESULT 12
US-10-273-707-47
; Sequence 47, Application US/10273707
; Publication No. US20030104448A1
; GENERAL INFORMATION:
; APPLICANT: HARVEY, Richard, C.
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FOR DETECTING GENETIC MARKERS
; FILE REFERENCE: GP097-03.DV1
; CURRENT APPLICATION NUMBER: US/10/273,707
; PRIOR FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: 09/493,491
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/117,640 US
; PRIOR FILING DATE: 1999-01-28
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 47
; LENGTH: 55
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; NAME/KEY: promoter
; LOCATION: (1)..(28)
US-10-273-707-47

Query Match          53.7%; Score 29; DB 15; Length 55;
Best Local Similarity 75.9%; Pred. No. 1.1e-06;
Matches 22; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 UAAUUUAUACGACUCACUUAAGGGAGAC 29
Db 1 TAAATTAATACGACTCACTATAGGGAGAC 29

RESULT 13
US-09-833-782-3
; Sequence 3, Application US/09833782
; Publication No. US20020040131A1
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; FILE REFERENCE: GP097-03.DV1
; CURRENT APPLICATION NUMBER: US/10/273,707
; PRIOR FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: 09/493,491
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/117,640 US
; PRIOR FILING DATE: 1999-01-28
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 49
; LENGTH: 54
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; NAME/KEY: promoter
; LOCATION: (1)..(28)
US-10-273-707-49

Query Match          53.7%; Score 29; DB 15; Length 54;
Best Local Similarity 75.9%; Pred. No. 1.1e-06;
Matches 22; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 UAAUUUAUACGACUCACUUAAGGGAGAC 29
Db 1 TAAATTAATACGACTCACTATAGGGAGAC 29

RESULT 12
US-10-273-707-47
; Sequence 47, Application US/10273707
; Publication No. US20030104448A1
; GENERAL INFORMATION:
; APPLICANT: HARVEY, Richard, C.
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FOR DETECTING GENETIC MARKERS
; FILE REFERENCE: GP097-03.DV1
; CURRENT APPLICATION NUMBER: US/10/273,707
; PRIOR FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: 09/493,491
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/117,640 US
; PRIOR FILING DATE: 1999-01-28
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 47
; LENGTH: 55
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; NAME/KEY: promoter
; LOCATION: (1)..(28)
US-10-273-707-47

Query Match          53.7%; Score 29; DB 15; Length 55;
Best Local Similarity 75.9%; Pred. No. 1.1e-06;
Matches 22; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 UAAUUUAUACGACUCACUUAAGGGAGAC 29
Db 1 TAAATTAATACGACTCACTATAGGGAGAC 29

RESULT 13
US-09-833-782-3
; Sequence 3, Application US/09833782
; Publication No. US20020040131A1
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; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Wilganowski, Nathaniel L.
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: Novel Human Metalloprotease and Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0161-USA
; CURRENT APPLICATION NUMBER: US/09/833,782
; CURRENT FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: US 60/196,319
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 6306
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-833-782-3

Query Match      53.7%; Score 29; DB 13; Length 6306;
Best Local Similarity 75.9%; Pred. No. 1.2e-06;
Matches 22; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 2 AAAUUAUACGACUCACUAGGGAGACU 30
Db 86 AAATTAATACGACTCACTATAGGAGACT 114

RESULT 14
US-10-273-707-44
; Sequence 44, Application US/10273707
; Publication No. US20030104448A1
; GENERAL INFORMATION:
; APPLICANT: HARVEY, Richard, C.
; APPLICANT: CLARK, JR., Thomas, J.
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FOR DETECTING GENETIC MARKERS
; FILE REFERENCE: GP097-03.DV1
; CURRENT APPLICATION NUMBER: US/10/273,707
; CURRENT FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: 09/493,491
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/117,640 US
; PRIOR FILING DATE: 1999-01-28
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 44
; LENGTH: 28
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: construct
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (1)..(28)
US-10-273-707-44

Query Match      51.9%; Score 28; DB 15; Length 28;
Best Local Similarity 75.0%; Pred. No. 3.9e-06;
Matches 21; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 UAAUUAUACGACUCACUAGGGAGGA 28
Db 1 TAAATTAATACGACTCACTATAGGAGGA 28

RESULT 15
US-09-876-527-29
; Sequence 29, Application US/09876527
; Patent No. US20020102616A1
; GENERAL INFORMATION:
; APPLICANT: Kindsvogel, Wayne
; APPLICANT: Jelinek, Laura J.

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; Sheppard, Paul O.
; Hagopian, William A.
; LaGasse, James M.
; TITLE OF INVENTION: ISLET CELL ANTIGEN 1851
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/876,527
; FILING DATE: 07-Jun-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/811,481
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Lingenfelter, Susan
; REGISTRATION NUMBER: P-41,156
; REFERENCE/DOCKET NUMBER: 95-36
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6675
; TELEFAX: 206-442-6678
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; IMMEDIATE SOURCE:
; CLONE: ZC11197
; SEQUENCE DESCRIPTION: SEQ ID NO: 29:
US-09-876-527-29

Query Match      51.9%; Score 28; DB 9; Length 30;
Best Local Similarity 78.6%; Pred. No. 3.9e-06;
Matches 22; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 2 AAAUUAUACGACUCACUAGGGAGAC 29
Db 1 AAATTAATACGACTCACTATAGGAGAC 28

Search completed: May 27, 2004, 14:58:24
Job time : 284.177 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 26, 2004, 15:22:41 ; Search time 1906.62 Seconds  
(without alignments)  
845,770 Million cell updates/sec

Title: US-09-121-239-2

Perfect score: 54

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Gapop 60.0 , Gapext 60.0

Searched: 27513289 seqs, 14931090276 residues

Word size : 0

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

EST:

1: em\_estba:\*

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6: em\_estpl:\*

7: em\_estro:\*

8: em\_htc:\*

9: gb\_est1:\*

10: gb\_est2:\*

11: gb\_htc:\*

12: gb\_est3:\*

13: gb\_est4:\*

14: gb\_est5:\*

15: em\_estfun:\*

16: em\_estom:\*

17: em\_gss\_hum:\*

18: em\_gss\_inv:\*

19: em\_gss\_pln:\*

20: em\_gss\_vrt:\*

21: em\_gss\_fun:\*

22: em\_gss\_nam:\*

23: em\_gss\_mus:\*

24: em\_gss\_pro:\*

25: em\_gss\_rod:\*

26: em\_gss\_phg:\*

27: em\_gss\_vrl:\*

28: gb\_gsl1:\*

29: gb\_gsl2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	29	53.7	560	29	CC966861
C 2	29	53.7	571	29	CC964269
C 3	29	53.7	585	29	CC947693
C 4	29	53.7	592	29	CC961654

FEATURES

C	5	29	53.7	604	29	CC952121	CC952121	BOIB185TR
C	6	29	53.7	610	29	CC948768	CC948768	BOIDG32TR
C	7	29	53.7	612	29	CC947463	CC947463	CC947463
C	8	29	53.7	617	29	CC967304	CC967304	BOIFK41TR
C	9	29	53.7	621	29	CC968451	CC968451	BOIFB27TR
C	10	29	53.7	642	29	CC944751	CC944751	BOIBU81TR
C	11	29	53.7	642	29	CC948396	CC948396	BOICQ54TR
C	12	29	53.7	644	29	CC949404	CC949404	BOIGZ19TR
C	13	29	53.7	644	29	CC951454	CC951454	BOIFB62TR
C	14	29	53.7	649	29	CC962886	CC962886	BOIGN54TR
C	15	29	53.7	651	29	CC961061	CC961061	BOICX68TR
C	16	29	53.7	684	29	CC945503	CC945503	BOIDK74TR
C	17	29	53.7	687	29	CC948738	CC948738	BOIFD28TR
C	18	29	53.7	688	29	CC944195	CC944195	BOIBL59TR
C	19	29	53.7	693	29	CC944485	CC944485	BOIBL39TR
C	20	29	53.7	705	29	CC951566	CC951566	BOIEJ65TR
C	21	29	53.7	705	29	CC958824	CC958824	BOIBM11TR
C	22	29	53.7	718	29	CC954347	CC954347	BOIBW60TR
C	23	29	53.7	719	29	CC968802	CC968802	BOICJ62TR
C	24	29	53.7	727	29	CC969001	CC969001	BOICR93TR
C	25	29	53.7	735	29	CC958105	CC958105	BOIGX30TR
C	26	29	53.7	735	29	CC961701	CC961701	BOIDQ39TR
C	27	29	53.7	830	29	CC953502	CC953502	BOIGT40TR
C	28	29	53.7	830	29	CC968053	CC968053	BOICE19TR
C	29	29	53.7	859	29	CC958532	CC958532	BOIFG34TR
C	30	28	51.9	143	13	BQ102727	BQ102727	UUGC0111
C	31	28	51.9	181	10	BE391582	BE391582	601282148
C	32	28	51.9	182	10	BE262878	BE262878	601148014
C	33	28	51.9	183	10	BF976190	BF976190	602245057
C	34	28	51.9	185	10	BE314661	BE314661	601146777
C	35	28	51.9	188	12	BG475075	BG475075	602491094
C	36	28	51.9	195	10	BE397962	BE397962	601290494
C	37	28	51.9	203	10	BF974085	BF974085	602240343
C	38	28	51.9	204	10	BE410828	BE410828	601301490
C	39	28	51.9	206	10	BE398063	BE398063	601290252
C	40	28	51.9	227	10	BF027436	BF027436	601872556
C	41	28	51.9	267	13	BQ102748	BQ102748	UUGC0132
C	42	28	51.9	272	10	BE391744	BE391744	601282029
C	43	28	51.9	310	13	BQ102753	BQ102753	UUGC0137
C	44	28	51.9	329	13	BQ102710	BQ102710	UUGC0094
C	45	28	51.9	334	12	BG425691	BG425691	602448292

ALIGNMENTS

RESULT 1  
CC966861/c  
LOCUS  
DEFINITION  
BOIFL85TR BO.1.4.1.6 KB nuc Brassica oleracea genomic clone  
BOIFL85, genomic survey sequence.  
ACCESSION  
CC966861  
VERSION  
CC966861.1 GI:33819522  
KEYWORDS  
GSS.  
SOURCE  
Brassica oleracea  
ORGANISM  
Brassica oleracea  
REFERENCE  
1 (bases 1 to 560)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.  
AUTHORS  
Town, C.D., Van Aken, S., Utterback, T., Koo, H. and Fraser, C.M.  
TITLE  
Whole genome shotgun sequencing of Brassica oleracea  
JOURNAL  
Unpublished (2001)  
COMMENT  
Contact: Chris Town  
TIGR  
9712 Medical Center Drive, Rockville, MD 20850, USA.  
Tel: 301-838-3523  
Fax: 301-838-0208  
Email: cdtown@tigr.org  
DNA is from a doubled haploid provided by Tom Osborn.  
Seq primer: TP  
Class: sheared ends.  
Location/Qualifiers

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source
1..560
/organism="Brassica oleracea"
/mol_type="genomic DNA"
/strain="TO1000DH3"
/db_xref="taxon:3712"
/clone="BOIFL85"
/clone_lib="BO_1.4_1.6_KB_nuc"
/note="Vector: PHOS2; Site 1: BstXI; 1.4-1.6 kb sheared
nuclear DNA inserted into PHOS2 using BstXI linkers"

ORIGIN
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Best Local Similarity 75.9%; Pred. NO. 8.1e-06;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AAUUAUACGACUCACUUAUAGGAGACUC 31
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Db 177 AATTAATACGACTCACTATAGGAGACTC 149

RESULT 2
CC964269/c
LOCUS
DEFINITION
BOIEN76TR BO_1.4_1.6_KB_nuc Brassica oleracea genomic clone
BOIEN76, genomic survey sequence.
ACCESSION
CC964269
VERSION
1 GI:33814428
KEYWORDS
GSS.
SOURCE
Brassica oleracea
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE
1 (bases 1 to 571)
AUTHORS
Town,C.D., Van Aken,S., Utterback,T., Koo,H. and Fraser,C.M.
TITLE
Whole genome shotgun sequencing of Brassica oleracea
JOURNAL
Unpublished (2001)
COMMENT
Contact: Chris Town
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TR
Class: sheared ends.

FEATURES
source
Location/Qualifiers
1..571
/organism="Brassica oleracea"
/mol_type="genomic DNA"
/strain="TO1000DH3"
/db_xref="taxon:3712"
/clone="BOIEN76"
/clone_lib="BO_1.4_1.6_KB_nuc"
/note="Vector: PHOS2; Site 1: BstXI; 1.4-1.6 kb sheared
nuclear DNA inserted into PHOS2 using BstXI linkers"

ORIGIN
Query Match      53.7%; Score 29; DB 29; Length 571;
Best Local Similarity 75.9%; Pred. NO. 8.1e-06;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AAUUAUACGACUCACUUAUAGGAGACUC 31
   ||:|||||:|||||:|||||:|||||:|
Db 179 AATTAATACGACTCACTATAGGAGACTC 151

RESULT 3
CC947693/c
LOCUS
DEFINITION
BOIEQ41TR BO_1.4_1.6_KB_nuc Brassica oleracea genomic clone
BOIEQ41, genomic survey sequence.
ACCESSION
CC947693

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VERSION
CC947693.1 GI:33781675
KEYWORDS
GSS.
SOURCE
Brassica oleracea
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE
1 (bases 1 to 595)
AUTHORS
Town,C.D., Van Aken,S., Utterback,T., Koo,H. and Fraser,C.M.
TITLE
Whole genome shotgun sequencing of Brassica oleracea
JOURNAL
Unpublished (2001)
COMMENT
Contact: Chris Town
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TR
Class: sheared ends.

FEATURES
source
Location/Qualifiers
1..595
/organism="Brassica oleracea"
/mol_type="genomic DNA"
/strain="TO1000DH3"
/db_xref="taxon:3712"
/clone="BOIEQ41"
/clone_lib="BO_1.4_1.6_KB_nuc"
/note="Vector: PHOS2; Site 1: BstXI; 1.4-1.6 kb sheared
nuclear DNA inserted into PHOS2 using BstXI linkers"

ORIGIN
Query Match      53.7%; Score 29; DB 29; Length 585;
Best Local Similarity 75.9%; Pred. NO. 8.2e-06;
Matches 22; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 3 AAUUAUACGACUCACUUAUAGGAGACUC 31
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Db 177 AATTAATACGACTCACTATAGGAGACTC 149

RESULT 4
CC961654/c
LOCUS
DEFINITION
BOIDB28TR BO_1.4_1.6_KB_nuc Brassica oleracea genomic clone
BOIDB28, genomic survey sequence.
ACCESSION
CC961654
VERSION
1 GI:33809231
KEYWORDS
GSS.
SOURCE
Brassica oleracea
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE
1 (bases 1 to 592)
AUTHORS
Town,C.D., Van Aken,S., Utterback,T., Koo,H. and Fraser,C.M.
TITLE
Whole genome shotgun sequencing of Brassica oleracea
JOURNAL
Unpublished (2001)
COMMENT
Contact: Chris Town
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TR
Class: sheared ends.

FEATURES
source
Location/Qualifiers
1..592
/organism="Brassica oleracea"
/mol_type="genomic DNA"
/strain="TO1000DH3"
/db_xref="taxon:3712"

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/clone="BOIDB28"
/clone_lib="BO_1.4_1.6_KB_nuc"
/note="Vector: pHOS2; Site 1: BstXI; 1.4-1.6 kb sheared
nuclear DNA inserted into pHOS2 using BstXI linkers"

ORIGIN
Query Match      53.7%; Score 29; DB 29; Length 592;
Best Local Similarity 75.9%; Pred. No. 8.2e-06;
Matches 22; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 3 AAUUAUACGACUCACUUAUAGGAGACUC 31
||:||||:||||:||||:||||:||||:|
Db 184 AATTAATACGACTCACTATAGGAGACTC 156

RESULT 5
CC952121/c
LOCUS CC952121 604 bp DNA linear GSS 18-AUG-2003
DEFINITION BOIB185TR BO_1.4_1.6_KB_nuc Brassica oleracea genomic clone
BOIB185, genomic survey sequence.
ACCESSION CC952121
VERSION CC952121.1 GI:33790560
KEYWORDS GSS.
SOURCE Brassica oleracea
ORGANISM Brassica oleracea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE 1 (bases 1 to 604)
AUTHORS Town,C.D., Van Aken,S., Utterback,T., Koo,H. and Fraser,C.M.
TITLE Whole genome shotgun sequencing of Brassica oleracea
JOURNAL Unpublished (2001)
COMMENT Other GSSs: BOIB185TF
Contact: Chris Town
TIGR
712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TR
Class: sheared ends.

FEATURES             source
    Location/Qualifiers
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            /organism="Brassica oleracea"
            /mol_type="genomic DNA"
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            /db_xref="taxon:3712"
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            /clone_lib="BO_1.4_1.6_KB_nuc"
            /note="Vector: pHOS2; Site 1: BstXI; 1.4-1.6 kb sheared
            nuclear DNA inserted into pHOS2 using BstXI linkers"

ORIGIN
Query Match      53.7%; Score 29; DB 29; Length 604;
Best Local Similarity 75.9%; Pred. No. 8.2e-06;
Matches 22; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 3 AAUUAUACGACUCACUUAUAGGAGACUC 31
||:||||:||||:||||:||||:||||:|
Db 185 AATTAATACGACTCACTATAGGAGACTC 157

RESULT 6
CC948768/c
LOCUS CC948768 610 bp DNA linear GSS 18-AUG-2003
DEFINITION BOIDG32TR BO_1.4_1.6_KB_nuc Brassica oleracea genomic clone
BOIDG32, genomic survey sequence.
ACCESSION CC948768
VERSION CC948768.1 GI:33783814
KEYWORDS GSS.
SOURCE Brassica oleracea
ORGANISM Brassica oleracea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE 1 (bases 1 to 610)
AUTHORS Town,C.D., Van Aken,S., Utterback,T., Koo,H. and Fraser,C.M.
TITLE Whole genome shotgun sequencing of Brassica oleracea
JOURNAL Unpublished (2001)
COMMENT Other GSSs: BOIDG32TF
Contact: Chris Town
TIGR
712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TR
Class: sheared ends.

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Matches 22; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 3 AAUUAUACGACUCACUUAUAGGAGACUC 31
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Db 185 AATTAATACGACTCACTATAGGAGACTC 157

RESULT 7
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DEFINITION BOIGK06TR BO_1.4_1.6_KB_nuc Brassica oleracea genomic clone
BOIGK06, genomic survey sequence.
ACCESSION CC947463
VERSION CC947463.1 GI:33781217
KEYWORDS GSS.
SOURCE Brassica oleracea
ORGANISM Brassica oleracea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE 1 (bases 1 to 612)
AUTHORS Town,C.D., Van Aken,S., Utterback,T., Koo,H. and Fraser,C.M.
TITLE Whole genome shotgun sequencing of Brassica oleracea
JOURNAL Unpublished (2001)
COMMENT Other GSSs: BOIGK06TF
Contact: Chris Town
TIGR
712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TR
Class: sheared ends.

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            nuclear DNA inserted into pHOS2 using BstXI linkers"

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Best Local Similarity 75.9%; Pred. No. 8.2e-06;
Matches 22; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 3 AAUUAUACGACUCACUUAUAGGAGACUC 31
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Db 270 AATTAATACGACTCACTATAGGAGACTC 242

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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE 1 (bases 1 to 610)
AUTHORS Town,C.D., Van Aken,S., Utterback,T., Koo,H. and Fraser,C.M.
TITLE Whole genome shotgun sequencing of Brassica oleracea
JOURNAL Unpublished (2001)
COMMENT Other GSSs: BOIDG32TF
Contact: Chris Town
TIGR
712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TR
Class: sheared ends.

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            /clone_lib="BO_1.4_1.6_KB_nuc"
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            nuclear DNA inserted into pHOS2 using BstXI linkers"

ORIGIN
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Best Local Similarity 75.9%; Pred. No. 8.2e-06;
Matches 22; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 3 AAUUAUACGACUCACUUAUAGGAGACUC 31
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Db 270 AATTAATACGACTCACTATAGGAGACTC 242

RESULT 7
CC947463/c
LOCUS CC947463 612 bp DNA linear GSS 18-AUG-2003
DEFINITION BOIGK06TR BO_1.4_1.6_KB_nuc Brassica oleracea genomic clone
BOIGK06, genomic survey sequence.
ACCESSION CC947463
VERSION CC947463.1 GI:33781217
KEYWORDS GSS.
SOURCE Brassica oleracea
ORGANISM Brassica oleracea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE 1 (bases 1 to 612)
AUTHORS Town,C.D., Van Aken,S., Utterback,T., Koo,H. and Fraser,C.M.
TITLE Whole genome shotgun sequencing of Brassica oleracea
JOURNAL Unpublished (2001)
COMMENT Other GSSs: BOIGK06TF
Contact: Chris Town
TIGR
712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TR
Class: sheared ends.

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            /clone_lib="BO_1.4_1.6_KB_nuc"
            /note="Vector: pHOS2; Site 1: BstXI; 1.4-1.6 kb sheared
            nuclear DNA inserted into pHOS2 using BstXI linkers"

ORIGIN
Query Match      53.7%; Score 29; DB 29; Length 610;
Best Local Similarity 75.9%; Pred. No. 8.2e-06;
Matches 22; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

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Db 270 AATTAATACGACTCACTATAGGAGACTC 242

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Db 307 AATTATACGACTCACTATAGGAGACTC 279  
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## RESULT 14

CC962886/c

LOCUS

DEFINITION

BOIGN54TR BO 1.4 1.6 KB nuc Brassica oleracea genomic clone

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

1 (bases 1 to 649)

Town, C.D., Van Aken, S., Utterback, T., Koo, H. and Fraser, C.M.

Whole genome shotgun sequencing of Brassica oleracea

JOURNAL

COMMENT

Contact: Chris Town

TIGR 9712 Medical Center Drive, Rockville, MD 20850, USA.

Tel: 301-838-3523

Fax: 301-838-0208

Email: cdtown@tigr.org

DNA is from a doubled haploid provided by Tom Osborn.

Seq primer: TR

Class: sheared ends.

## FEATURES

source

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/organism="Brassica oleracea"

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nuclear DNA inserted into pHOS2 using BstXI linkers"

## ORIGIN

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 Best Local Similarity 75.9%; Pred. No. 8.4e-06;  
 Matches 22; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 3 AAUUAUACGACUCACUAGGGAGACUC 31

||:||||:||||:||||:||||:||||:|

Db 184 AATTATACGACTCACTATAGGAGACTC 156

## RESULT 15

CC961061/c

LOCUS

DEFINITION

BOICX68TR BO 1.4 1.6 KB nuc Brassica oleracea genomic clone

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

1 (bases 1 to 651)

Town, C.D., Van Aken, S., Utterback, T., Koo, H. and Fraser, C.M.

Whole genome shotgun sequencing of Brassica oleracea

JOURNAL

COMMENT

Contact: Chris Town

TIGR 9712 Medical Center Drive, Rockville, MD 20850, USA.

Tel: 301-838-3523

Fax: 301-838-0208

Email: cdtown@tigr.org  
 DNA is from a doubled haploid provided by Tom Osborn.

Seq primer: TR

Class: sheared ends.

## FEATURES

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/note="Vector: pHOS2; Site 1: BstXI; 1.4-1.6 kb sheared

nuclear DNA inserted into pHOS2 using BstXI linkers"

## ORIGIN

Query Match 53.7%; Score 29; DB 29; Length 651;  
 Best Local Similarity 75.9%; Pred. No. 8.4e-06;  
 Matches 22; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 3 AAUUAUACGACUCACUAGGGAGACUC 31

||:||||:||||:||||:||||:||||:|

Db 184 AATTATACGACTCACTATAGGAGACTC 156

Search completed: May 26, 2004, 22:44:18

Job time: 1906.62 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 26, 2004, 16:00:31 ; Search time 574.63 Seconds  
(without alignments)  
2036.547 Million cell updates/sec

Title: US-09-121-239-20

Perfect score: 27  
Sequence: 1 ACTGACCCCTGAGGCTCAAGTCAGA 27

Scoring table: OLIGO\_NUC  
Gapop\_60.0 , Gapext\_60.0

Searched: 3470272 seqs, 21671516995 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

GenEmbl.\*

- 1: gb\_ba.\*
- 2: gb\_htg.\*
- 3: gb\_in.\*
- 4: gb\_om.\*
- 5: gb\_ov.\*
- 6: gb\_pat.\*
- 7: gb\_ph.\*
- 8: gb\_pl.\*
- 9: gb\_pr.\*
- 10: gb\_ro.\*
- 11: gb\_ste.\*
- 12: gb\_sy.\*
- 13: gb\_un.\*
- 14: gb\_vi.\*
- 15: em\_ba.\*
- 16: em\_fun.\*
- 17: em\_hum.\*
- 18: em\_in.\*
- 19: em\_mu.\*
- 20: em\_om.\*
- 21: em\_or.\*
- 22: em\_ov.\*
- 23: em\_pat.\*
- 24: em\_ph.\*
- 25: em\_pl.\*
- 26: em\_ro.\*
- 27: em\_ste.\*
- 28: em\_un.\*
- 29: em\_vi.\*
- 30: em\_htg\_hum.\*
- 31: em\_htg\_inv.\*
- 32: em\_htg\_other.\*
- 33: em\_htg\_mus.\*
- 34: em\_htg\_pln.\*
- 35: em\_htg\_rod.\*
- 36: em\_htg\_mam.\*
- 37: em\_htg\_vrt.\*
- 38: em\_sy.\*
- 39: em\_htgo\_hum.\*
- 40: em\_htgo\_mus.\*
- 41: em\_htgo\_other.\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	27	100.0	27	6	BD222542	BD222542 Methods f
2	27	100.0	27	6	BD222543	BD222543 Methods f
3	27	100.0	27	6	BD222544	BD222544 Methods f
4	27	100.0	27	6	BD222545	BD222545 Methods f
5	27	100.0	54	6	BD222523	BD222523 Methods f
6	27	100.0	54	6	BD222524	BD222524 Methods f
7	27	100.0	54	6	BD222525	BD222525 Methods f
8	27	100.0	54	6	BD222526	BD222526 Methods f
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10	27	100.0	153	9	HUMABLB	M14754 Human abl m
11	27	100.0	204	9	HUMBCRA2	M25948 Human chron
12	27	100.0	205	6	I02402	I02402 Sequence 1
13	27	100.0	234	9	HUMCABLA1	M13098 Homo sapien
14	27	100.0	257	6	I58633	I58633 Sequence 1
15	27	100.0	257	6	I96199	I96199 Sequence 36
16	27	100.0	266	6	I58636	I58636 Sequence 4
17	27	100.0	266	6	I96200	I96200 Sequence 37
18	27	100.0	299	6	BD222547	BD222547 Methods f
19	27	100.0	350	6	BD222546	BD222546 Methods f
20	27	100.0	423	9	AB069693	AB069693 Homo sapi
21	27	100.0	468	9	HUMCMCABL	M25946 Human chron
22	27	100.0	468	9	HUMKS62A	M13096 Human chime
23	27	100.0	491	9	HUMALUBCR	M19730 Human acute
24	27	100.0	494	9	HUMABLC	M30833 Human abl p
25	27	100.0	532	9	HUMABLEA	M14753 Human abl m
26	27	100.0	549	9	HSBRREAP3	Z35761 Homo sapien
27	27	100.0	679	9	HUMABLB	M30832 Human bcr/a
28	27	100.0	854	9	HUMABLD	M30829 Human bcr/a
29	27	100.0	922	9	HSAL131467	AJ131467 Homo sapi
30	27	100.0	997	9	HSAL131466	AJ131466 Homo sapi
31	27	100.0	1078	6	A92081	A92081 Sequence 5
32	27	100.0	1079	6	AR230688	AR230688 Sequence 5
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34	27	100.0	3393	6	AX743957	AX743957 Sequence 35
35	27	100.0	3623	6	I96198	I96198 Sequence 35
36	27	100.0	3840	6	AX601393	AX601393 Sequence
37	27	100.0	3840	9	HUMABLA	M14752 Human c-abl
38	27	100.0	5527	6	AX411066	AX411066 Sequence
39	27	100.0	5527	9	HSABL	X16416 Human c-abl
40	27	100.0	5744	6	AX779943	AX779943 Sequence
41	27	100.0	84539	6	AX331986	AX331986 Sequence
42	27	100.0	84539	9	HSABLGR3	U07563 Human proto
43	27	100.0	176466	9	AL161733	AL161733 Human DNA
44	26	96.3	80	6	I58639	I58639 Sequence 7
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ALIGNMENTS

RESULT 1  
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LOCUS BD222542 27 bp DNA linear PAT 17-JUL-2003  
DEFINITION Methods for detecting and measuring spliced nucleic acids.  
ACCESSION BD222542  
VERSION BD222542.1 GI:33032312  
KEYWORDS JP 2002521037-A/20.  
SOURCE synthetic construct  
ORGANISM artificial sequences.  
REFERENCE 1 (bases 1 to 27)  
AUTHORS Harvey,R.C. and Eastman,P.S.  
TITLE Methods for detecting and measuring spliced nucleic acids  
JOURNAL Patent: JP 2002521037-A 20 16-JUL-2002;  
GEN PROBE INC

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COMMENT OS Artificial Sequence
PN JP 2002521037-A/20
PD 16-JUL-2002
PF 23-JUL-1999 JP 2000561364
PR 23-JUL-1998 US 09/121239
PI RICHARD C HARVEY, PAUL S EASTMAN
PC C12Q1/68, C12N15/09, C12N15/00
CC Description of Artificial Sequence: Primer sequence as in SEQ
CC ID NO:1 but
CC without T7 promoter sequence
FH Key Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 0.0001;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 ACTCAGACCCCTGAGGCTCAAAGTCAGA 27
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LOCUS
DEFINITION Methods for detecting and measuring spliced nucleic acids.
ACCESSION BD222543
VERSION JP 2002521037-A/21
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 27)
AUTHORS Harvey, R.C. and Eastman, P.S.
TITLE Methods for detecting and measuring spliced nucleic acids
JOURNAL Patent: JP 2002521037-A 21 16-JUL-2002;
GEN PROBE INC
COMMENT OS Artificial Sequence
PN JP 2002521037-A/21
PD 16-JUL-2002
PF 23-JUL-1999 JP 2000561364
PR 23-JUL-1998 US 09/121239
PI RICHARD C HARVEY, PAUL S EASTMAN
PC C12Q1/68, C12N15/09, C12N15/00
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DB 1 ACTCAGACCCCTGAGGCTCAAAGTCAGA 27
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LOCUS
DEFINITION Methods for detecting and measuring spliced nucleic acids.
ACCESSION BD222544
VERSION JP 2002521037-A/22
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 27)
AUTHORS Harvey, R.C. and Eastman, P.S.
TITLE Methods for detecting and measuring spliced nucleic acids
JOURNAL Patent: JP 2002521037-A 22 16-JUL-2002;
GEN PROBE INC
COMMENT OS Artificial Sequence
PN JP 2002521037-A/22
PD 16-JUL-2002
PF 23-JUL-1999 JP 2000561364
PR 23-JUL-1998 US 09/121239
PI RICHARD C HARVEY, PAUL S EASTMAN
PC C12Q1/68, C12N15/09, C12N15/00
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CC ID NO:20
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Best Local Similarity 100.0%; Pred. No. 0.0001;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 27 ACTCAGACCCCTGAGGCTCAAAGTCAGA 1
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RESULT 4
BD222545/c 27 bp RNA linear PAT 17-JUL-2003
LOCUS
DEFINITION Methods for detecting and measuring spliced nucleic acids.
ACCESSION BD222545
VERSION JP 2002521037-A/23
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 27)
AUTHORS Harvey, R.C. and Eastman, P.S.
TITLE Methods for detecting and measuring spliced nucleic acids
JOURNAL Patent: JP 2002521037-A 23 16-JUL-2002;
GEN PROBE INC
COMMENT OS Artificial Sequence
PN JP 2002521037-A/23
PD 16-JUL-2002
PF 23-JUL-1999 JP 2000561364
PR 23-JUL-1998 US 09/121239
PI RICHARD C HARVEY, PAUL S EASTMAN
PC C12Q1/68, C12N15/09, C12N15/00
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CC 22
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FT /organism='Artificial Sequence'.
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Best Local Similarity 100.0%; Pred. No. 0.0001;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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27 ACTCAGACCCCTGAGGCTCAAAAGTCAGA 1

RESULT 5
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LOCUS          54 bp      DNA      linear      PAT 17-JUL-2003
DEFINITION    Methods for detecting and measuring spliced nucleic acids.
ACCESSION     BD222523
VERSION       BD222523.1 GI:33032293
KEYWORDS      JP 2002521037-A/1.
SOURCE        synthetic construct
ORGANISM      artificial sequences.
REFERENCE     1 (bases 1 to 54)
AUTHORS       Harvey,R.C. and Eastman,P.S.
TITLE         Methods for detecting and measuring spliced nucleic acids
JOURNAL       Patent: JP 2002521037-A 1 16-JUL-2002;
GEN PROBE INC
COMMENT       OS Artificial Sequence
               PN JP 2002521037-A/1
               PD 16-JUL-2002
               PF 23-JUL-1999 JP 2000561364
               PR 23-JUL-1998 US 09/121239
               PI RICHARD C HARVEY, PAUL S EASTMAN
               PC C12Q1/68,C12N15/09,C12N15/00
               CC Description of Artificial Sequence: Synthetic promoter primer
               CC including T7
               CC promoter sequence at residues 1-27
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Query Match          100.0%; Score 27; DB 6; Length 54;
Best Local Similarity 100.0%; Pred. No. 8.8e-05;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 6
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LOCUS          54 bp      RNA      linear      PAT 17-JUL-2003
DEFINITION    Methods for detecting and measuring spliced nucleic acids.
ACCESSION     BD222524
VERSION       BD222524.1 GI:33032294
KEYWORDS      JP 2002521037-A/2.
SOURCE        synthetic construct
ORGANISM      artificial sequences.
REFERENCE     1 (bases 1 to 54)
AUTHORS       Harvey,R.C. and Eastman,P.S.
TITLE         Methods for detecting and measuring spliced nucleic acids
JOURNAL       Patent: JP 2002521037-A 2 16-JUL-2002;
GEN PROBE INC
COMMENT       OS Artificial Sequence
               PN JP 2002521037-A/2
               PD 16-JUL-2002
               PF 23-JUL-1999 JP 2000561364
               PR 23-JUL-1998 US 09/121239
               PI RICHARD C HARVEY, PAUL S EASTMAN
               PC C12Q1/68,C12N15/09,C12N15/00
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ORIGIN
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Best Local Similarity 100.0%; Pred. No. 8.8e-05;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACTCAGACCCCTGAGGCTCAAAAGTCAGA 27
    |||
28 ACTCAGACCCCTGAGGCTCAAAAGTCAGA 1

RESULT 7
BD222525/c
LOCUS          54 bp      DNA      linear      PAT 17-JUL-2003
DEFINITION    Methods for detecting and measuring spliced nucleic acids.
ACCESSION     BD222525
VERSION       BD222525.1 GI:33032295
KEYWORDS      JP 2002521037-A/3.
SOURCE        synthetic construct
ORGANISM      artificial sequences.
REFERENCE     1 (bases 1 to 54)
AUTHORS       Harvey,R.C. and Eastman,P.S.
TITLE         Methods for detecting and measuring spliced nucleic acids
JOURNAL       Patent: JP 2002521037-A 3 16-JUL-2002;
GEN PROBE INC
COMMENT       OS Artificial Sequence
               PN JP 2002521037-A/3
               PD 16-JUL-2002
               PF 23-JUL-1999 JP 2000561364
               PR 23-JUL-1998 US 09/121239
               PI RICHARD C HARVEY, PAUL S EASTMAN
               PC C12Q1/68,C12N15/09,C12N15/00
               CC Description of Artificial Sequence: Reverse complement of SEQ
               CC ID NO:1
               FH Key Location/Qualifiers
               FT source 1..54
               /organism='Artificial Sequence'.

FEATURES             source
    Location/Qualifiers
    1..54
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    /mol_type="genomic DNA"
    /db_xref="taxon:32630"

ORIGIN
Query Match          100.0%; Score 27; DB 6; Length 54;
Best Local Similarity 100.0%; Pred. No. 8.8e-05;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACTCAGACCCCTGAGGCTCAAAAGTCAGA 27
    |||
27 ACTCAGACCCCTGAGGCTCAAAAGTCAGA 1

RESULT 8
BD222526/c
LOCUS          54 bp      RNA      linear      PAT 17-JUL-2003
DEFINITION    Methods for detecting and measuring spliced nucleic acids.
ACCESSION     BD222526
VERSION       BD222526.1 GI:33032296
KEYWORDS      JP 2002521037-A/2.
SOURCE        synthetic construct
ORGANISM      artificial sequences.
REFERENCE     1 (bases 1 to 54)
AUTHORS       Harvey,R.C. and Eastman,P.S.
TITLE         Methods for detecting and measuring spliced nucleic acids
JOURNAL       Patent: JP 2002521037-A 2 16-JUL-2002;
GEN PROBE INC
COMMENT       OS Artificial Sequence
               PN JP 2002521037-A/2
               PD 16-JUL-2002
               PF 23-JUL-1999 JP 2000561364
               PR 23-JUL-1998 US 09/121239
               PI RICHARD C HARVEY, PAUL S EASTMAN
               PC C12Q1/68,C12N15/09,C12N15/00
               CC Description of Artificial Sequence: Reverse complement of SEQ
               CC ID NO:1
               FH Key Location/Qualifiers
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               /organism='Artificial Sequence'.

FEATURES             source
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    /db_xref="taxon:32630"

ORIGIN
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Best Local Similarity 100.0%; Pred. No. 8.8e-05;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACTCAGACCCCTGAGGCTCAAAAGTCAGA 27
    |||
27 ACTCAGACCCCTGAGGCTCAAAAGTCAGA 1

RESULT 9
BD222527/c
LOCUS          54 bp      DNA      linear      PAT 17-JUL-2003
DEFINITION    Methods for detecting and measuring spliced nucleic acids.
ACCESSION     BD222527
VERSION       BD222527.1 GI:33032297
KEYWORDS      JP 2002521037-A/3.
SOURCE        synthetic construct
ORGANISM      artificial sequences.
REFERENCE     1 (bases 1 to 54)
AUTHORS       Harvey,R.C. and Eastman,P.S.
TITLE         Methods for detecting and measuring spliced nucleic acids
JOURNAL       Patent: JP 2002521037-A 3 16-JUL-2002;
GEN PROBE INC
COMMENT       OS Artificial Sequence
               PN JP 2002521037-A/3
               PD 16-JUL-2002
               PF 23-JUL-1999 JP 2000561364
               PR 23-JUL-1998 US 09/121239
               PI RICHARD C HARVEY, PAUL S EASTMAN
               PC C12Q1/68,C12N15/09,C12N15/00
               CC Description of Artificial Sequence: Reverse complement of SEQ
               CC ID NO:1
               FH Key Location/Qualifiers
               FT source 1..54
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FEATURES             source
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    /mol_type="genomic DNA"
    /db_xref="taxon:32630"

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Best Local Similarity 100.0%; Pred. No. 8.8e-05;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACTCAGACCCCTGAGGCTCAAAAGTCAGA 27
    |||
27 ACTCAGACCCCTGAGGCTCAAAAGTCAGA 1

RESULT 10
BD222528/c
LOCUS          54 bp      RNA      linear      PAT 17-JUL-2003
DEFINITION    Methods for detecting and measuring spliced nucleic acids.
ACCESSION     BD222528
VERSION       BD222528.1 GI:33032298
KEYWORDS      JP 2002521037-A/2.
SOURCE        synthetic construct
ORGANISM      artificial sequences.
REFERENCE     1 (bases 1 to 54)
AUTHORS       Harvey,R.C. and Eastman,P.S.
TITLE         Methods for detecting and measuring spliced nucleic acids
JOURNAL       Patent: JP 2002521037-A 2 16-JUL-2002;
GEN PROBE INC
COMMENT       OS Artificial Sequence
               PN JP 2002521037-A/2
               PD 16-JUL-2002
               PF 23-JUL-1999 JP 2000561364
               PR 23-JUL-1998 US 09/121239
               PI RICHARD C HARVEY, PAUL S EASTMAN
               PC C12Q1/68,C12N15/09,C12N15/00
               CC Description of Artificial Sequence: Reverse complement of SEQ
               CC ID NO:1
               FH Key Location/Qualifiers
               FT source 1..54
               /organism='Artificial Sequence'.

FEATURES             source
    Location/Qualifiers
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    /db_xref="taxon:32630"

ORIGIN
Query Match          100.0%; Score 27; DB 6; Length 54;
Best Local Similarity 100.0%; Pred. No. 8.8e-05;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACTCAGACCCCTGAGGCTCAAAAGTCAGA 27
    |||
27 ACTCAGACCCCTGAGGCTCAAAAGTCAGA 1

RESULT 11
BD222529/c
LOCUS          54 bp      DNA      linear      PAT 17-JUL-2003
DEFINITION    Methods for detecting and measuring spliced nucleic acids.
ACCESSION     BD222529
VERSION       BD222529.1 GI:33032299
KEYWORDS      JP 2002521037-A/3.
SOURCE        synthetic construct
ORGANISM      artificial sequences.
REFERENCE     1 (bases 1 to 54)
AUTHORS       Harvey,R.C. and Eastman,P.S.
TITLE         Methods for detecting and measuring spliced nucleic acids
JOURNAL       Patent: JP 2002521037-A 3 16-JUL-2002;
GEN PROBE INC
COMMENT       OS Artificial Sequence
               PN JP 2002521037-A/3
               PD 16-JUL-2002
               PF 23-JUL-1999 JP 2000561364
               PR 23-JUL-1998 US 09/121239
               PI RICHARD C HARVEY, PAUL S EASTMAN
               PC C12Q1/68,C12N15/09,C12N15/00
               CC Description of Artificial Sequence: Reverse complement of SEQ
               CC ID NO:1
               FH Key Location/Qualifiers
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               /organism='Artificial Sequence'.

FEATURES             source
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    /db_xref="taxon:32630"

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Query Match          100.0%; Score 27; DB 6; Length 54;
Best Local Similarity 100.0%; Pred. No. 8.8e-05;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACTCAGACCCCTGAGGCTCAAAAGTCAGA 27
    |||
27 ACTCAGACCCCTGAGGCTCAAAAGTCAGA 1

RESULT 12
BD222530/c
LOCUS          54 bp      RNA     
```



SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.  
AUTHORS 1 (bases 1 to 204)  
De Klein, A., Hermans, A., Bootsma, D., Grosveld, G., Heisterkamp, N.,  
Stam, K., and Groffen, J.  
TITLE The role of the Philadelphia translocation in chronic myelocytic  
leukemia  
JOURNAL Ann. Clin. Res. 18 (5-6), 278-283 (1986)  
MEDLINE 87183193  
PUBMED 3471171  
COMMENT Original source text: Human fibroblast cell line K562, cDNA to  
mRNA, clone pV1-3.  
FEATURES  
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Location/Qualifiers  
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/db\_xref="taxon:9606"  
order(M25947.1:76..90,1..15)  
16..189  
intron About 500 bp downstream of segment 1.  
exon  
Query Match 100.0%; Score 27; DB 9; Length 204;  
Best Local Similarity 100.0%; Pred. No. 6.5e-05;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
ORIGIN  
Query Match 100.0%; Score 27; DB 9; Length 204;  
Best Local Similarity 100.0%; Pred. No. 6.3e-05;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ACTCAGACCTGAGGCTCAAGTCAGA 27  
|||||  
Db 65 ACTCAGACCTGAGGCTCAAGTCAGA 39  
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RESULT 12  
102402/c  
LOCUS Sequence 1 from Patent US 4874853. linear PAT 21-MAY-1993  
DEFINITION  
ACCESSION 102402  
VERSION 102402.1 GI:270541  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 205)  
AUTHORS Rossi, J.J.  
TITLE Synthetic oligonucleotides useful in diagnosis of chronic  
myelogenous leukemia  
JOURNAL Patent: US 4874853-A 1 17-OCT-1989;  
City of Hope; Duarte, CA  
FEATURES  
source  
1..205  
Location/Qualifiers  
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ORIGIN  
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Best Local Similarity 100.0%; Pred. No. 6.5e-05;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ACTCAGACCTGAGGCTCAAGTCAGA 27  
|||||  
Db 156 ACTCAGACCTGAGGCTCAAGTCAGA 130  
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RESULT 13  
HUMCABL1/c  
LOCUS HUMCABL1 234 bp DNA linear PRI 04-MAY-2000  
DEFINITION Homo sapiens c-abl (ABL1) gene, exon al.  
ACCESSION M13098  
VERSION M13098.1 GI:179747  
KEYWORDS  
SEGMENT 1 of 2  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 234)  
AUTHORS Grosveld, G., Verwoerd, T., van Aghoven, T., de Klein, A.,  
Ranachandran, K.L., Heisterkamp, N., Stam, K. and Groffen, J.  
TITLE The chronic myelocytic cell line K562 contains a breakpoint in bcr  
and produces a chimeric bcr/c-abl transcript  
JOURNAL Mol. Cell. Biol. 6 (2), 607-616 (1986)  
MEDLINE 87064346  
PUBMED 3023859  
FEATURES  
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1..234  
Location/Qualifiers  
/organism="Homo sapiens"  
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/note="c-abl"  
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intron  
ORIGIN  
Query Match 100.0%; Score 27; DB 9; Length 234;  
Best Local Similarity 100.0%; Pred. No. 6.3e-05;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ACTCAGACCTGAGGCTCAAGTCAGA 27  
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Db 80 ACTCAGACCTGAGGCTCAAGTCAGA 54  
|||||  
RESULT 14  
158633/c  
LOCUS Sequence 1 from patent US 5652222. linear PAT 07-OCT-1997  
DEFINITION  
ACCESSION 158633  
VERSION 158633.1 GI:2477871  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 257)  
AUTHORS Calabretta, B. and Gewirtz, A.M.  
TITLE Selective inhibition of leukemic cell proliferation by bcr-abl  
antisense oligonucleotides  
JOURNAL Patent: US 5652222-A 1 29-JUL-1997;  
Location/Qualifiers  
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Location/Qualifiers  
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Best Local Similarity 100.0%; Pred. No. 6.2e-05;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ACTCAGACCTGAGGCTCAAGTCAGA 27  
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Db 81 ACTCAGACCTGAGGCTCAAGTCAGA 55  
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RESULT 15  
196199/c  
LOCUS Sequence 36 from patent US 5734039. linear PAT 01-DEC-1998  
DEFINITION  
ACCESSION 196199  
VERSION 196199.1 GI:3940669  
KEYWORDS

SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 257)  
AUTHORS Calabretta, B. and Skorski, T.  
TITLE Antisense oligonucleotides targeting cooperating oncogenes  
JOURNAL Patent: US 5734039-A 36 31-MAR-1998;  
FEATURES Location/Qualifiers  
source  
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QY 1 ACTCAGACCCCTGAGGCTCAAAGTCAGA 27  
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Db 81 ACTCAGACCCCTGAGGCTCAAAGTCAGA 55  
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Job time : 575.63 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: May 26, 2004, 14:55:11 ; Search time 120.416 Seconds  
(without alignments)  
952.539 Million cell updates/sec

Title: US-09-121-239-20

Perfect score: 27

Sequence: 1 ACTGAGCCTGAGGCTCAAGTCA 27

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 3373863 seqs, 2124099041 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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1: Geneseqn1980s.\*  
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5: Geneseqn2001bs.\*  
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7: Geneseqn2003as.\*  
8: Geneseqn2003bs.\*  
9: Geneseqn2003cs.\*  
10: Geneseqn2004s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	27	100.0	27	3 AAZ60861	Aaz60861 Oligonuc
C 2	27	100.0	27	3 AAZ60862	Aaz60862 Oligonuc
C 3	27	100.0	27	3 AAZ60860	Aaz60860 Oligonuc
C 4	27	100.0	27	3 AAZ60859	Aaz60859 Oligonuc
C 5	27	100.0	54	3 AAZ60843	Aaz60843 Oligonuc
C 6	27	100.0	54	3 AAZ60841	Aaz60841 Oligonuc
C 7	27	100.0	54	3 AAZ60840	Aaz60840 Oligonuc
C 8	27	100.0	54	3 AAZ60842	Aaz60842 Oligonuc
C 9	27	100.0	205	1 AAN91666	Aan91666 bcr-abl f
C 10	27	100.0	257	2 AAQ34625	Aaq34625 Human bcr
C 11	27	100.0	257	2 AAV20458	Aav20458 Human bcr
C 12	27	100.0	266	2 AAQ34628	Aaq34628 Human bcr
C 13	27	100.0	266	2 AAV20459	Aav20459 Human bcr
C 14	27	100.0	299	3 AAZ60864	Aaz60864 Region su
C 15	27	100.0	350	3 AAZ60863	Aaz60863 Region su
C 16	27	100.0	423	6 ABS73179	Abs73179 DNA encod
C 17	27	100.0	468	6 ABS73171	Abs73171 Human tra
C 18	27	100.0	549	6 ABS73314	Abs73314 DNA encod
C 19	27	100.0	679	6 ABS73172	Abs73172 DNA encod
C 20	27	100.0	854	6 ABS73170	Abs73170 DNA encod
C 21	27	100.0	921	5 AAS85025	Aas85025 DNA encod
C 22	27	100.0	922	6 ABS73180	Abs73180 DNA encod
C 23	27	100.0	997	6 ABS73173	Abs73173 DNA encod

C 24	27	100.0	1024	7 ABZ82900	Abz82900 Toxicolog
C 25	27	100.0	1079	5 AAS85026	Aas85026 DNA encod
C 26	27	100.0	1079	6 ABS73181	Abs73181 DNA encod
C 27	27	100.0	1097	2 AAT91764	Aat91764 Chimeric
C 28	27	100.0	1212	5 AAS85028	Aas85028 DNA encod
C 29	27	100.0	3323	7 ABZ18519	Abz18519 Group III
C 30	27	100.0	3380	7 ABZ18520	Abz18520 Group III
C 31	27	100.0	3393	7 ABX95815	Abx95815 CDNA enco
C 32	27	100.0	3623	2 AAV20457	Aav20457 Human c-a
C 33	27	100.0	3780	2 AAT61864	Aat61864 c-abl gen
C 34	27	100.0	3840	7 AAD52781	Aad52781 Human Abl
C 35	27	100.0	5434	6 ABV77964	Abv77964 Hypoxia-r
C 36	27	100.0	5520	2 AAT61865	Aat61865 c-abl gen
C 37	27	100.0	5527	6 ABN97215	Abn97215 Gene #371
C 38	27	100.0	84539	6 ABL64158	Abi64158 Stomach c
C 39	26	96.3	80	2 AAQ34631	Aaq34631 Human bcr
C 40	26	96.3	80	2 AAV20460	Aav20460 Human bcr
C 41	25	92.6	200	2 AAT88785	Aat88785 Leukemic
C 42	24	88.9	50	2 AAQ86626	Aaq86626 CML chrom
C 43	24	88.9	50	2 AAT15571	Aat15571 CML-2 chr
C 44	24	88.9	50	2 AAT42417	Aat42417 CML chrom
C 45	24	88.9	50	2 AAV66349	Aav66349 CML-2 chr

## ALIGNMENTS

RESULT 1  
AAZ60861/c  
ID AAZ60861 standard; DNA; 27 BP.  
XX  
AC AAZ60861;  
XX  
DT 16-MAY-2000 (first entry)  
XX  
DE Oligonucleotide used to detect bcr b3-abl fusion transcripts.  
XX  
KW Fusion transcript; translocation; bcr b3 region; abl gene;  
KW amplification assay; detection assay; medical diagnosis;  
KW clinical monitoring; chimeric RNA; fusion RNA; condition marker;  
KW disease marker; cancer; leukemia; ss.  
XX  
OS Synthetic.  
XX  
FN WO200005419-A1.  
XX  
PD 03-FEB-2000.  
XX  
PF 23-JUL-1999; 99WO-US016832.  
XX  
PR 23-JUL-1998; 98US-00121239.  
XX  
PA (GENP-) GEN-PROBE INC.  
XX  
PI Harvey RC, Eastman PS;  
XX  
DR WPI; 2000-182730/16.  
XX  
PT Novel methods for preparing RNA from biological samples, used for the  
PT detection and measurement of nucleic acids and fusion nucleic acids.  
XX  
PS Claim 19; Page 43; 49pp; English.  
XX  
CC Oligonucleotides AAZ60840-62 and AAZ60865-66 are used in the method of  
CC the invention to detect fusion transcripts produced from a translocation  
CC between the bcr b3 region and the abl gene. The specification describes a  
CC method for detecting a fusion nucleic acid (particularly chimeric mRNA  
CC species), in a biological sample. The method comprises contacting a  
CC sample of fusion nucleic acid with primers, amplifying the hybridized  
CC fusion nucleic acid, and detecting the target hybrid. The method is used  
CC for the simple and rapid preparation of RNA from a biological sample,  
CC particularly from the cytoplasm of eukaryotic cells, which is suitable  
CC for use in an amplification and detection assay. The methods are used for

CC the analysis and detection of nucleic acids in biological samples. The  
 CC methods are useful in the human medical and veterinary fields, for  
 CC medical diagnoses and clinical monitoring of a patient's response to  
 CC therapy where a disease or medical condition is associated with a  
 CC particular type and/or level of mRNA present in the sample. The methods  
 CC are also useful for detecting or quantifying fusion or chimeric RNA  
 CC species, and for detecting a translocation as a marker for a given  
 CC condition or disease, e.g. translocations associate with cancers,  
 CC particularly forms of leukemia  
 XX  
 SQ Sequence 27 BP; 4 A; 6 C; 8 G; 9 T; 0 U; 0 Other;

Query Match 100.0%; Score 27; DB 3; Length 27;  
 Best Local Similarity 100.0%; Pred. No. 3.9e-05;  
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACTCAGACCTGAGGCTCAAAGTCAGA 27  
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 Db 27 ACTCAGACCTGAGGCTCAAAGTCAGA 1

RESULT 2  
 AAZ60862/c  
 ID AAZ60862 standard; RNA; 27 BP.  
 XX  
 AC AAZ60862;  
 XX  
 DT 16-MAY-2000 (first entry)  
 DE  
 DE Oligonucleotide used to detect bcr b3-abl fusion transcripts.  
 XX  
 XX Fusion transcript; translocation; bcr b3 region; abl gene;  
 KW amplification assay; detection assay; medical diagnosis;  
 KW clinical monitoring; chimeric RNA; fusion RNA; condition marker;  
 KW disease marker; cancer; leukemia; ss.  
 XX  
 OS Synthetic.

XX  
 XX WO200005418-A1.  
 XX  
 PD 03-FEB-2000.  
 XX  
 PF 23-JUL-1999; 99WO-US016832.  
 XX  
 PR 23-JUL-1998; 98US-00121239.  
 XX  
 PA (GENP-) GEN-PROBE INC.  
 XX  
 PI Harvey RC, Eastman PS;  
 XX  
 DR WPI; 2000-182730/16.  
 XX  
 PT Novel methods for preparing RNA from biological samples, used for the  
 PT detection and measurement of nucleic acids and fusion nucleic acids.  
 XX  
 PS Claim 19; Page 44; 49pp; English.

XX  
 CC Oligonucleotides AAZ60840-62 and AAZ60865-66 are used in the method of  
 CC the invention to detect fusion transcripts produced from a translocation  
 CC between the bcr b3 region and the abl gene. The specification describes a  
 CC method for detecting a fusion nucleic acid (particularly chimeric mRNA  
 CC species), in a biological sample. The method comprises contacting a  
 CC sample of fusion nucleic acid with primers, amplifying the hybridized  
 CC fusion nucleic acid, and detecting the target hybrid. The method is used  
 CC for the simple and rapid preparation of RNA from a biological sample,  
 CC particularly from the cytoplasm of eukaryotic cells, which is suitable  
 CC for use in an amplification and detection assay. The methods are used for  
 CC the analysis and detection of nucleic acids in biological samples. The  
 CC methods are useful in the human medical and veterinary fields, for  
 CC medical diagnoses and clinical monitoring of a patient's response to  
 CC therapy where a disease or medical condition is associated with a  
 CC particular type and/or level of mRNA present in the sample. The methods  
 CC are also useful for detecting or quantifying fusion or chimeric RNA  
 CC species, and for detecting a translocation as a marker for a given  
 CC condition or disease, e.g. translocations associate with cancers,  
 CC particularly forms of leukemia

CC species, and for detecting a translocation as a marker for a given  
 CC condition or disease, e.g. translocations associate with cancers,  
 CC particularly forms of leukemia  
 XX  
 SQ Sequence 27 BP; 4 A; 6 C; 8 G; 0 T; 9 U; 0 Other;

Query Match 100.0%; Score 27; DB 3; Length 27;  
 Best Local Similarity 100.0%; Pred. No. 3.9e-05;  
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACTCAGACCTGAGGCTCAAAGTCAGA 27  
 |||||  
 Db 27 ACTCAGACCTGAGGCTCAAAGTCAGA 1

RESULT 3  
 AAZ60860  
 ID AAZ60860 standard; RNA; 27 BP.  
 XX  
 AC AAZ60860;  
 XX  
 DT 16-MAY-2000 (first entry)  
 DE  
 DE Oligonucleotide used to detect bcr b3-abl fusion transcripts.  
 XX  
 XX Fusion transcript; translocation; bcr b3 region; abl gene;  
 KW amplification assay; detection assay; medical diagnosis;  
 KW clinical monitoring; chimeric RNA; fusion RNA; condition marker;  
 KW disease marker; cancer; leukemia; ss.  
 XX  
 OS Synthetic.

XX  
 XX WO200005418-A1.  
 XX  
 PD 03-FEB-2000.  
 XX  
 PF 23-JUL-1999; 99WO-US016832.  
 XX  
 PR 23-JUL-1998; 98US-00121239.  
 XX  
 PA (GENP-) GEN-PROBE INC.

XX  
 PI Harvey RC, Eastman PS;  
 XX  
 DR WPI; 2000-182730/16.

XX  
 PT Novel methods for preparing RNA from biological samples, used for the  
 PT detection and measurement of nucleic acids and fusion nucleic acids.  
 XX  
 PS Claim 19; Page 43; 49pp; English.

XX  
 CC Oligonucleotides AAZ60840-62 and AAZ60865-66 are used in the method of  
 CC the invention to detect fusion transcripts produced from a translocation  
 CC between the bcr b3 region and the abl gene. The specification describes a  
 CC method for detecting a fusion nucleic acid (particularly chimeric mRNA  
 CC species), in a biological sample. The method comprises contacting a  
 CC sample of fusion nucleic acid with primers, amplifying the hybridized  
 CC fusion nucleic acid, and detecting the target hybrid. The method is used  
 CC for the simple and rapid preparation of RNA from a biological sample,  
 CC particularly from the cytoplasm of eukaryotic cells, which is suitable  
 CC for use in an amplification and detection assay. The methods are used for  
 CC the analysis and detection of nucleic acids in biological samples. The  
 CC methods are useful in the human medical and veterinary fields, for  
 CC medical diagnoses and clinical monitoring of a patient's response to  
 CC therapy where a disease or medical condition is associated with a  
 CC particular type and/or level of mRNA present in the sample. The methods  
 CC are also useful for detecting or quantifying fusion or chimeric RNA  
 CC species, and for detecting a translocation as a marker for a given  
 CC condition or disease, e.g. translocations associate with cancers,  
 CC particularly forms of leukemia

XX  
 SQ Sequence 27 BP; 9 A; 8 C; 6 G; 0 T; 4 U; 0 Other;

Query Match 100.0%; Score 27; DB 3; Length 27;  
 Best Local Similarity 85.2%; Pred. No. 3.9e-05;  
 Matches 23; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACTCAGACCTGAGGCTCAAGTCAGA 27  
 ||:|||||:||||:||||:||||:||||  
 DB 1 ACUCAGACCCUGAGGCUCAAGUCAGA 27

RESULT 4  
 ID AAZ60859 standard; DNA; 27 BP.  
 XX AAZ60859;  
 AC AAZ60859;  
 XX 16-MAY-2000 (first entry)  
 DT 16-MAY-2000 (first entry)  
 XX Oligonucleotide used to detect bcr b3-abl fusion transcripts.  
 DE Fusion transcript; translocation; bcr b3 region; abl gene;  
 XX amplification assay; detection assay; medical diagnosis;  
 KW clinical monitoring; chimeric RNA; fusion RNA; condition marker;  
 KW disease marker; cancer; leukemia; ss.  
 XX Synthetic.  
 OS WO200005418-A1.  
 XX WO200005418-A1.  
 PN 03-FEB-2000.  
 PD 23-JUL-1999; 99WO-US016832.  
 PF 23-JUL-1998; 98US-00121239.  
 PR (GENP-) GEN-PROBE INC.  
 PA Harvey RC, Eastman PS;  
 PI WPI; 2000-182730/16.  
 DR Novel methods for preparing RNA from biological samples, used for the  
 PT detection and measurement of nucleic acids and fusion nucleic acids.  
 PT Claim 19; Page 43; 49pp; English.  
 PS Oligonucleotides AAZ60840-62 and AAZ60865-66 are used in the method of  
 CC the invention to detect fusion transcripts produced from a translocation  
 CC between the bcr b3 region and the abl gene. The specification describes a  
 CC method for detecting a fusion nucleic acid (particularly chimeric mRNA  
 CC sample of fusion nucleic acid with primers, amplifying the hybridized  
 CC fusion nucleic acid, and detecting the target hybrid. The method is used  
 CC for the simple and rapid preparation of RNA from a biological sample,  
 CC particularly from the cytoplasm of eukaryotic cells, which is suitable  
 CC for use in an amplification and detection assay. The methods are used for  
 CC the analysis and detection of nucleic acids in biological samples. The  
 CC methods are useful in the human medical and veterinary fields, for  
 CC medical diagnoses and clinical monitoring of a patient's response to  
 CC therapy where a disease or medical condition is associated with a  
 CC particular type and/or level of mRNA present in the sample. The methods  
 CC are also useful for detecting or quantifying fusion or chimeric RNA  
 CC species, and for detecting a translocation as a marker for a given  
 CC condition or disease, e.g. translocations associate with cancers,  
 CC particularly forms of leukemia

QY Sequence 27 BP; 9 A; 8 C; 6 G; 4 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 27; DB 3; Length 27;  
 Best Local Similarity 100.0%; Pred. No. 3.9e-05;  
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACTCAGACCTGAGGCTCAAGTCAGA 27  
 |||||||||||||||||||||||||||||

DB 1 ACTCAGACCTGAGGCTCAAGTCAGA 27

RESULT 5  
 ID AAZ60843/c standard; RNA; 54 BP.  
 XX AAZ60843;  
 AC AAZ60843;  
 XX 16-MAY-2000 (first entry)  
 DT Oligonucleotide used to detect bcr b3-abl fusion transcripts.  
 DE Fusion transcript; translocation; bcr b3 region; abl gene;  
 XX amplification assay; detection assay; medical diagnosis;  
 KW clinical monitoring; chimeric RNA; fusion RNA; condition marker;  
 KW disease marker; cancer; leukemia; ss.  
 XX Synthetic.  
 OS WO200005418-A1.  
 XX WO200005418-A1.  
 PN 03-FEB-2000.  
 PD 23-JUL-1999; 99WO-US016832.  
 PF 23-JUL-1998; 98US-00121239.  
 PR (GENP-) GEN-PROBE INC.  
 PA Harvey RC, Eastman PS;  
 PI WPI; 2000-182730/16.  
 DR Novel methods for preparing RNA from biological samples, used for the  
 PT detection and measurement of nucleic acids and fusion nucleic acids.  
 PT Claim 19; Page 40; 49pp; English.  
 PS Oligonucleotides AAZ60840-62 and AAZ60865-66 are used in the method of  
 CC the invention to detect fusion transcripts produced from a translocation  
 CC between the bcr b3 region and the abl gene. The specification describes a  
 CC method for detecting a fusion nucleic acid (particularly chimeric mRNA  
 CC sample of fusion nucleic acid with primers, amplifying the hybridized  
 CC fusion nucleic acid, and detecting the target hybrid. The method is used  
 CC for the simple and rapid preparation of RNA from a biological sample,  
 CC particularly from the cytoplasm of eukaryotic cells, which is suitable  
 CC for use in an amplification and detection assay. The methods are used for  
 CC the analysis and detection of nucleic acids in biological samples. The  
 CC methods are useful in the human medical and veterinary fields, for  
 CC medical diagnoses and clinical monitoring of a patient's response to  
 CC therapy where a disease or medical condition is associated with a  
 CC particular type and/or level of mRNA present in the sample. The methods  
 CC are also useful for detecting or quantifying fusion or chimeric RNA  
 CC species, and for detecting a translocation as a marker for a given  
 CC condition or disease, e.g. translocations associate with cancers,  
 CC particularly forms of leukemia

QY Sequence 54 BP; 11 A; 11 C; 12 G; 0 T; 20 U; 0 Other;  
 Query Match 100.0%; Score 27; DB 3; Length 54;  
 Best Local Similarity 100.0%; Pred. No. 3.8e-05;  
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACTCAGACCTGAGGCTCAAGTCAGA 27  
 |||||||||||||||||||||||||||||  
 DB 27 ACTCAGACCTGAGGCTCAAGTCAGA 1

RESULT 6  
 ID AAZ60841 standard; RNA; 54 BP.





```
OS Synthetic.
PN WO200005418-A1.
XX
XX
PD 03-FEB-2000.
XX
XX 23-JUL-1999; 99WO-US016832.
PF
XX 23-JUL-1998; 98US-00121239.
PR
XX (GENP-) GEN-PROBE INC.
PA
XX Harvey RC, Eastman PS;
PI
XX WPI; 2000-182730/16.
DR
XX
XX Novel methods for preparing RNA from biological samples, used for the
PT detection and measurement of nucleic acids and fusion nucleic acids.
XX
XX Claim 19; Page 40; 49pp; English.
PS
XX Oligonucleotides AAZ60840-62 and AAZ60865-66 are used in the method of
CC the invention to detect fusion transcripts produced from a translocation
CC between the bcr b3 region and the abl gene. The specification describes a
CC method for detecting a fusion nucleic acid (particularly chimeric mRNA
CC species), in a biological sample. The method comprises contacting a
CC sample of fusion nucleic acid with primers, amplifying the hybridized
CC fusion nucleic acid, and detecting the target hybrid. The method is used
CC for the simple and rapid preparation of RNA from a biological sample,
CC particularly from the cytoplasm of eukaryotic cells, which is suitable
CC for use in an amplification and detection assay. The methods are used for
CC the analysis and detection of nucleic acids in biological samples. The
CC methods are useful in the human medical and veterinary fields, for
CC medical diagnoses and clinical monitoring of a patient's response to
CC therapy where a disease or medical condition is associated with a
CC particular type and/or level of mRNA present in the sample. The methods
CC are also useful for detecting or quantifying fusion or chimeric RNA
CC species, and for detecting a translocation as a marker for a given
CC condition or disease, e.g. translocations associate with cancers,
CC particularly forms of leukemia
XX
SQ Sequence 54 BP; 11 A; 11 C; 12 G; 20 T; 0 U; 0 Other;

Query Match 100.0%; Score 27; DB 3; Length 54;
Best Local Similarity 100.0%; Pred. NO. 3.8e-05;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACTCAGACCCCTGAGGCTCAAGTCAGA 27
Db 27 ACTCAGACCCCTGAGGCTCAAGTCAGA 1

RESULT 9
AA91666/c
ID AA91666 standard; DNA; 205 BP.
XX
XX AA91666;
AC
XX 14-MAR-1990 (first entry)
DT
XX Bcr-abl fusion message for leukaemia.
DE
XX Reciprocal translocation.
KW
XX Homo sapiens.
OS
XX Key Location/Qualifiers
FH exon 1..31
FT /tag= a
FT /note= "bcr exon 2"
FT exon 32..106
FT /tag= b
FT /note= "bcr exon 3"
FT
```

```
FT exon 106..205
FT /tag= b
FT /note= "abl exon 2"
XX
XX EP338713-A.
PN
XX 25-OCT-1989.
PD
XX 11-APR-1989; 89EP-00303538.
PF
XX 18-APR-1988; 88US-00182434.
PR
XX (CITY ) CITY OF HOPE.
PA
XX Rossi JJ;
PI
XX WPI; 1989-311152/43.
DR
XX New synthetic oligonucleotide probes - used for detection of BCR-ABL RNA
PT from blood or bone marrow or chronic myelogenous leukaemia patients.
XX
XX Disclosure; Page 3; 4pp; English.
PS
XX Part of 8 kb RNA transcript, showing the fusion of abl and bcr. The abl
CC gene is from human chromosome 9, and this is spliced to a region on
CC chromosome 22 called the breakpoint cluster region (bcr). CML has
CC reciprocal translocation of human chromosomes 9 and 22
XX
SQ Sequence 205 BP; 50 A; 55 C; 52 G; 48 T; 0 U; 0 Other;

Query Match 100.0%; Score 27; DB 1; Length 205;
Best Local Similarity 100.0%; Pred. NO. 3.8e-05;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACTCAGACCCCTGAGGCTCAAGTCAGA 27
Db 156 ACTCAGACCCCTGAGGCTCAAGTCAGA 130

RESULT 10
AAQ34625/c
ID AAQ34625 standard; cDNA; 257 BP.
XX
XX AAQ34625;
AC
XX 25-MAR-2003 (revised)
DT
XX 10-MAY-1993 (first entry)
DT
XX Human bcr-abl junction.
DE
XX Leukaemia; treatment; blast crisis; specific; CML; translocation;
KW Philadelphia chromosome; chronic myeloid; chronic myelogenous; leukemia;
XX ss.
XX Homo sapiens.
OS
XX Key Location/Qualifiers
FH misc_feature 23..40
FT /tag= b
FT /note= "breakpoint junction target sequence"
FT misc_feature 31..32
FT /tag= a
FT /note= "bcr-abl breakpoint"
XX
XX WO9222303-A1.
PN
XX 23-DEC-1992.
PD
XX 15-JUN-1992; 92WO-US005035.
PF
XX 18-JUN-1991; 91US-00718302.
PR
XX 14-APR-1992; 92US-00869911.
XX
```

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PA (UTEM ) UNIV TEMPLE.
XX
XX Calabretta B, Gewirtz AM;
XX
XX WPI; 1993-017893/02.
DR
XX Treating Ph1-positive leukaemia(s) using bcr-abl anti-sense oligo-
PT nucleotide(s) - to selectively inhibit leukaemic cell proliferation
PT without adversely affecting normal haematopoiesis.
XX
XX Disclosure; Fig 1; 74pp; English.
XX
XX This is the sequence around the bcr-abl junction derived from a group of
CC five chronic myeloid leukaemia (CML) patients in blast crisis. It is the
CC L-6 type junction, formed by fusion of bcr exon 2 to c-abl exon 2.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 257 BP; 72 A; 62 C; 64 G; 59 T; 0 U; 0 Other;
SQ
    Query Match      100.0%; Score 27; DB 2; Length 257;
    Best Local Similarity 100.0%; Pred. No. 3.8e-05;
    Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACTCAGACCTGAGGCTCAAAAGTCAGA 27
    |||||||||||||||||||||||||||
Db 81 ACTCAGACCTGAGGCTCAAAAGTCAGA 55

RESULT 11
AAV20458/c
ID AAV20458 standard; DNA; 257 BP.
XX
XX AAV20458;
AC
XX 17-JUN-1998 (first entry)
DT
XX Human bcr-abl oncogene b2a2 genotype.
DE
XX Human; oncogene; proto-oncogene; neoplastic disease; anticancer; cancer;
KW antisense oligonucleotide; bcr-abl; ds.
XX
XX Homo sapiens.
OS
XX
XX US5734039-A.
PN
XX
XX 31-MAR-1998.
PD
XX
XX 15-SEP-1994; 94US-00306691.
PF
XX
XX 15-SEP-1994; 94US-00306691.
PR
XX
XX (UYJE-) UNIV JEFFERSON THOMAS.
PA
XX Calabretta B, Skorski T;
PI
XX
XX WPI; 1998-229882/20.
DR
XX
XX Anticancer composition comprising two anti-sense oligo:nucleotide(s) -
PT targeting cytoplasmic and nuclear oncogene(s).
PT
XX
XX Claim 1; Col 109-110; 92pp; English.
PS
XX
XX The present sequence represents an oncogene from the present invention.
CC The present invention describes a composition which comprises two
CC antisense oligonucleotides. The first oligonucleotide is specific for a
CC cytoplasmic oncogene or proto-oncogene selected from ras, raf, EGF-1, c-
CC fms, c-ros, c-kit, c-met, c-trk, c-src, c-abl, bcr-abl, c-fgr and c-yes.
CC The second oligonucleotide is specific for a nuclear oncogene or proto-
CC oncogene selected from myc, jun, c-ets, c-fos, c-myb, B-myb, c-rel, c-
CC vav, c-ski, c-spi, cyclin D1, PML/RAR alpha, AML1/MTG8, E2A/p12 and ALL-
CC 1/AF-4. The composition is used for treating cancer. The combination of
CC antisense oligonucleotides has synergistically enhanced ability to
CC inhibit growth of cancer cells

PA (UTEM ) UNIV TEMPLE.
XX
XX Sequence 257 BP; 72 A; 62 C; 64 G; 59 T; 0 U; 0 Other;
SQ
    Query Match      100.0%; Score 27; DB 2; Length 257;
    Best Local Similarity 100.0%; Pred. No. 3.8e-05;
    Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACTCAGACCTGAGGCTCAAAAGTCAGA 27
    |||||||||||||||||||||||||||
Db 81 ACTCAGACCTGAGGCTCAAAAGTCAGA 55

RESULT 12
AAQ34628/c
ID AAQ34628 standard; cDNA; 266 BP.
XX
XX AAQ34628;
AC
XX 25-MAR-2003 (revised)
DT
XX 10-MAY-1993 (first entry)
DT
XX Human bcr-abl junction.
DE
XX
XX Leukaemia; treatment; blast crisis; specific; CML; translocation;
KW Philadelphia chromosome; chronic myeloid; chronic myelogenous; leukemia;
KW ss.
XX
XX Synthetic.
OS
XX
XX Key
FH misc_feature 31..49 Location/Qualifiers
FT misc_feature /tag= b
FT /notes= "breakpoint junction target sequence"
FT misc_feature 40..41
FT /tag= a
FT /notes= "bcr-abl breakpoint"
FT
XX
XX WO9222303-A1.
PN
XX
XX 23-DEC-1992.
PD
XX
XX 15-JUN-1992; 92WO-US005035.
PF
XX
XX 18-JUN-1991; 91US-00718302.
PR
XX 14-APR-1992; 92US-00869911.
XX
XX (UTEM ) UNIV TEMPLE.
PA
XX Calabretta B, Gewirtz AM;
PI
XX
XX WPI; 1993-017893/02.
DR
XX
XX Treating Ph1-positive leukaemia(s) using bcr-abl anti-sense oligo-
PT nucleotide(s) - to selectively inhibit leukaemic cell proliferation
PT without adversely affecting normal haematopoiesis.
XX
XX Disclosure; Page 50; 74pp; English.
XX
XX This is the sequence around the bcr-abl junction derived from two chronic
CC myeloid leukaemia (CML) patients in blast crisis. It is the K-28 type
CC junction, formed by fusion of bcr exon 3 to c-abl exon 2. (Updated on 25-
CC MAR-2003 to correct PN field.)
XX
XX Sequence 266 BP; 72 A; 64 C; 66 G; 64 T; 0 U; 0 Other;
SQ
    Query Match      100.0%; Score 27; DB 2; Length 266;
    Best Local Similarity 100.0%; Pred. No. 3.8e-05;
    Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACTCAGACCTGAGGCTCAAAAGTCAGA 27
    |||||||||||||||||||||||||||
Db 90 ACTCAGACCTGAGGCTCAAAAGTCAGA 64

```

OS	Unidentified.
XX	
PN	WO200005418-A1.
XX	
PD	03-FEB-2000.
XX	
PF	23-JUL-1999; 99WO-US016832.
XX	
PR	23-JUL-1998; 98US-00121239.
XX	
PA	(GENP-) GEN-PROBE INC.
XX	
PI	Harvey RC, Eastman PS;
XX	
DR	WPI; 2000-182730/16.
XX	
PT	Novel methods for preparing RNA from biological samples, used for the detection and measurement of nucleic acids and fusion nucleic acids.
XX	
PS	Disclosure; Fig 3; 49pp; English.
XX	
CC	The present sequence represents a region surrounding a potential splice junction in a normal abl transcript. The specification describes oligonucleotides which are used to detect fusion transcripts produced from a translocation between the bcr b3 region and the abl gene. The CC specification also describes a method for detecting a fusion nucleic acid (particularly chimeric mRNA species), in a biological sample. The method comprises contacting a sample of fusion nucleic acid with primers, amplifying the hybridized fusion nucleic acid, and detecting the target hybrid. The method is used for the simple and rapid preparation of RNA from a biological sample, particularly from the cytoplasm of eukaryotic cells, which is suitable for use in an amplification and detection assay. The methods are used for the analysis and detection of nucleic acids in biological samples. The methods are useful in the human medical and veterinary fields, for medical diagnoses and clinical monitoring of a patient's response to therapy where a disease or medical condition is associated with a particular type and/or level of mRNA present in the sample. The methods are also useful for detecting or quantifying fusion or chimeric RNA species, and for detecting a translocation as a marker for a given condition or disease, e.g. translocations associate with cancers, particularly forms of leukemia
XX	
SQ	Sequence 299 BP; 77 A; 70 C; 81 G; 71 T; 0 U; 0 Other;
	Query Match 100.0%; Score 27; DB 3; Length 299;
	Best Local Similarity 100.0%; Pred. No. 3.8e-05;
	Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY	1 ACTCAGACCTGAGGCTCAAAAGTCAGA 27 
Dd	201 ACTCAGACCTGAGGCTCAAAAGTCAGA 175 
	RESULT 15
ID	AZ60863/c
XX	AZ60863 standard; DNA; 350 BP.
XX	
AC	AZ60863;
XX	
DT	16-MAY-2000 (first entry)
XX	
DE	Region surrounding a bcr-abl splice junction.
XX	
KW	Fusion transcript; translocation; bcr b3 region; abl gene;
KW	amplification assay; detection assay; medical diagnosis;
KW	clinical monitoring; chimeric RNA; fusion RNA; condition marker;
XX	disease marker; cancer; leukemia; ss.
OS	Unidentified.
XX	
PN	WO200005418-A1.
XX	
PD	03-FEB-2000.
XX	
OS	Unidentified.
XX	
PN	WO200005418-A1.
XX	
PD	03-FEB-2000.
XX	
PF	23-JUL-1999; 99WO-US016832.
XX	
PR	23-JUL-1998; 98US-00121239.
XX	
PA	(GENP-) GEN-PROBE INC.
XX	
PI	Harvey RC, Eastman PS;
XX	
DR	WPI; 2000-182730/16.
XX	
PT	Novel methods for preparing RNA from biological samples, used for the detection and measurement of nucleic acids and fusion nucleic acids.
XX	
PS	Disclosure; Fig 3; 49pp; English.
XX	
CC	The present sequence represents a composition which comprises two antisense oligonucleotides. The first oligonucleotide is specific for a cytoplasmic oncogene or proto-oncogene selected from ras, raf, EGF-1, c-fms, c-ros, c-kit, c-met, c-trk, c-src, c-abl, bcr-abl, c-fgr and c-vyes. The second oligonucleotide is specific for a nuclear oncogene or proto-oncogene selected from myc, jun, cets, c-fos, c-myb, B-myb, c-rel, c-vav, c-ski, c-spi, cyclin D1, PML/RAR alpha, AML1/MTG8, E2A/pri and ALL-1/AP-4. The composition is used for treating cancer. The combination of antisense oligonucleotides has synergistically enhanced ability to inhibit growth of cancer cells
XX	
SQ	Sequence 266 BP; 72 A; 64 C; 66 G; 64 T; 0 U; 0 Other;
	Query Match 100.0%; Score 27; DB 2; Length 266;
	Best Local Similarity 100.0%; Pred. No. 3.8e-05;
	Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY	1 ACTCAGACCTGAGGCTCAAAAGTCAGA 27 
Dd	90 ACTCAGACCTGAGGCTCAAAAGTCAGA 64 
	RESULT 14
ID	AZ60864/c
XX	AZ60864 standard; DNA; 299 BP.
XX	
AC	AZ60864;
XX	
DT	16-MAY-2000 (first entry)
XX	
DE	Region surrounding a splice junction in a normal abl transcript.
XX	
KW	Fusion transcript; translocation; bcr b3 region; abl gene;
KW	amplification assay; detection assay; medical diagnosis;
KW	clinical monitoring; chimeric RNA; fusion RNA; condition marker;
XX	disease marker; cancer; leukemia; ss.
OS	Unidentified.
XX	
PN	WO200005418-A1.
XX	
PD	03-FEB-2000.
XX	
PF	23-JUL-1999; 99WO-US016832.
XX	
PR	23-JUL-1998; 98US-00121239.
XX	
PA	(UYJE-) UNIV JEFFERSON THOMAS.
XX	
PI	Calabretta B, Skorski T;
XX	
DR	WPI; 1998-229882/20.
XX	
PT	Anticancer composition comprising two anti-sense oligo:nucleotide(s) - targeting cytoplasmic and nuclear oncogene(s).
XX	
PS	Claim 1; Col 109-110; 92pp; English.
XX	
CC	The present sequence represents an oncogene from the present invention. The present invention describes a composition which comprises two antisense oligonucleotides. The first oligonucleotide is specific for a cytoplasmic oncogene or proto-oncogene selected from ras, raf, EGF-1, c-fms, c-ros, c-kit, c-met, c-trk, c-src, c-abl, bcr-abl, c-fgr and c-vyes. The second oligonucleotide is specific for a nuclear oncogene or proto-oncogene selected from myc, jun, cets, c-fos, c-myb, B-myb, c-rel, c-vav, c-ski, c-spi, cyclin D1, PML/RAR alpha, AML1/MTG8, E2A/pri and ALL-1/AP-4. The composition is used for treating cancer. The combination of antisense oligonucleotides has synergistically enhanced ability to inhibit growth of cancer cells
XX	
SQ	Sequence 266 BP; 72 A; 64 C; 66 G; 64 T; 0 U; 0 Other;
	Query Match 100.0%; Score 27; DB 2; Length 266;
	Best Local Similarity 100.0%; Pred. No. 3.8e-05;
	Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY	1 ACTCAGACCTGAGGCTCAAAAGTCAGA 27 
Dd	90 ACTCAGACCTGAGGCTCAAAAGTCAGA 64 
	RESULT 14
ID	AZ60864/c
XX	AZ60864 standard; DNA; 299 BP.
XX	
AC	AZ60864;
XX	
DT	16-MAY-2000 (first entry)
XX	
DE	Region surrounding a splice junction in a normal abl transcript.
XX	
KW	Fusion transcript; translocation; bcr b3 region; abl gene;
KW	amplification assay; detection assay; medical diagnosis;
KW	clinical monitoring; chimeric RNA; fusion RNA; condition marker;
XX	disease marker; cancer; leukemia; ss.
OS	Unidentified.
XX	
PN	WO200005418-A1.
XX	
PD	03-FEB-2000.
XX	
PF	23-JUL-1999; 99WO-US016832.
XX	
PR	23-JUL

XX 23-JUL-1999; 99WO-US016832.  
 XX 23-JUL-1998; 98US-00121239.  
 PR (GENP-) GEN-PROBE INC.  
 XX Harvey RC, Eastman PS;  
 XX WPI; 2000-192730/16.  
 XX Novel methods for preparing RNA from biological samples, used for the  
 PT detection and measurement of nucleic acids and fusion nucleic acids.  
 PS Disclosure; Fig 2; 49pp; English.  
 XX The present sequence represents a region surrounding a bcr-able splice  
 CC junction. The specification describes oligonucleotides which are used to  
 CC detect fusion transcripts produced from a translocation between the bcr  
 CC b3 region and the abl gene. The specification also describes a method for  
 CC detecting a fusion nucleic acid (particularly chimeric mRNA species), in  
 CC a biological sample. The method comprises contacting a sample of fusion  
 CC nucleic acid with primers, amplifying the hybridized fusion nucleic acid,  
 CC and detecting the target hybrid. The method is used for the simple and  
 CC rapid preparation of RNA from a biological sample, particularly from the  
 CC cytoplasm of eukaryotic cells, which is suitable for use in an  
 CC amplification and detection assay. The methods are used for the analysis  
 CC and detection of nucleic acids in biological samples. The methods are  
 CC useful in the human medical and veterinary fields, for medical diagnoses  
 CC and clinical monitoring of a patient's response to therapy where a disease  
 CC or medical condition is associated with a particular type and/or level of  
 CC mRNA present in the sample. The methods are also useful for detecting or  
 CC quantifying fusion or chimeric RNA species, and for detecting a  
 CC translocation as a marker for a given condition or disease, e.g.  
 CC translocations associate with cancers, particularly forms of leukemia  
 XX SQ Sequence 350 BP; 85 A; 92 C; 89 G; 84 T; 0 U; 0 Other;

Query Match 100.0%; Score 27; DB 3; Length 350;  
 Best Local Similarity 100.0%; Pred. No. 3.8e-05;  
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 ACTCAGACCCCTGAGGCTCAAAGTCAGA 27  
 Db 251 ACTCAGACCCCTGAGGCTCAAAGTCAGA 225

Search completed: May 26, 2004, 16:52:25  
 Job time : 120.416 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: May 26, 2004, 16:02:51 ; Search time 22.7559 Seconds  
(without alignments)  
658.454 Million cell updates/sec

Title: US-09-121-239-20

Perfect score: 27  
Sequence: 1 ACTCAGACCTGAGGCTCAAGTCAGA 27

Scoring table: OLIGO\_NUC  
Gapop\_60.0 , Gapext 60.0

Searched: 682709 seqs, 277475446 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents NA.\*  
1: /cgn2\_6/prodata/2/ina/5A COMB.seq.\*  
2: /cgn2\_6/prodata/2/ina/5B COMB.seq.\*  
3: /cgn2\_6/prodata/2/ina/6A COMB.seq.\*  
4: /cgn2\_6/prodata/2/ina/6B COMB.seq.\*  
5: /cgn2\_6/prodata/2/ina/PCTUS COMB.seq.\*  
6: /cgn2\_6/prodata/2/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	27	100.0	204	5	PCT-US93-06251-5
C 2	27	100.0	257	1	US-08-152-621-1
C 3	27	100.0	257	1	US-08-306-691B-36
C 4	27	100.0	257	5	PCT-US92-05035-1
C 5	27	100.0	266	1	US-08-152-621-4
C 6	27	100.0	266	1	US-08-306-691B-37
C 7	27	100.0	266	5	PCT-US92-05035-4
C 8	27	100.0	1078	4	US-09-310-842-1
C 9	27	100.0	3623	1	US-08-306-691B-35
C 10	26	96.3	80	1	US-08-152-621-7
C 11	26	96.3	80	1	US-08-306-691B-38
C 12	26	96.3	80	5	PCT-US92-05035-7
C 13	24	88.9	50	4	US-09-168-947-45
C 14	22	81.5	22	1	US-08-013-419-1
C 15	22	81.5	22	1	US-08-122-795B-10
C 16	22	81.5	22	1	US-08-525-818-1
C 17	22	81.5	22	1	US-09-028-184-1
C 18	22	81.5	22	5	PCT-US94-00680-1
C 19	22	81.5	22	5	PCT-US94-0963A-10
C 20	17	63.0	56	1	US-07-940-652-19
C 21	17	63.0	56	1	US-08-255-553-19
C 22	16	59.3	2992	2	US-08-841-349-10
C 23	16	59.3	2992	4	US-09-431-184A-10
C 24	15	55.6	20	1	US-08-761-131-7
C 25	15	55.6	21	3	US-07-784-222-2
C 26	15	55.6	21	4	US-09-502-954-2
C 27	15	55.6	40	1	US-08-761-131-1

C 28	15	55.6	40	1	US-08-761-131-2	Sequence 2, Appli
C 29	15	55.6	818	4	US-09-599-360B-37	Sequence 37, Appli
C 30	15	55.6	822	4	US-09-621-976-1361	Sequence 1361, Ap
C 31	15	55.6	2214	4	US-09-489-847-113	Sequence 113, App
C 32	15	55.6	2227	4	US-09-489-847-130	Sequence 30, Appl
C 33	15	55.6	7052	4	US-09-526-193A-22	Sequence 22, Appl
C 34	14	51.9	426	4	US-09-621-976-18309	Sequence 18309, A
C 35	14	51.9	474	4	US-09-615-192A-264	Sequence 264, App
C 36	14	51.9	888	4	US-09-171-209-7	Sequence 7, Appli
C 37	14	51.9	973	4	US-09-599-360B-71	Sequence 71, Appl
C 38	14	51.9	1910	2	US-08-808-931-17	Sequence 17, Appl
C 39	14	51.9	1910	3	US-08-808-323-17	Sequence 17, Appl
C 40	14	51.9	1910	3	US-09-050-603A-17	Sequence 17, Appl
C 41	14	51.9	1910	3	US-09-102-420B-17	Sequence 17, Appl
C 42	14	51.9	1910	4	US-09-497-698-17	Sequence 17, Appl
C 43	14	51.9	2050	4	US-09-620-312D-761	Sequence 761, App
C 44	14	51.9	2150	2	US-08-318-837-1	Sequence 1, Appli
C 45	14	51.9	2606	2	US-08-808-931-26	Sequence 26, Appl

## ALIGNMENTS

RESULT 1  
PCT-US93-06251-5/c  
; Sequence 5, Application PC/TUS9306251  
; GENERAL INFORMATION:  
; APPLICANT: Wickstrom, Eric and Rife, Jason P.  
; TITLE OF INVENTION: Trivalent Synthesis of Oligonucleotides Containing  
; TITLE OF INVENTION: Stereospecific Alkylphosphonates and Arylphosphonates  
; NUMBER OF SEQUENCES: 93  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER  
; STREET: 400 Garden City Plaza  
; CITY: Garden City  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 11530  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US93/06251  
; FILING DATE: 19930630  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Digiglio, Frank S.  
; REGISTRATION NUMBER: 31,346  
; REFERENCE/DOCKET NUMBER: 8586  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 516-742-4343  
; TELEFAX: 516-742-4366  
; TELEX: 230 901 SANS UR  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 204 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
PCT-US93-06251-5

Query Match 100.0%; Score 27; DB 5; Length 204;

Best Local Similarity 100.0%; Pred.No.1.2e-06; Indels 0; Gaps 0;  
Matches 27; Conservative 0; Mismatches 0;

QY 1 ACTCAGACCTGAGGCTCAAGTCAGA 27

Db 65 ACTCAGACCTGAGGCTCAAGTCAGA 39

RESULT 2  
US-08-152-621-1/c  
; Sequence 1, Application US/08152621  
; Patent No. 5652222  
; GENERAL INFORMATION:  
; APPLICANT: Calabretta, Bruno  
; APPLICANT: Gewirtz, Alan M.  
; TITLE OF INVENTION: Selective Inhibition of  
; TITLE OF INVENTION: Leukemic Cell Proliferation by bcr-abl  
; TITLE OF INVENTION: Antisense Oligonucleotides  
; NUMBER OF SEQUENCES: 34  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SEIDEL, GONDA, LAVORGNA  
; ADDRESSEE: & MONACO, P.C.  
; STREET: 1800 Two Penn Center  
; CITY: Philadelphia  
; STATE: Pennsylvania  
; COUNTRY: U.S.A.  
; ZIP: 19102  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb  
; COMPUTER: IBM PS/2  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: WordPerfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/152,621  
; FILING DATE: No. 5652222ember 15, 1993  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/718,302  
; FILING DATE: June 18, 1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Monaco, Daniel A.  
; REGISTRATION NUMBER: 30,480  
; REFERENCE/DOCKET NUMBER: 6056-120 (CT.) 1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (215) 568-8383  
; TELEFAX: (215) 568-5549  
; TELEX: No. 565222e  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 257 Nucleotides  
; TYPE: nucleic acid  
; STRANDEDNESS: single stranded  
; TOPOLOGY: linear  
; US-08-152-621-1

Query Match 100.0%; Score 27; DB 1; Length 257;  
Best Local Similarity 100.0%; Pred. No. 1.2e-06;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 ACTCAGACCTGAGGCTCAAAGTCAGA 27  
Db 81 ACTCAGACCTGAGGCTCAAAGTCAGA 55

RESULT 3  
US-08-306-691B-36/c  
; Sequence 36, Application US/08306691B  
; Patent No. 5734039  
; GENERAL INFORMATION:  
; APPLICANT: Calabretta, Bruno  
; APPLICANT: Skorski, Tomasz  
; TITLE OF INVENTION: ANTISENSE  
; TITLE OF INVENTION: OLIGONUCLEOTIDES TARGETING COOPERATING ONCOGENES  
; NUMBER OF SEQUENCES: 55  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Seidel, Gonda, Lavorgna & Monaco, P.C.  
; STREET: Two Penn Center, Suite 1800  
; CITY: Philadelphia  
; STATE: Pennsylvania  
; COUNTRY: U.S.A.  
; ZIP: 19102

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb  
; COMPUTER: IBM PS/2  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: WordPerfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/306,691B  
; FILING DATE: September 15, 1994  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Monaco, Daniel A.  
; REGISTRATION NUMBER: 30,480  
; REFERENCE/DOCKET NUMBER: 8321-8  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (215) 568-8383  
; TELEFAX: (215) 568-5549  
; TELEX: No. 5734039e  
; INFORMATION FOR SEQ ID NO: 36:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 257 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; US-08-306-691B-36

Query Match 100.0%; Score 27; DB 1; Length 257;  
Best Local Similarity 100.0%; Pred. No. 1.2e-06;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 ACTCAGACCTGAGGCTCAAAGTCAGA 27  
Db 81 ACTCAGACCTGAGGCTCAAAGTCAGA 55

RESULT 4  
PCT-US92-05035-1/c  
; Sequence 1, Application PC/TUS9205035  
; GENERAL INFORMATION:  
; APPLICANT: Calabretta, Bruno  
; APPLICANT: Gewirtz, Alan M.  
; TITLE OF INVENTION: Selective Inhibition of  
; TITLE OF INVENTION: Leukemic Cell Proliferation by bcr-abl  
; TITLE OF INVENTION: Antisense Oligonucleotides  
; NUMBER OF SEQUENCES: 34  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Temple University - Of The Common-  
; ADDRESSEE: wealth System of Higher Education  
; STREET: 406 University Services Building  
; CITY: Philadelphia  
; STATE: Pennsylvania  
; COUNTRY: U.S.A.  
; ZIP: 19122  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb  
; COMPUTER: IBM PS/2  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: WordPerfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US92/05035  
; FILING DATE: 19920615  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/718,302  
; FILING DATE: June 18, 1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/869,911  
; FILING DATE: April 14, 1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Monaco, Daniel A.  
; REGISTRATION NUMBER: 30,480

REFERENCE/DOCKET NUMBER: 6056-120 (CIP) 1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (215) 568-8383  
TELEFAX: (215) 568-5549  
TELEX: None  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 257 Nucleotides  
TYPE: NUCLEIC ACID  
STRANDEDNESS: single stranded  
TOPOLOGY: linear  
PCT-US92-05035-1

Query Match 100.0%; Score 27; DB 5; Length 257;  
Best Local Similarity 100.0%; Pred. No. 1.2e-06;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACTCAGACCTGAGGCTCAAAAGTCAGA 27  
Db 81 ACTCAGACCTGAGGCTCAAAAGTCAGA 55

RESULT 5

US-08-152-621-4/c  
Sequence 4, Application US/08152621  
Patent No. 5652222  
GENERAL INFORMATION:  
APPLICANT: Calabretta, Bruno  
TITLE OF INVENTION: Selective Inhibition of  
Leukemic Cell Proliferation by bcr-abl  
TITLE OF INVENTION: Leukemic Cell Proliferation by bcr-abl  
NUMBER OF SEQUENCES: 34  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SEIDEL, GONDA, LAVORGNA  
ADDRESSEE: & MONACO, P.C.  
STREET: 1800 Two Penn Center  
CITY: Philadelphia  
STATE: Pennsylvania  
COUNTRY: U.S.A.  
ZIP: 19102

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb  
COMPUTER: IBM PS/2  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: WordPerfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/152,621  
FILING DATE: June 18, 1991  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/718,302  
FILING DATE: June 18, 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Monaco, Daniel A.  
REGISTRATION NUMBER: 30,480  
REFERENCE/DOCKET NUMBER: 6056-120 (CT.) 1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (215) 568-8383  
TELEFAX: (215) 568-5549  
TELEX: No. 5652222e

INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 266 Nucleotides  
TYPE: nucleic acid  
STRANDEDNESS: single stranded  
TOPOLOGY: linear  
US-08-152-621-4

Query Match 100.0%; Score 27; DB 1; Length 266;  
Best Local Similarity 100.0%; Pred. No. 1.2e-06;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACTCAGACCTGAGGCTCAAAAGTCAGA 27  
Db 90 ACTCAGACCTGAGGCTCAAAAGTCAGA 64

RESULT 6

US-08-306-691B-37/c  
Sequence 37, Application US/08306691B  
Patent No. 5734039  
GENERAL INFORMATION:  
APPLICANT: Calabretta, Bruno  
TITLE OF INVENTION: ANTISENSE  
TITLE OF INVENTION: OLIGONUCLEOTIDES TARGETING COOPERATING ONCOGENES  
NUMBER OF SEQUENCES: 55  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Seidel, Gonda, Lavorgna & Monaco, P.C.  
STREET: Two Penn Center, Suite 1800  
CITY: Philadelphia  
STATE: Pennsylvania  
COUNTRY: U.S.A.  
ZIP: 19102

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb  
COMPUTER: IBM PS/2  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: WordPerfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/306,691B  
FILING DATE: September 15, 1994  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Monaco, Daniel A.  
REGISTRATION NUMBER: 30,480  
REFERENCE/DOCKET NUMBER: 8321-8  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (215) 568-8383  
TELEFAX: (215) 568-5549  
TELEX: No. 5734039e  
INFORMATION FOR SEQ ID NO: 37:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 266 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-306-691B-37

Query Match 100.0%; Score 27; DB 1; Length 266;  
Best Local Similarity 100.0%; Pred. No. 1.2e-06;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACTCAGACCTGAGGCTCAAAAGTCAGA 27  
Db 90 ACTCAGACCTGAGGCTCAAAAGTCAGA 64

RESULT 7

PCT-US92-05035-4/c  
Sequence 4, Application PC/TUS9205035  
GENERAL INFORMATION:  
APPLICANT: Calabretta, Bruno  
TITLE OF INVENTION: Selective Inhibition of  
Leukemic Cell Proliferation by bcr-abl  
TITLE OF INVENTION: Antisense Oligonucleotides  
NUMBER OF SEQUENCES: 34  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Temple University - Of The Common-  
wealth System of Higher Education  
STREET: 406 University Services Building

CITY: Philadelphia  
STATE: Pennsylvania  
COUNTRY: U.S.A.  
ZIP: 19122  
COMPUTER READABLE FORM: 3.50 inch, 720 Kb  
MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb  
COMPUTER: IBM PS/2  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: WordPerfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US92/05035  
FILING DATE: 19920615  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/718,302  
FILING DATE: June 18, 1991  
APPLICATION DATA:  
APPLICATION NUMBER: 07/869,911  
FILING DATE: April 14, 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Monaco, Daniel A.  
REGISTRATION NUMBER: 30,480  
REFERENCE/DOCKET NUMBER: 6056-120 (CIP) 1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (215) 568-8383  
TELEFAX: (215) 568-5549  
TELEX: None  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 266 Nucleotides  
TYPE: NUCLEIC ACID  
STRANDEDNESS: single stranded  
TOPOLOGY: linear  
PCT-US92-05035-4  
Query Match 100.0%; Score 27; DB 5; Length 266;  
Best Local Similarity 100.0%; Pred. No. 1.2e-06;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ACTCAGACCCCTGAGGCTCAAAAGTCAGA 27  
Db 90 ACTCAGACCCCTGAGGCTCAAAAGTCAGA 64  
RESULT 8  
US-09-310-842-1/C  
Sequence 1, Application US/09310842A  
Patent No. 6451593  
GENERAL INFORMATION:  
APPLICANT: Wittig, Prof. Burghardt  
APPLICANT: Jungmans, Claas  
TITLE OF INVENTION: Design Principle for Constructing Expression Constructs for Gene  
FILE REFERENCE: XI 597/99  
CURRENT FILING DATE: 1999-05-12  
EARLIER APPLICATION NUMBER: DE 196 48 625.4  
EARLIER FILING DATE: 1996-11-13  
NUMBER OF SEQ ID NOS: 13  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 1  
LENGTH: 1078  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
NAME/KEY: gene  
LOCATION: (1)..(1078)  
OTHER INFORMATION: bcr3=abl2; Oligo DNA Dumbbell  
FEATURE:  
NAME/KEY: misc binding  
LOCATION: (1)..(2)  
OTHER INFORMATION: intramolecular binding site; the T-nucleotides at position 1 to  
OTHER INFORMATION: 2 can be modified with amino or caroxy features

FEATURE:  
NAME/KEY: misc binding  
LOCATION: (1077)..(1078)  
OTHER INFORMATION: intramolecular binding site; the T-nucleotides at position 1077  
OTHER INFORMATION: to 1078 can be modified with amino or caroxy features  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Strandness: both; nucleic  
OTHER INFORMATION: acid (linear), hypothetical: No. 6451593 anti-sense: NO  
US-09-310-842-1  
Query Match 100.0%; Score 27; DB 4; Length 1078;  
Best Local Similarity 100.0%; Pred. No. 1.2e-06;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ACTCAGACCCCTGAGGCTCAAAAGTCAGA 27  
Db 824 ACTCAGACCCCTGAGGCTCAAAAGTCAGA 798  
RESULT 9  
US-08-306-691B-35/c  
Sequence 35, Application US/08306691B  
Patent No. 5734039  
GENERAL INFORMATION:  
APPLICANT: Calabretta, Bruno  
APPLICANT: Skorski, Tomasz  
TITLE OF INVENTION: ANTISENSE  
TITLE OF INVENTION: OLIGONUCLEOTIDES TARGETING COOPERATING ONCOGENES  
NUMBER OF SEQUENCES: 55  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Seidel, Gonda, Lavorigna & Monaco, P.C.  
CITY: Philadelphia  
STATE: Pennsylvania  
COUNTRY: U.S.A.  
ZIP: 19102  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb  
COMPUTER: IBM PS/2  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: WordPerfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/306,691B  
FILING DATE: September 15, 1994  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Monaco, Daniel A.  
REGISTRATION NUMBER: 30,480  
REFERENCE/DOCKET NUMBER: 8321-8  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (215) 568-8383  
TELEFAX: (215) 568-5549  
TELEX: No. 5734039e  
INFORMATION FOR SEQ ID NO: 35:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3623 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
US-08-306-691B-35  
Query Match 100.0%; Score 27; DB 1; Length 3623;  
Best Local Similarity 100.0%; Pred. No. 1.3e-06;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ACTCAGACCCCTGAGGCTCAAAAGTCAGA 27  
Db 276 ACTCAGACCCCTGAGGCTCAAAAGTCAGA 250



RESULT 10  
US-08-152-621-7/c  
; Sequence 7, Application US/08152621  
; Patent No. 5652222  
; GENERAL INFORMATION:  
; APPLICANT: Calabretta, Bruno  
; APPLICANT: Gewirtz, Alan M.  
; TITLE OF INVENTION: Selective Inhibition of  
; TITLE OF INVENTION: Leukemic Cell Proliferation by bcr-abl  
; TITLE OF INVENTION: Antisense Oligonucleotides  
; NUMBER OF SEQUENCES: 34  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SEIDEL, GONDA, LAVORGNA  
; ADDRESSEE: & MONACO, P.C.  
; STREET: 1800 Two Penn Center  
; CITY: Philadelphia  
; STATE: Pennsylvania  
; COUNTRY: U.S.A.  
; ZIP: 19102  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb  
; COMPUTER: IBM PS/2  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: WordPerfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/152,621  
; FILING DATE: NO. 5652222ember 15, 1993  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/718,302  
; FILING DATE: June 18, 1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Monaco, Daniel A.  
; REGISTRATION NUMBER: 30,480  
; REFERENCE/DOCKET NUMBER: 6056-120 (CT.) 1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (215) 568-8383  
; TELEFAX: (215) 568-5549  
; TELEX: No. 5652222e  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 80 Nucleotides  
; TYPE: nucleic acid  
; STRANDEDNESS: single stranded  
; TOPOLOGY: linear  
US-08-152-621-7

Query Match 96.3%; Score 26; DB 1; Length 80;  
Best Local Similarity 100.0%; Pred. No. 4.3e-06;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CTCAGACCCCTGAGGCTCAAAGTCAGA 27  
Db 80 CTCAGACCCCTGAGGCTCAAAGTCAGA 55

RESULT 11  
US-08-306-691B-38/c  
; Sequence 38, Application US/08306691B  
; Patent No. 5734039  
; GENERAL INFORMATION:  
; APPLICANT: Calabretta, Bruno  
; APPLICANT: Skorski, Tomasz  
; TITLE OF INVENTION: ANTISENSE  
; TITLE OF INVENTION: OLIGONUCLEOTIDES TARGETING COOPERATING ONCOGENES  
; NUMBER OF SEQUENCES: 55  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Seidel, Gonda, Lavorgna & Monaco, P.C.  
; STREET: Two Penn Center, Suite 1800  
; CITY: Philadelphia  
; STATE: Pennsylvania  
; COUNTRY: U.S.A.  
; ZIP: 19102

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb  
COMPUTER: IBM PS/2  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: WordPerfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/306,691B  
FILING DATE: September 15, 1994  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Monaco, Daniel A.  
REGISTRATION NUMBER: 30,480  
REFERENCE/DOCKET NUMBER: 8321-8  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (215) 568-8383  
TELEFAX: (215) 568-5549  
TELEX: No. 5734039e  
INFORMATION FOR SEQ ID NO: 38:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 80 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-306-691B-38

Query Match 96.3%; Score 26; DB 1; Length 80;  
Best Local Similarity 100.0%; Pred. No. 4.3e-06;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CTCAGACCCCTGAGGCTCAAAGTCAGA 27  
Db 80 CTCAGACCCCTGAGGCTCAAAGTCAGA 55

RESULT 12  
PCT-US92-05035-7/c  
; Sequence 7, Application PC/TUS9205035  
; GENERAL INFORMATION:  
; APPLICANT: Calabretta, Bruno  
; APPLICANT: Gewirtz, Alan M.  
; TITLE OF INVENTION: Selective Inhibition of  
; TITLE OF INVENTION: Leukemic Cell Proliferation by bcr-abl  
; TITLE OF INVENTION: Antisense Oligonucleotides  
; NUMBER OF SEQUENCES: 34  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Temple University - Of The Common-  
; ADDRESSEE: wealth System of Higher Education  
; STREET: 406 University Services Building  
; CITY: Philadelphia  
; STATE: Pennsylvania  
; COUNTRY: U.S.A.  
; ZIP: 19122  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb  
; COMPUTER: IBM PS/2  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: WordPerfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US92/05035  
; FILING DATE: 19920615  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/718,302  
; FILING DATE: June 18, 1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/869,911  
; FILING DATE: April 14, 1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Monaco, Daniel A.  
; REGISTRATION NUMBER: 30,480

```
; REFERENCE/DOCKET NUMBER: 6056-120 (CIP) 1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-8383
; TELEFAX: (215) 568-5549
; TELEX: None
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 80 Nucleotides
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single stranded
; TOPOLOGY: linear
PCT-US92-05035-7

Query Match          96.3%; Score 26; DB 5; Length 80;
Best Local Similarity 100.0%; Pred. No. 4.3e-06;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  2 CTCAGACCCCTGAGGCTCAAAGTCAGA 27
    |||||
Db   80 CTCAGACCCCTGAGGCTCAAAGTCAGA 55

RESULT 13
US-09-168-947-45
; Sequence 45, Application US/09168947
; Patent No. 6585734
; GENERAL INFORMATION:
; APPLICANT: KACIAN, DANIEL L.
; APPLICANT: FULTZ, TIMOTHY J.
; APPLICANT: MCDONOUGH, SHERROL H.
; TITLE OF INVENTION: DETECTION OF HIV
; FILE REFERENCE: 218/130
; CURRENT APPLICATION NUMBER: US/09/168,947
; CURRENT FILING DATE: 1998-10-08
; EARLIER APPLICATION NUMBER: 08/469,067
; EARLIER FILING DATE: 1995-06-06
; EARLIER APPLICATION NUMBER: 07/550,837
; EARLIER FILING DATE: 1990-07-10
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 45
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthesized nucleic acid molecule
US-09-168-947-45

Query Match          88.9%; Score 24; DB 4; Length 50;
Best Local Similarity 100.0%; Pred. No. 5.7e-05;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1 ACTCAGACCCCTGAGGCTCAAAGTC 24
    |||||
Db   27 ACTCAGACCCCTGAGGCTCAAAGTC 50

RESULT 14
US-08-013-419-1
; Sequence 1, Application US/08013419
; Patent No. 5300635
; GENERAL INFORMATION:
; APPLICANT: Macfarlane, Donald E.
; TITLE OF INVENTION: Product and Process for Isolating RNA
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Howson and Howson
; STREET: Spring House Corporate Center, P.O. Box 457
; CITY: Spring House
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19477
; COMPUTER READABLE FORM:
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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/013,419
; FILING DATE: 19930201
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Bak, Mary E.
; REGISTRATION NUMBER: 31,215
; REFERENCE/DOCKET NUMBER: URIF1USA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-540-9206
; TELEFAX: 215-540-5818
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
US-08-013-419-1

Query Match          81.5%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.00077;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  3 TCAGACCCCTGAGGCTCAAAGTC 24
    |||||
Db   1 TCAGACCCCTGAGGCTCAAAGTC 22

RESULT 15
US-08-122-795B-10
; Sequence 10, Application US/08122795B
; Patent No. 5635385
; GENERAL INFORMATION:
; APPLICANT: Lance H. Leopold
; APPLICANT: Scott K. Shore
; APPLICANT: Moolle V. R. Reddy
; APPLICANT: E. Premkumar Reddy
; TITLE OF INVENTION: MULTI-UNIT RIBOZYME
; TITLE OF INVENTION: INHIBITION OF ONCOGENE EXPRESSION
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seidel, Gonda, Lavorigna
; ADDRESSEE: & Monaco, P.C.
; STREET: Two Penn Center Plaza, Suite 1800
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: U.S.A.
; ZIP: 19102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/122,795B
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 122,795
; FILING DATE: 15 September 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Monaco, Daniel A.
; REGISTRATION NUMBER: 30,480
; REFERENCE/DOCKET NUMBER: 6056-192
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-8383
; TELEFAX: (215) 568-5549
; TELEX: NO. 5635385e
```

; INFORMATION FOR SEQ ID NO: 10:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 22 Nucleotides

; TYPE: nucleic acid

; STRANDEDNESS: single stranded

; TOPOLOGY: linear

US-08-122-795B-10

Query Match

Best Local Similarity 81.5%; Score 22; DB 1; Length 22;

Matches 22; Conservativity 100.0%; Pred. No. 0.00077;

Mismatches 0; Indels 0; Gaps 0;

QY 3 TCAGACCTGAGGCTCAAGTC 24

DB 1 TCAGACCTGAGGCTCAAGTC 22

Search completed: May 27, 2004, 02:25:16

Job time : 23.7559 secs

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US-10-228-811-1/c
; Sequence 1, Application US/10228811
; Publication No. US20030054392A1
; GENERAL INFORMATION:
; APPLICANT: Wittig, Prof. Burghardt
; APPLICANT: Jungmans, Claas
; TITLE OF INVENTION: Design Principle for Constructing Expression Constructs for Gene
; TITLE OF INVENTION: Therapy
; FILE REFERENCE: XI 597/99
; CURRENT APPLICATION NUMBER: US/10/228,811
; CURRENT FILING DATE: 2002-08-27
; PRIOR APPLICATION NUMBER: DE 196 48 625.4
; PRIOR FILING DATE: 1996-11-13
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1078
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: gene
; LOCATION: (1)..(1078)
; OTHER INFORMATION: bcr3=abl2; Oligo DNA Dumbbell
; FEATURE:
; NAME/KEY: misc binding
; LOCATION: (1)..(2)
; OTHER INFORMATION: intramolecular binding site; the T-nucleotides at position 1 to
; OTHER INFORMATION: 2 can be modified with amino or caroxy features
; FEATURE:
; NAME/KEY: misc binding
; LOCATION: (1077)..(1078)
; OTHER INFORMATION: intramolecular binding site; the T-nucleotides at position 1077
; OTHER INFORMATION: to 1078 can be modified with amino or caroxy features
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Strandness: both; nucleic
; OTHER INFORMATION: acid (linear), hypothetical: No. US20030054392A1 anti-sense: No.

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## US-10-228-811-1

Query Match 100.0%; Score 27; DB 15; Length 1078;  
Best Local Similarity 100.0%; Pred. No. 5.7e-06;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACTCAGACCCCTGAGGCTCAAGTCAGA 27  
|||||  
Db 824 ACTCAGACCCCTGAGGCTCAAGTCAGA 798  
|||||

## RESULT 2

US-10-263-480-1/c  
; Sequence 1, Application US/10263480  
; Publication No. US20030170851A1  
; GENERAL INFORMATION:  
; APPLICANT: NO. US20030170851A1artis AG  
; TITLE OF INVENTION: Organic Compounds  
; FILE REFERENCE: Case 4-32175PI/PROV  
; CURRENT APPLICATION NUMBER: US/10/263,480  
; CURRENT FILING DATE: 2002-10-03  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 1  
; LENGTH: 3393  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(3393)  
US-10-263-480-1

Query Match 100.0%; Score 27; DB 15; Length 3393;  
Best Local Similarity 100.0%; Pred. No. 5e-06;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACTCAGACCCCTGAGGCTCAAGTCAGA 27  
|||||  
Db 129 ACTCAGACCCCTGAGGCTCAAGTCAGA 103  
|||||

## RESULT 3

US-10-457-954-5/c  
; Sequence 5, Application US/10457954  
; Publication No. US20040005623A1  
; GENERAL INFORMATION:  
; APPLICANT: Longley, B. Jack  
; TITLE OF INVENTION: Method of determining tumor sensitivities to therapeutic drugs  
; FILE REFERENCE: 960296.98890  
; CURRENT APPLICATION NUMBER: US/10/457,954  
; CURRENT FILING DATE: 2003-06-10  
; PRIOR APPLICATION NUMBER: 60/387,370  
; PRIOR FILING DATE: 2002-06-10  
; PRIOR APPLICATION NUMBER: 60/387,406  
; PRIOR FILING DATE: 2002-06-10  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 5  
; LENGTH: 3450  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(3447)  
; FEATURE:  
; NAME/KEY: misc structure  
; LOCATION: (730)..(765)  
; OTHER INFORMATION: encode amino acids 244-255 for forming the sides of the enzymatic  
; OTHER INFORMATION: pocket  
; FEATURE:  
; NAME/KEY: misc structure  
; LOCATION: (931)..(1077)  
; OTHER INFORMATION: encode amino acids 311-359 for forming the sides of the enzymatic

## ; OTHER INFORMATION: pocket

## ; FEATURE:

; NAME/KEY: misc structure

; LOCATION: (1141)..(1206)

; OTHER INFORMATION: encode amino acids 381-402 for forming the enzymatic pocket's

; OTHER INFORMATION: activation loop

US-10-457-954-5

Query Match 100.0%; Score 27; DB 16; Length 3450;  
Best Local Similarity 100.0%; Pred. No. 5e-06;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACTCAGACCCCTGAGGCTCAAGTCAGA 27  
|||||  
Db 186 ACTCAGACCCCTGAGGCTCAAGTCAGA 160  
|||||

## RESULT 4

US-10-204-041-3/c  
; Sequence 3, Application US/10204041  
; Publication No. US20030176443A1  
; GENERAL INFORMATION:  
; APPLICANT: STEIN-GERLACH, MATTHIAS  
; APPLICANT: SALASSIDIS, KONSTADINOS  
; APPLICANT: BACHER, GERALD  
; APPLICANT: MULLER, STEFAN  
; TITLE OF INVENTION: Pyridylpyrimidine Derivatives as Effective Compounds Against Prion  
; TITLE OF INVENTION: Infections and Prion Diseases  
; FILE REFERENCE: AXM-007.1P US  
; CURRENT APPLICATION NUMBER: US/10/204,041  
; CURRENT FILING DATE: 2002-08-16  
; PRIOR APPLICATION NUMBER: EP 0111858.5  
; PRIOR FILING DATE: 2001-05-16  
; PRIOR APPLICATION NUMBER: PCT/EP02/05420  
; PRIOR FILING DATE: 2002-05-16  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 3  
; LENGTH: 3840  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-204-041-3

Query Match 100.0%; Score 27; DB 15; Length 3840;  
Best Local Similarity 100.0%; Pred. No. 4.9e-06;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACTCAGACCCCTGAGGCTCAAGTCAGA 27  
|||||  
Db 493 ACTCAGACCCCTGAGGCTCAAGTCAGA 467  
|||||

## RESULT 5

US-10-170-385-182/c  
; Sequence 182, Application US/10170385  
; Publication No. US20030203372A1  
; GENERAL INFORMATION:  
; APPLICANT: Ward, Neil Raymond  
; APPLICANT: Mundy, Christopher Robert  
; APPLICANT: Kan, On  
; APPLICANT: Harris, Robert Alan  
; APPLICANT: White, Jonathan  
; APPLICANT: Binley, Katie Mary  
; APPLICANT: Rayner, William Nigel  
; APPLICANT: Naylor, Stuart  
; APPLICANT: Kingsman, Susan Mary  
; APPLICANT: Krige, David  
; TITLE OF INVENTION: ANALYSIS METHOD  
; FILE REFERENCE: 532682000100  
; CURRENT APPLICATION NUMBER: US/10/170,385  
; CURRENT FILING DATE: 2002-06-12  
; PRIOR APPLICATION NUMBER: PCT/GB02/01662  
; PRIOR FILING DATE: 2002-04-08

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; PRIOR APPLICATION NUMBER: PCT/GB01/05458
; PRIOR FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 549
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 182
; LENGTH: 5434
; TYPE: DNA
; ORGANISM: Homo Sapiens
; US-10-170-385-182

Query Match      100.0%; Score 27; DB 13; Length 5434;
Best Local Similarity 100.0%; Pred. No. 4.7e-06;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACTCAGACCTGAGGCTCAAAGTCAGA 27
Db 183 ACTCAGACCTGAGGCTCAAAGTCAGA 157

RESULT 6
US-09-880-107-3710/c
; Sequence 3710, Application US/09880107
; Patent No. US20020142981A1
; GENERAL INFORMATION:
; APPLICANT: Horne, Darci T.
; APPLICANT: Vockley, Joseph G.
; APPLICANT: Scherf, Uwe
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
; FILE REFERENCE: 44921-5028-WO
; CURRENT APPLICATION NUMBER: US/09/880,107
; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: US 60/211,379
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: US 60/237,054
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 3950
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3710
; LENGTH: 5527
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20020142981A1 X16416
; US-09-880-107-3710

Query Match      100.0%; Score 27; DB 9; Length 5527;
Best Local Similarity 100.0%; Pred. No. 4.7e-06;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACTCAGACCTGAGGCTCAAAGTCAGA 27
Db 276 ACTCAGACCTGAGGCTCAAAGTCAGA 250

RESULT 7
US-10-439-703-5/c
; Sequence 5, Application US/10439703
; Publication No. US20040018527A1
; GENERAL INFORMATION:
; APPLICANT: Chang, Jenny
; APPLICANT: O'Connell, Peter
; TITLE OF INVENTION: Differential Patterns of Gene Expression that Predict for Docetax
; FILE REFERENCE: HO-P2482US1/10205813
; CURRENT APPLICATION NUMBER: US/10/439,703
; CURRENT FILING DATE: 2003-05-16
; PRIOR APPLICATION NUMBER: US 60/381,141
; PRIOR FILING DATE: 2002-05-17
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 5744
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; TYPE: DNA
; ORGANISM: Human
; US-10-439-703-5

Query Match      100.0%; Score 27; DB 16; Length 5744;
Best Local Similarity 100.0%; Pred. No. 4.7e-06;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACTCAGACCTGAGGCTCAAAGTCAGA 27
Db 493 ACTCAGACCTGAGGCTCAAAGTCAGA 467

RESULT 8
US-09-962-436-36/c
; Sequence 36, Application US/09962436
; Patent No. US20020081301A1
; GENERAL INFORMATION:
; APPLICANT: Soppet, Daniel
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu
; FILE REFERENCE: 689290-75
; CURRENT APPLICATION NUMBER: US/09/962,436
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/60/235,082
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/234,924
; PRIOR FILING DATE: 2000-09-25
; NUMBER OF SEQ ID NOS: 568
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 36
; LENGTH: 84539
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-962-436-36

Query Match      100.0%; Score 27; DB 9; Length 84539;
Best Local Similarity 100.0%; Pred. No. 3.4e-06;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACTCAGACCTGAGGCTCAAAGTCAGA 27
Db 49938 ACTCAGACCTGAGGCTCAAAGTCAGA 49912

RESULT 9
US-10-244-490-45
; Sequence 45, Application US/10244490
; Publication No. US20030152916A1
; GENERAL INFORMATION:
; APPLICANT: KACIAN, DANIEL L.
; APPLICANT: FULTZ, TIMOTHY J.
; APPLICANT: MCDONOUGH, SHERROL H.
; TITLE OF INVENTION: DETECTION OF HIV
; FILE REFERENCE: 218/130
; CURRENT APPLICATION NUMBER: US/10/244,490
; CURRENT FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: US/09/168,947
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 08/469,067
; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: 07/550,837
; PRIOR FILING DATE: 1990-07-10
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 45
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthesized nucleic acid molecule
; US-10-244-490-45
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Query Match 88.9%; Score 24; DB 15; Length 50;  
Best Local Similarity 100.0%; Pred. No. 0.00042;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACTGAGCCCTGAGGCTCAAGTC 24  
|||||  
DB 27 ACTGAGCCCTGAGGCTCAAGTC 50

## RESULT 10

US-09-995-912-4  
; Sequence 4, Application US/09995912  
; Patent No. US20020137076A1  
; GENERAL INFORMATION:  
; APPLICANT: Shultz, John W.  
; APPLICANT: Lewis, Martin K.  
; APPLICANT: Andrews, Christine  
; TITLE OF INVENTION: RNA Polymers and Uses Thereof  
; FILE REFERENCE: PRMG-06684  
; CURRENT APPLICATION NUMBER: US/09/995,912  
; CURRENT FILING DATE: 2001-11-28  
; PRIOR APPLICATION NUMBER: 60/253,451  
; PRIOR FILING DATE: 2000-11-28  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: Patentin version 3.1  
; SEQ ID NO 4  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic  
US-09-995-912-4

Query Match 81.5%; Score 22; DB 9; Length 22;  
Best Local Similarity 100.0%; Pred. No. 0.0065;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TCAGACCCCTGAGGCTCAAGTC 24  
|||||  
DB 1 TCAGACCCCTGAGGCTCAAGTC 22

## RESULT 11

US-09-747-165-3  
; Sequence 3, Application US/09747165  
; Publication No. US20020192645A1  
; GENERAL INFORMATION:  
; APPLICANT: TSENG, RICHARD W.  
; APPLICANT: SAMOSZUK, MICHAEL K.  
; TITLE OF INVENTION: BCR-ABL GENE REARRANGEMENT ASSAY METHOD  
; FILE REFERENCE: 034827/0302  
; CURRENT APPLICATION NUMBER: US/09/747,165  
; CURRENT FILING DATE: 2001-09-24  
; PRIOR APPLICATION NUMBER: 60/173,050  
; PRIOR FILING DATE: 1999-12-24  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 3  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Primer  
US-09-747-165-3

Query Match 81.5%; Score 22; DB 9; Length 22;  
Best Local Similarity 100.0%; Pred. No. 0.0065;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TCAGACCCCTGAGGCTCAAGTC 24  
|||||  
DB 1 TCAGACCCCTGAGGCTCAAGTC 22

## RESULT 12

US-10-382-634-20  
; Sequence 20, Application US/10382634  
; Publication No. US20040038921A1  
; GENERAL INFORMATION:  
; APPLICANT: Kreutzer, Roalnd  
; TITLE OF INVENTION: Composition and Method for Inhibiting Expression of a Target Gene  
; FILE REFERENCE: 20200/2062  
; CURRENT APPLICATION NUMBER: US/10/382,634  
; CURRENT FILING DATE: 2003-03-07  
; PRIOR APPLICATION NUMBER: DE 101 55 280.7  
; PRIOR FILING DATE: 2001-10-26  
; PRIOR APPLICATION NUMBER: DE 101 58 411.3  
; PRIOR FILING DATE: 2001-11-29  
; PRIOR APPLICATION NUMBER: DE 101 60 151.4  
; PRIOR FILING DATE: 2001-12-07  
; PRIOR APPLICATION NUMBER: DE 102 30 996.5  
; PRIOR FILING DATE: 2002-07-09  
; PRIOR APPLICATION NUMBER: PCT/EP02/00152  
; PRIOR FILING DATE: 2002-01-09  
; PRIOR APPLICATION NUMBER: PCT/EP02/00151  
; PRIOR FILING DATE: 2002-01-09  
; PRIOR APPLICATION NUMBER: PCT/EP02/11971  
; PRIOR FILING DATE: 2002-10-25  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: Patentin version 3.2  
; SEQ ID NO 20  
; LENGTH: 21  
; TYPE: DNA  
; ORGANISM: artificial sequence  
; FEATURE:  
; OTHER INFORMATION: PRIMER  
US-10-382-634-20

Query Match 77.8%; Score 21; DB 13; Length 21;  
Best Local Similarity 100.0%; Pred. No. 0.024;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TCAGACCCCTGAGGCTCAAGT 23  
|||||  
DB 1 TCAGACCCCTGAGGCTCAAGT 21

## RESULT 13

US-10-349-320-19  
; Sequence 19, Application US/10349320  
; Publication No. US20030190654A1  
; GENERAL INFORMATION:  
; APPLICANT: Heidenreich, Olaf  
; TITLE OF INVENTION: DOUBLE-STRANDED RNA (dsRNA) AND METHOD OF USE  
; FILE REFERENCE: 20200/2112  
; CURRENT APPLICATION NUMBER: US/10/349,320  
; CURRENT FILING DATE: 2003-01-22  
; PRIOR APPLICATION NUMBER: DE 102 02 419.7  
; PRIOR FILING DATE: 2002-01-22  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: Patentin version 3.1  
; SEQ ID NO 19  
; LENGTH: 21  
; TYPE: DNA  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: primer  
US-10-349-320-19

Query Match 77.8%; Score 21; DB 15; Length 21;  
Best Local Similarity 100.0%; Pred. No. 0.024;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TCAGACCCCTGAGGCTCAAGT 23  
|||||  
DB 1 TCAGACCCCTGAGGCTCAAGT 21



## RESULT 14

US-09-918-995-19841/c  
; Sequence 19841, Application US/0918995  
; Publication No. US20030073623A1  
; GENERAL INFORMATION:  
; APPLICANT: Hyseq, Inc.  
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED  
; FILE REFERENCE: 20411-756  
; CURRENT APPLICATION NUMBER: US/09/918,995  
; PRIOR FILING DATE: 2001-07-30  
; PRIOR APPLICATION NUMBER: US/09/235,076  
; PRIOR FILING DATE: 1999-01-20  
; NUMBER OF SEQ ID NOS: 38054  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 19841  
; LENGTH: 468  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1)-(468)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-918-995-19841

Query Match 59.3%; Score 16; DB 10; Length 468;  
Best Local Similarity 100.0%; Pred. No. 12;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 CTGAGGCTCAAAAGTCA 25

DB 331 CTGAGGCTCAAAAGTCA 316

## RESULT 15

US-10-027-632-163921  
; Sequence 163921, Application US/10027632  
; Publication No. US20020198371A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
; FILE REFERENCE: 108827.129  
; CURRENT APPLICATION NUMBER: US/10/027,632  
; PRIOR FILING DATE: 2002-04-30  
; PRIOR APPLICATION NUMBER: US 60/218,006  
; PRIOR FILING DATE: 2000-07-12  
; PRIOR APPLICATION NUMBER: US 60/198,676  
; PRIOR FILING DATE: 2000-04-20  
; PRIOR APPLICATION NUMBER: US 60/193,483  
; PRIOR FILING DATE: 2000-03-29  
; PRIOR APPLICATION NUMBER: US 60/185,218  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/167,363  
; PRIOR FILING DATE: 1999-11-23  
; PRIOR APPLICATION NUMBER: US 60/156,358  
; PRIOR FILING DATE: 1999-09-28  
; PRIOR APPLICATION NUMBER: US 60/146,002  
; PRIOR FILING DATE: 1999-08-09  
; NUMBER OF SEQ ID NOS: 325720  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 163921  
; LENGTH: 639  
; TYPE: DNA  
; ORGANISM: Human  
US-10-027-632-163921

Query Match 59.3%; Score 16; DB 13; Length 639;  
Best Local Similarity 100.0%; Pred. No. 12;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CAGACCCCTGAGGCTCA 19  
DB 522 CAGACCCCTGAGGCTCA 537

Search completed: May 27, 2004, 14:58:32  
Job time : 143.089 secs

**THIS PAGE BLANK (USPTO)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 26, 2004, 15:22:41 ; Search time 953.308 Seconds  
(without alignments)  
845.770 Million cell updates/sec

Title: US-09-121-239-20

Perfect score: 27  
Sequence: 1 ACTGACCTGAGGCTCAAGTCAGA 27

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 27513289 seqs, 14931090276 residues

Word size : 0

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

EST:\*

1: em\_estba:\*

2: em\_esthum:\*

3: em\_estin:\*

4: em\_estmu:\*

5: em\_estov:\*

6: em\_estpl:\*

7: em\_estro:\*

8: em\_htc:\*

9: gb\_est1:\*

10: gb\_est2:\*

11: gb\_htc:\*

12: gb\_est3:\*

13: gb\_est4:\*

14: gb\_est5:\*

15: em\_estfun:\*

16: em\_estom:\*

17: em\_gss\_hum:\*

18: em\_gss\_inv:\*

19: em\_gss\_pin:\*

20: em\_gss\_vrt:\*

21: em\_gss\_fun:\*

22: em\_gss\_nam:\*

23: em\_gss\_mus:\*

24: em\_gss\_pro:\*

25: em\_gss\_rod:\*

26: em\_gss\_phg:\*

27: em\_gss\_vrl:\*

28: gb\_gss1:\*

29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	27	100.0	157	10	AW386252 CM4-PT001
C 2	27	100.0	404	14	H81820 Y868e09.t1
C 3	27	100.0	421	12	BM832613 K-EST0107
C 4	27	100.0	781	13	BM097261 BX097261

5	19	70.4	181	10	BE927145
6	19	70.4	875	10	BF973844
C 7	18	66.7	686	12	BI332596
C 8	18	66.7	851	10	BF531871
C 9	17	63.0	539	29	CE192426
C 10	17	63.0	542	29	CE536813
C 11	17	63.0	714	29	CE270642
C 12	17	63.0	778	29	CNS072JP
C 13	17	63.0	780	12	BG206281
C 14	17	63.0	788	28	B2865134
C 15	17	63.0	824	12	BI246488
C 16	17	63.0	874	29	AG160977
C 17	16	59.3	129	14	CF250190
C 18	16	59.3	174	10	BB782656
C 19	16	59.3	192	10	BE522588
C 20	16	59.3	206	12	BI740150
C 21	16	59.3	210	9	AV222166
C 22	16	59.3	238	10	BE525308
C 23	16	59.3	240	10	BE525590
C 24	16	59.3	241	10	BE525578
C 25	16	59.3	241	10	BE530312
C 26	16	59.3	243	10	BB439432
C 27	16	59.3	244	10	BE525566
C 28	16	59.3	247	10	BE525452
C 29	16	59.3	250	10	BE529949
C 30	16	59.3	259	10	BE528577
C 31	16	59.3	265	9	AV140149
C 32	16	59.3	284	9	AV364585
C 33	16	59.3	290	10	BB441430
C 34	16	59.3	297	10	BE522587
C 35	16	59.3	300	10	BE248616
C 36	16	59.3	305	10	BB731714
C 37	16	59.3	306	10	BE524258
C 38	16	59.3	312	13	BY415640
C 39	16	59.3	321	10	BB043130
C 40	16	59.3	321	10	BE523402
C 41	16	59.3	324	9	AI482323
C 42	16	59.3	330	10	BE525407
C 43	16	59.3	331	10	BE525064
C 44	16	59.3	341	9	AJ444339
C 45	16	59.3	341	10	BE525372

#### ALIGNMENTS

RESULT 1  
AW386252/c 157 bp mRNA linear EST 04-FEB-2000  
CM4-PT0015-071299-057-d10 PT0015 Homo sapiens cDNA, mRNA sequence.  
AW386252  
AW386252.1 GI:6890976  
EST.  
Homo sapiens (human)  
ORGANISM  
REFERENCE  
1 (bases 1 to 157)  
HCGP <http://www.ludwig.org.br/ORESTES>.  
The FAPESP/LICR Human Cancer Genome Project  
Unpublished (1999)  
CONTACT: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: [asimpson@ludwig.org.br](mailto:asimpson@ludwig.org.br)  
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL  
(<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CM4&t2=CM4-PT0015-071299-057-d10&t3=1999-12-07&t4=1>)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

```

Seq primer: puc 18 forward
High quality sequence start: 2
High quality sequence stop: 157.
FEATURES
    source
        1..157
            /organism="Homo sapiens"
            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /dev_stage="Adult"
            /clone_lib="PT0015"
            /note="Organ: pnet; Vector: puc18; Site 1: SmaI; Site 2:
            SmaI; A mini-library was made by cloning products derived
            from ORSTES PCR (U.S. Letters Patent application No.
            196,716 - Ludwig Institute for Cancer Research) profiles
            into the pUC 18 vector. Reverse transcription of tissue
            mRNA and cDNA amplification were performed under low
            stringency conditions."
ORIGIN
    Query Match      100.0%; Score 27; DB 10; Length 157;
    Best Local Similarity 100.0%; Pred. No. 6.8e-05;
    Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACTCAGACCTGAGGCTCAAAGTCAGA 27
    |||||
Db 117 ACTCAGACCTGAGGCTCAAAGTCAGA 91

RESULT 2
H81820
LOCUS      404 bp mRNA linear EST 09-NOV-1995
DEFINITION Ys68e09.r1 Soares retina N2b4HR Homo sapiens cDNA clone
IMAGE:219976 5' similar to gb:U14752 PRTO-ONCOGENE
TYROSINE-PROTEIN KINASE ABL (HUMAN);, mRNA sequence.
H81820
ACCESSION H81820.1 GI:1059909
VERSION    1
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
REFERENCE   1 (bases 1 to 404)
AUTHORS    Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevasakis,E., Waterston,R., Williamson,A., Wohldmann,P. and
Wilson,R.
TITLE      The WashU-Merck EST Project
JOURNAL    Unpublished (1995)
COMMENT    Contact: Wilson RK
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence stops: 382
Source: IMAGE Consortium LNL
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.lni.gov) for further information.
Insert Length: 1427 Std Error: 0.00
Seq primer: M13RP1
High quality sequence stop: 382.
FEATURES
    source
        1..404
            /organism="Homo sapiens"
            /mol_type="mRNA"
            /db_xref="GDB:3847969"
            /db_xref="taxon:9606"
            /clone="IMAGE:219976"
            /sex="male"
            /tissue_type="retina"
            /dev_stage="55 year old"
            /lab_host="DH10B (ampicillin resistant)"

```

```

/clone_lib="Soares retina N2b4HR"
/note="Organ: eye; Vector: pT7T3D (Pharmacia) with a
modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTTCATCTGAAGTGGAGCGCGCGCTTTTTTTTTTTTTTTT 3'],
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT7T3 vector
(Pharmacia). The retinas were obtained from a 55 year old
Caucasian and total cellular poly(A)+ RNA was extracted 6
hrs after their removal. The retina RNA was kindly
provided by Roderick R. McInnes M.D. Ph.D. from the
University of Toronto. Library constructed by Bento
Soares and M.Fatima Bonaudo."
ORIGIN
    Query Match      100.0%; Score 27; DB 14; Length 404;
    Best Local Similarity 100.0%; Pred. No. 8.8e-05;
    Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACTCAGACCTGAGGCTCAAAGTCAGA 27
    |||||
Db 75 ACTCAGACCTGAGGCTCAAAGTCAGA 101

RESULT 3
BM832613/c
LOCUS      421 bp mRNA linear EST 06-MAR-2002
DEFINITION K-EST0107122 S11SNUI Homo sapiens cDNA clone S11SNUI-47-E02 5',
mRNA sequence.
BM832613
ACCESSION BM832613.1 GI:19189022
VERSION    1
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
REFERENCE   1 (bases 1 to 421)
AUTHORS    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
Kim,Y.S.
TITLE      21C Frontier Korean EST Project 2001
JOURNAL    Unpublished (2002)
COMMENT    Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 47 row: E column: 02
High quality sequence stop: 421.
FEATURES
    source
        1..421
            /organism="Homo sapiens"
            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /clone="S11SNUI-47-E02"
            /sex="M"
            /tissue_type="Stomach"
            /cell_type="Lymphoblast-like"
            /cell_line="SNU-1"
            /lab_host="Top10p"
            /clone_lib="S11SNUI"
            /note="Organ: Stomach; Vector: pME18-FL3; Site 1: XhoI;
            Site 2: XhoI; The poly (A)+ RNA was dephosphorylated with
            bacterial alkaline phosphatase (BAP) and then decapped
            with tobacco acid pyrophosphatase (TAP). The decapped
            intact mRNA was ligated with DNA-RNA linker including Sfil
            site by treatment of T4 RNA ligase and the first strand
            cDNA was synthesized with Superscript II using Sfil
            oligo-dT primer. After first strand synthesis, RNA was
            degraded by NaOH treatment and cDNA was amplified by PCR

```

reaction. The PCR products were digested with SfiI and cloned into DraIII- digested pME18S-FL3 vector. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10<sup>®</sup> by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."

## ORIGIN

Query Match 100.0%; Score 27; DB 12; Length 421;  
Best Local Similarity 100.0%; Pred. No. 8.9e-05;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACTCAGACCTGAGGCTCAAGTCAGA 27  
|||||  
DB 306 ACTCAGACCTGAGGCTCAAGTCAGA 280

## RESULT 4

EX097261

DEFINITION BX097261 Soares retina N2b4HR Homo sapiens cDNA clone  
IMAGE:998C17436 ; IMAGE:219976, mRNA sequence.

ACCESSION BX097261

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 781)

Ebert, L., Heil, O., Hennig, S., Neubert, P., Partsch, E., Peters, M.,  
Radelof, U., Schneider, D. and Korn, B.

Human Unigeneset - RZPD3

Unpublished (2003)

COMMENT

Contact: Ina Rolfs  
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH

Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany

RZPD; IMAGE998C17436.

RZPDLIB; I.M.A.G.E. cDNA Clone Collection;

Human Unigeneset - RZPD3 (RZPDLIB No.972)

http://www.rzpd.de/CloneCards/cgi-

bin/showLib.pl.cgi?response?libNo=972 Contact: Ina Rolfs

RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH

Heubnerweg 6, D-14059 Berlin, Germany

Tel: +49 30 32639 101

Fax: +49 30 32639 111

www.rzpd.de

This clone is available royalty-free from RZPD;  
contact RZPD (clone@rzpd.de) for further information. Seq primer:

M13r, Primer sequence: TTTCACAGGAAACAGCTATGAC.

Location/Qualifiers

## FEATURES

source

1..781

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE998C17436 ; IMAGE:219976"

/sex="male"

/tissue type="retina"

/dev\_stage="55 year old"

/lab\_host="DH10B (ampicillin resistant)"

/clone\_lib="Soares retina N2b4HR"

/note="Organ: eye; Vector: pT7T3D (Pharmacia) with a  
modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st

strand cDNA was primed with a Not I - oligo(dT) primer [5'  
TGTTACCATCTGAGTGGGCGCGCGCTTTTCTTTTCTTTT 3'].

double-stranded cDNA was size selected, ligated to Eco RI

adapters (Pharmacia), digested with Not I and cloned into

the Not I and Eco RI sites of a modified pT7T3 vector

(Pharmacia). The retinas were obtained from a 55 year old

Caucasian and total cellular poly(A)<sup>+</sup> RNA was extracted 6

hrs after their removal. The retina RNA was kindly

provided by Roderick R. McInnes M.D. Ph.D. from the

University of Toronto. Library constructed by Bento

## ORIGIN

Query Match 100.0%; Score 27; DB 13; Length 781;  
Best Local Similarity 100.0%; Pred. No. 0.00011;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACTCAGACCTGAGGCTCAAGTCAGA 27  
|||||  
DB 55 ACTCAGACCTGAGGCTCAAGTCAGA 81

## RESULT 5

BE927145

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 181)

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,

Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,

Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,

Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V.,

O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and

Simpson, A.J.

Shotgun sequencing of the human transcriptome with ORF expressed

sequence tags

JOURNAL

MEDLINE

PUBMED

COMMENT

Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics

Ludwig Institute for Cancer Research

Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,

Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome

Project. This entry can be seen in the following URL

(http://www.ludwig.org.br/scripts/gethtml2.pl?t1=&t2=RC4-CN0007-010

900-015-e08&t3=2000-09-01&t4=1)

Seq primer: puc 18 forward

High quality sequence start: 57

High quality sequence stop: 130.

Location/Qualifiers

1..181

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/dev\_stage="Adult"

/clone\_lib="CN0007"

/note="Organ: colon normal; Vector: puc18; Site 1: SmaI;

Site 2: SmaI; A mini-library was made by cloning products

derived from ORESTES PCR (U.S. Letters Patent application

No. 196,716 - Ludwig Institute for Cancer Research)

profiles into the pUC 18 vector. Reverse transcription of

tissue mRNA and cDNA amplification were performed under

low stringency conditions."

## ORIGIN

Query Match 70.4%; Score 19; DB 10; Length 181;  
Best Local Similarity 100.0%; Pred. No. 2.2;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACTCAGACCTGAGGCTCA 19  
|||||  
DB 91 ACTCAGACCTGAGGCTCA 109



Site\_2: Salt; Cloned unidirectionally. Primer: Oligo dT.  
Average insert size 1.9 Kb. Constructed by Life  
Technologies. Note: this is a NCI\_CGAP Library."

## ORIGIN

Query Match 66.7%; Score 18; DB 10; Length 851;  
Best Local Similarity 100.0%; Pred. No. 12;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 AGACCCCTGAGGCTCAAAG 22  
|||||

Db 587 AGACCCCTGAGGCTCAAAG 570  
|||||

## RESULT 9

CE192426 539 bp DNA linear GSS 25-SEP-2003  
LOCUS tigr-gss-dog-17000371470877 Dog Library Canis familiaris genomic,  
DEFINITION genomic survey sequence.

ACCESSION CE192426 GI:35348079

VERSION CE192426

KEYWORDS GSS.

SOURCE Canis familiaris (dog)

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

Kirkness, E.F., Bafna, V., Halpern, A.L., Levy, S., Remington, K.,

Rusch, D.B., Delcher, A.L., Pop, M., Wang, W., Fraser, C.M. and

Venter, J.C.

The dog genome: survey sequencing and comparative analysis

Science 301 (5641), 1898-1903 (2003)

22875432

PUBMED 14512627

## COMMENT

Contact: Kirkness EF

The Institute for Genomic Research

Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,

Rockville, MD 20850, USA

Tel: 301-838-0200

Fax: 301-838-0208

Email: ekirknes@tigr.org

Class: shotgun.

## FEATURES

source

1..539

/organism="Canis familiaris"

/mol\_type="genomic DNA"

/strain="Standard Poodle"

/db\_xref="taxon:9615"

/clone\_lib="Dog Library"

/note="Site\_1: BstXI; Libraries were prepared from

peripheral blood"

## ORIGIN

Query Match 63.0%; Score 17; DB 29; Length 539;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ACTCAGACCTGAGGCT 17  
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Db 362 ACTCAGACCTGAGGCT 346  
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## RESULT 10

CE536813/c 542 bp DNA linear GSS 28-SEP-2003  
LOCUS tigr-gss-dog-17000365931015 Dog Library Canis familiaris genomic,  
DEFINITION genomic survey sequence.

ACCESSION CE536813

VERSION CE536813.1 GI:36853594

KEYWORDS GSS.

SOURCE Canis familiaris (dog)

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

1 (bases 1 to 542)

Kirkness, E.F., Bafna, V., Halpern, A.L., Levy, S., Remington, K.,

Rusch, D.B., Delcher, A.L., Pop, M., Wang, W., Fraser, C.M. and

Venter, J.C.

The dog genome: survey sequencing and comparative analysis

Science 301 (5641), 1898-1903 (2003)

22875432

PUBMED 14512627

## COMMENT

Contact: Kirkness EF

The Institute for Genomic Research

Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,

Rockville, MD 20850, USA

Tel: 301-838-0200

Fax: 301-838-0208

Email: ekirknes@tigr.org

Class: shotgun.

## FEATURES

source

1..542

/organism="Canis familiaris"

/mol\_type="genomic DNA"

/strain="Standard Poodle"

/db\_xref="taxon:9615"

/clone\_lib="Dog Library"

/note="Site\_1: BstXI; Libraries were prepared from

peripheral blood"

## ORIGIN

Query Match 63.0%; Score 17; DB 29; Length 542;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TCAGACCTGAGGCTCA 19  
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Db 65 TCAGACCTGAGGCTCA 49  
|||||

## RESULT 11

CE270642 714 bp DNA linear GSS 26-SEP-2003  
LOCUS tigr-gss-dog-1700033537646 Dog Library Canis familiaris genomic,  
DEFINITION genomic survey sequence.

ACCESSION CE270642 GI:36002203

VERSION CE270642

KEYWORDS GSS.

SOURCE Canis familiaris (dog)

ORGANISM Canis familiaris

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

1 (bases 1 to 714)

Kirkness, E.F., Bafna, V., Halpern, A.L., Levy, S., Remington, K.,

Rusch, D.B., Delcher, A.L., Pop, M., Wang, W., Fraser, C.M. and

Venter, J.C.

The dog genome: survey sequencing and comparative analysis

Science 301 (5641), 1898-1903 (2003)

22875432

PUBMED 14512627

## COMMENT

Contact: Kirkness EF

The Institute for Genomic Research

Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,

Rockville, MD 20850, USA

Tel: 301-838-0200

Fax: 301-838-0208

Email: ekirknes@tigr.org

Class: shotgun.

## FEATURES

source

1..714

/organism="Canis familiaris"

/mol\_type="genomic DNA"

/strain="Standard Poodle"

/db\_xref="taxon:9615"

/clone\_lib="Dog Library"

/note="Site\_1: BstXI; Libraries were prepared from

peripheral blood"

/evidence=not\_experimental

## ORIGIN

Query Match 63.0%; Score 17; DB 29; Length 714;  
 Best Local Similarity 100.0%; Pred. No. 43;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TCAGACCCCTGAGGCTCA 19  
 |||||  
 Db 469 TCAGACCCCTGAGGCTCA 485

## RESULT 12

CNS072JP/c 778 bp DNA linear GSS 07-JUL-2001  
 LOCUS clone BA0AB012A05 of library BA0AB from strain CLIB 210 of  
 DEFINITION Kluyveromyces lactis, genomic survey sequence.  
 ACCESSION AL426299  
 VERSION AL426299.1 GI:12209493  
 KEYWORDS GSS.  
 SOURCE Kluyveromyces lactis  
 ORGANISM Kluyveromyces lactis

REFERENCE 1 (bases 1 to 778)  
 AUTHORS Souciet J.L., Aigle M., Artiguenave F., Blandin G.,  
 Bolotin-Fukuhara M., Bon E., Brottier P., Casaregola S.,  
 de-Montigny J., Dujon B., Durrens P., Lepingle A., Llorente B.,  
 Malpertuy A., Neuveglise C., Oxier-Kalogeropoulos O., Potier S.,  
 Saurin W., Tekala F., Toffano-Nioche C., Wesolowski-Louvel M.,  
 Wincker P. and Weissenbach J.

TITLE Genomic exploration of the hemiascomycetous yeasts: 1. A set of  
 yeast species for molecular evolution studies  
 JOURNAL FEBS Lett. 487 (1), 3-12 (2000)  
 MEDLINE 20584711  
 PUBMED 11152876

## REFERENCE

2 (bases 1 to 778)  
 AUTHORS Bolotin-Fukuhara M., Toffano-Nioche C., Artiguenave F.,  
 Duchateau-Nguyen G., Lemaire M., Marmeisse R., Montrocher R.,  
 Robert C., Ternier M., Wincker P. and Wesolowski-Louvel M.  
 TITLE Genomic exploration of the hemiascomycetous yeasts: 11.  
 JOURNAL Kluyveromyces lactis  
 MEDLINE FEBS Lett. 487 (1), 66-70 (2000)  
 PUBMED 20584721

## REFERENCE

3 (bases 1 to 778)  
 Genoscope.  
 Direct Submission  
 Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage,  
 2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail :  
 seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

## COMMENT

This GSS is part of a random genomic sequencing program of thirteen  
 yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces  
 exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii,  
 Saccharomyces kluyveri, Kluyveromyces marxianus var. marxianus, Pichia  
 lactis var. lactis, Kluyveromyces thermotolerans, Kluyveromyces  
 angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila,  
 Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to  
 5 kb were prepared and both extremities were sequenced. See  
 keywords for description of this sequence and for the sequence of  
 the other extremity of this insert.

## FEATURES

Location/Qualifiers  
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 /organism="Kluyveromyces lactis"  
 /mol\_type="genomic DNA"  
 /strain="CLIB 210"  
 /variety="lactis"  
 /db\_xref="taxon:28985"  
 /clone="BA0AB012A05"  
 /clone\_lib="BA0AB"

## misc\_feature

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 /note="similar to Saccharomyces cerevisiae ORF YGR120c [  
 SEC35 ; required for ER to golgi vesicle docking ]"

## ORIGIN

Query Match 63.0%; Score 17; DB 29; Length 778;  
 Best Local Similarity 100.0%; Pred. No. 44;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 TGAGGCTCAAGTCAGA 27  
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 Db 534 TGAGGCTCAAGTCAGA 518

## RESULT 13

BG206281/c 780 bp mRNA linear EST 21-APR-2001  
 LOCUS RST5726 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.  
 DEFINITION BG206281  
 ACCESSION BG206281.1 GI:13727968  
 VERSION EST.  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 780)  
 AUTHORS Harrington J.J., Sherf B., Rundlett S., Jackson P.D., Perry R.,  
 Cain S., Leventhal C., Thornton M., Ramachandran R.,  
 Whittington J., Lerner L., Costanzo D., McElligott K., Booser S.,  
 Mays R., Smith E., Veloso N., Klika A., Hess J., Cothren K., Lo K.,  
 Offenbacher J., Danzig J. and Ducar M.

TITLE Creation of genome-wide protein expression libraries using random  
 activation of gene expression  
 JOURNAL Nat. Biotechnol. 19 (5), 440-445 (2001)  
 MEDLINE 21227151  
 PUBMED 11329013

## COMMENT

Contact: Scott J. Cain  
 Athersys, Inc.  
 3201 Carnegie Ave, Cleveland, OH 44115, USA  
 Tel: 216 431 9900  
 Fax: 216 361 9596  
 Email: scain@atersys.com  
 High quality sequence stop: 425.  
 Location/Qualifiers  
 1..780

source  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /cell\_line="HT1080"

/note="See 'Creation of Genome-wide Protein Expression  
 Libraries using Random Activation of Gene Expression',  
 Nature Biotechnology, in press. Note that even though the  
 cell type indicated is HT1080, since a random activation  
 method was used, these sequence tags are not necessarily  
 expressed in HT1080 under normal circumstances."

## ORIGIN

Query Match 63.0%; Score 17; DB 12; Length 780;  
 Best Local Similarity 100.0%; Pred. No. 44;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TCAGACCCCTGAGGCTCA 19  
 |||||  
 Db 76 TCAGACCCCTGAGGCTCA 60

## RESULT 14

BZ865134/c 788 bp DNA linear GSS 18-MAR-2003  
 LOCUS CH240 235MB.TJ CHORI-240 Bos taurus genomic clone CH240\_235M8,  
 DEFINITION genomic survey sequence.  
 ACCESSION BZ865134  
 VERSION BZ865134.1 GI:29092539  
 KEYWORDS GSS.



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SOURCE      Bos taurus (cow)
ORGANISM
REFERENCE   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS     Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
            Bovinae; Bos.
            1 (bases 1 to 788)
            Zhao, S., Shetty, J., Shateman, S., Tsengaye, G., Geer, K.,
            Shvartsbeyn, A., Gebregorgis, E., Chen, D., Riggs, F., de Jong, P.,
            Crawford, A.M. and McEwan, J.C.
            Bovine BAC End Sequences from Library CHORI-240
            Unpublished (2003)
            Contact: Shaying Zhao
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850, USA
            Tel: 301 838 0200
            Fax: 301 838 0208
            Email: szhao@tigr.org
            Clones are derived from the bovine BAC library CHORI-240
            (http://www.chori.org/bacpac/bovine240.htm). For BAC library
            availability, please contact Pieter de Jong (pdejong@mail.cho.org).
            Clones may be purchased from BACPAC Resources
            (http://www.chori.org/bacpac/ordering/information.htm). This work
            was undertaken as part of the International Bovine BAC Mapping
            Consortium (IBBMC) by AgResearch Ltd., New Zealand and The
            Institute of Genomic Research (TIGR), USA.
            Plate: 235 row: M column: 8
            Seq primer: SP6
            Class: BAC ends.
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            /clone="CH240-235M8"
            /sex="Male"
            /cell_type="Blood"
            /clone_lib="CHORI-240"
            /note="Vector: pTARBAC1.3; Site 1: MboI; Site 2: MboI;
            Hereford bull L1 Domino 99375; CHORI-240 Bovine BAC
            library (Male) produced by Pieter de Jong"

ORIGIN
Query Match      63.0%; Score 17; DB 28; Length 788;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 AGACCTGTAGGCTCAAA 21
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Db      293 AGACCTGTAGGCTCAAA 277

RESULT 15
BI246488/c
LOCUS
DEFINITION 602958537F1 NCI_CGAP_Li9 Mus musculus cDNA clone IMAGE:5124201 5',
            mRNA sequence.
ACCESSION  BI246488
VERSION    BI246488.1 GI:14790501
KEYWORDS
SOURCE     EST.
            Mus musculus (house mouse)
ORGANISM
            Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
            1 (bases 1 to 824)
            NIH-MGC http://mgc.nci.nih.gov/.
            National Institutes of Health, Mammalian Gene Collection (MGC)
            Unpublished (1999)
            Contact: Robert Strausberg, Ph.D.
            Email: cgabbs@mail.nih.gov
            Tissue Procurement: Jeffrey E. Green, M.D.
            cDNA Library Preparation: Life Technologies, Inc.

FEATURES
            source
            Location/Qualifiers
            1..824
            /organism="Mus musculus"
            /mol_type="mRNA"
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            /clone="IMAGE:5124201"
            /lab_host="DH10B (T1 phage-resistant)"
            /clone_lib="NCI CGAP Li9"
            /note="Organ: liver; Vector: pCMV-SPORT6; Site 1: NotI;
            Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
            Average insert size 1.9 kb. Constructed by Life
            Technologies. Note: this is a NCI_CGAP Library."

ORIGIN
Query Match      63.0%; Score 17; DB 12; Length 824;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 GACCCGTGAGGCTCAAG 22
      |||||
Db      567 GACCCGTGAGGCTCAAG 551

Search completed: May 26, 2004, 22:44:37
Job time : 956.308 secs

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FEATURES
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            1..824
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            /note="Organ: liver; Vector: pCMV-SPORT6; Site 1: NotI;
            Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
            Average insert size 1.9 kb. Constructed by Life
            Technologies. Note: this is a NCI_CGAP Library."

ORIGIN
Query Match      63.0%; Score 17; DB 12; Length 824;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 GACCCGTGAGGCTCAAG 22
      |||||
Db      567 GACCCGTGAGGCTCAAG 551

Search completed: May 26, 2004, 22:44:37
Job time : 956.308 secs

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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11303 row: j column: 10
High quality sequence stop: 714.

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 26, 2004, 16:00:31 ; Search time 574.63 Seconds  
(without alignments)  
2036.547 Million cell updates/sec

Title: US-09-121-239-21

Perfect score: 27  
Sequence: 1 ACUCAGACCTGAGGCUCAAAGUCAGA 27

Scoring table: OLIGO\_NUC  
Gapop\_60.0 , Gapext 60.0

Searched: 3470272 seqs, 21671516995 residues

Word size : 0  
Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : GenEmbl :

- 1: gb\_ba:\*
- 2: gb\_htg:\*
- 3: gb\_in:\*
- 4: gb\_om:\*
- 5: gb\_ov:\*
- 6: gb\_pat:\*
- 7: gb\_ph:\*
- 8: gb\_pl:\*
- 9: gb\_pr:\*
- 10: gb\_ro:\*
- 11: gb\_ste:\*
- 12: gb\_sy:\*
- 13: gb\_un:\*
- 14: gb\_vi:\*
- 15: em\_ba:\*
- 16: em\_fun:\*
- 17: em\_hum:\*
- 18: em\_in:\*
- 19: em\_mu:\*
- 20: em\_om:\*
- 21: em\_or:\*
- 22: em\_ov:\*
- 23: em\_pat:\*
- 24: em\_ph:\*
- 25: em\_pl:\*
- 26: em\_ro:\*
- 27: em\_ste:\*
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- 29: em\_vi:\*
- 30: em\_htg\_hum:\*
- 31: em\_htg\_inv:\*
- 32: em\_htg\_other:\*
- 33: em\_htg\_mus:\*
- 34: em\_htg\_pln:\*
- 35: em\_htg\_rod:\*
- 36: em\_htg\_mam:\*
- 37: em\_htg\_vrt:\*
- 38: em\_sy:\*
- 39: em\_htgo\_hum:\*
- 40: em\_htgo\_mus:\*
- 41: em\_htgo\_other:\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	27	100.0	27	6	BD222542	BD222542 Methods f
2	27	100.0	27	6	BD222543	BD222543 Methods f
3	27	100.0	27	6	BD222544	BD222544 Methods f
4	27	100.0	27	6	BD222545	BD222545 Methods f
5	27	100.0	54	6	BD222523	BD222523 Methods f
6	27	100.0	54	6	BD222524	BD222524 Methods f
7	27	100.0	54	6	BD222525	BD222525 Methods f
8	27	100.0	54	6	BD222526	BD222526 Methods f
9	27	100.0	102	9	HST9222FU	X07537 Human ALL t
10	27	100.0	153	9	HUMAB1BB	M14754 Human abl m
11	27	100.0	204	9	HUMBCRA2	M25948 Human chron
12	27	100.0	205	6	I02402	I02402 Sequence 1
13	27	100.0	234	9	HUMCABLA1	M13098 Homo sapien
14	27	100.0	257	6	I58633	I58633 Sequence 1
15	27	100.0	257	6	I96199	I96199 Sequence 36
16	27	100.0	266	6	I58636	I58636 Sequence 4
17	27	100.0	266	6	I96200	I96200 Sequence 37
18	27	100.0	299	6	BD222547	BD222547 Methods f
19	27	100.0	350	6	BD222546	BD222546 Methods f
20	27	100.0	423	9	AB069693	AB069693 Homo sapi
21	27	100.0	468	9	HUMCMLCABL	M25946 Human chron
22	27	100.0	468	9	HUMMK562A	M13096 Human chime
23	27	100.0	491	9	HUMALLBECR	M19730 Human acute
24	27	100.0	494	9	HUMABLC	M30833 Human abl p
25	27	100.0	532	9	HUMABLEA	M14753 Human abl m
26	27	100.0	549	9	HSBREAAP3	Z35761 Homo sapien
27	27	100.0	679	9	HUMABLB	M30832 Human bcr/a
28	27	100.0	854	9	HUMABLD	M30829 Human bcr/a
29	27	100.0	922	9	HSAL131467	AJ131467 Homo sapi
30	27	100.0	997	9	HSAL131466	AJ131466 Homo sapi
31	27	100.0	1078	6	A92081	A92081 Sequence 5
32	27	100.0	1078	6	AR230688	AR230688 Sequence
33	27	100.0	1079	9	AF113911	AF113911 Homo sapi
34	27	100.0	3393	6	AX743957	AX743957 Sequence
35	27	100.0	3623	6	I96198	I96198 Sequence 35
36	27	100.0	3840	6	AX601393	AX601393 Sequence
37	27	100.0	3840	9	HUMABLA	M14752 Human c-abl
38	27	100.0	5527	6	AX411066	AX411066 Sequence
39	27	100.0	5527	9	HSABL	X16416 Human c-abl
40	27	100.0	5744	6	AX779943	AX779943 Sequence
41	27	100.0	84539	6	AX3331986	AX3331986 Sequence
42	27	100.0	84539	9	HSABLGR3	U07563 Human proto
43	27	100.0	176466	9	AL161733	AL161733 Human DNA
44	26	96.3	80	6	I58639	I58639 Sequence 7
45	26	96.3	80	6	I96201	I96201 Sequence 38

ALIGNMENTS

RESULT 1  
BD222542  
LOCUS BD222542 27 bp DNA linear PAT 17-JUL-2003  
DEFINITION Methods for detecting and measuring spliced nucleic acids.  
ACCESSION BD222542  
VERSION BD222542.1 GI:33032312  
KEYWORDS JP 2002521037-A/20  
SOURCE synthetic construct  
ORGANISM artificial sequences.  
REFERENCE 1 (bases 1 to 27)  
AUTHORS Harvey, R.C. and Eastman, P.S.  
TITLE Methods for detecting and measuring spliced nucleic acids  
JOURNAL Patent: JP 2002521037-A 20 16-JUL-2002;  
GEN PROBE INC

```

COMMENT OS Artificial Sequence
PD JP 2002521037-A/20
PF 16-JUL-2002
PR 23-JUL-1999 JP 2000561364
PI 23-JUL-1998 US 09/121239
PT RICHARD C HARVEY, PAUL S EASTMAN
PC C12Q1/68, C12N15/09, C12N15/00
CC Description of Artificial Sequence: Primer sequence as in SEQ
CC ID NO:1 but
CC without T7 promoter sequence
FH Key Location/Qualifiers
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FEATURES
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Location/Qualifiers
1..27
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Best Local Similarity 85.2%; Pred. No. 0.0001;
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QY 1 ACUCAGACCCUGAGGCUCAAGUCAGA 27
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Db 1 ACTCAGACCTGAGGCTCAAGTCAGA 27
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DEFINITION Methods for detecting and measuring spliced nucleic acids.
ACCESSION BD222543
VERSION BD222543.1 GI:33032313
KEYWORDS JP 2002521037-A/21.
SOURCE synthetic construct
ORGANISM artificial construct
REFERENCE 1 (bases 1 to 27)
AUTHORS Harvey, R.C. and Eastman, P.S.
TITLE Methods for detecting and measuring spliced nucleic acids
JOURNAL Patent: JP 2002521037-A 21 16-JUL-2002;
GEN PROBE INC
COMMENT OS Artificial Sequence
PD JP 2002521037-A/21
PF 16-JUL-2002
PR 23-JUL-1999 JP 2000561364
PI 23-JUL-1998 US 09/121239
PT RICHARD C HARVEY, PAUL S EASTMAN
PC C12Q1/68, C12N15/09, C12N15/00
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CC 20
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source
Location/Qualifiers
1..27
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/db_xref="taxon:32630"
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Best Local Similarity 85.2%; Pred. No. 0.0001;
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QY 1 ACUCAGACCCUGAGGCUCAAGUCAGA 27
||:|||||:|||||:|||||:|||||
Db 1 ACTCAGACCTGAGGCTCAAGTCAGA 27
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RESULT 3
LOCUS BD222545/c 27 bp RNA linear PAT 17-JUL-2003
DEFINITION Methods for detecting and measuring spliced nucleic acids.
ACCESSION BD222545
VERSION BD222545.1 GI:33032315
KEYWORDS JP 2002521037-A/23.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 27)
AUTHORS Harvey, R.C. and Eastman, P.S.
TITLE Methods for detecting and measuring spliced nucleic acids
JOURNAL Patent: JP 2002521037-A 23 16-JUL-2002;
GEN PROBE INC
COMMENT OS Artificial Sequence
PD JP 2002521037-A/23
PF 16-JUL-2002
PR 23-JUL-1999 JP 2000561364
PI 23-JUL-1998 US 09/121239
PT RICHARD C HARVEY, PAUL S EASTMAN
PC C12Q1/68, C12N15/09, C12N15/00
CC Description of Artificial Sequence: RNA version of SEQ ID NO:
CC 22
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FT source 1..27
FT /organism="Artificial Sequence".
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source
Location/Qualifiers
1..27
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BD222544/c
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DEFINITION Methods for detecting and measuring spliced nucleic acids.
ACCESSION BD222544
VERSION BD222544.1 GI:33032314
KEYWORDS JP 2002521037-A/22.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 27)
AUTHORS Harvey, R.C. and Eastman, P.S.
TITLE Methods for detecting and measuring spliced nucleic acids
JOURNAL Patent: JP 2002521037-A 22 16-JUL-2002;
GEN PROBE INC
COMMENT OS Artificial Sequence
PD JP 2002521037-A/22
PF 16-JUL-2002
PR 23-JUL-1999 JP 2000561364
PI 23-JUL-1998 US 09/121239
PT RICHARD C HARVEY, PAUL S EASTMAN
PC C12Q1/68, C12N15/09, C12N15/00
CC Description of Artificial Sequence: Reverse complement of SEQ
CC ID NO:20
FH Key Location/Qualifiers
FT source 1..27
FT /organism="Artificial Sequence".
FEATURES
source
Location/Qualifiers
1..27
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/mol_type="genomic DNA"
/db_xref="taxon:32630"
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Query Match 100.0%; Score 27; DB 6; Length 27;
Best Local Similarity 85.2%; Pred. No. 0.0001;
Matches 23; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
QY 1 ACUCAGACCCUGAGGCUCAAGUCAGA 27
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Db 27 ACTCAGACCTGAGGCTCAAGTCAGA 1
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RESULT 4
LOCUS BD222545/c 27 bp RNA linear PAT 17-JUL-2003
DEFINITION Methods for detecting and measuring spliced nucleic acids.
ACCESSION BD222545
VERSION BD222545.1 GI:33032315
KEYWORDS JP 2002521037-A/23.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 27)
AUTHORS Harvey, R.C. and Eastman, P.S.
TITLE Methods for detecting and measuring spliced nucleic acids
JOURNAL Patent: JP 2002521037-A 23 16-JUL-2002;
GEN PROBE INC
COMMENT OS Artificial Sequence
PD JP 2002521037-A/23
PF 16-JUL-2002
PR 23-JUL-1999 JP 2000561364
PI 23-JUL-1998 US 09/121239
PT RICHARD C HARVEY, PAUL S EASTMAN
PC C12Q1/68, C12N15/09, C12N15/00
CC Description of Artificial Sequence: RNA version of SEQ ID NO:
CC 22
FH Key Location/Qualifiers
FT source 1..27
FT /organism="Artificial Sequence".
FEATURES
source
Location/Qualifiers
1..27
/organism="synthetic construct"
/mol_type="genomic RNA"

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ORIGIN
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Best Local Similarity 85.2%; Pred. No. 0.0001;
Matches 23; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACUCAGACCCUGAGGCUCAAAAGUCAGA 27
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Db 27 ACTCAGACCTGAGGCTCAAAGTCAGA 1

RESULT 5
LOCUS BD222523 54 bp DNA linear PAT 17-JUL-2003
DEFINITION Methods for detecting and measuring spliced nucleic acids.
ACCESSION BD222523
VERSION BD222523.1 GI:33032293
KEYWORDS JP 2002521037-A/1.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 54)
AUTHORS Harvey,R.C. and Eastman,P.S.
TITLE Methods for detecting and measuring spliced nucleic acids
JOURNAL Patent: JP 2002521037-A 1 16-JUL-2002;
GEN PROBE INC
COMMENT OS Artificial Sequence
PN JP 2002521037-A/1
PD 16-JUL-2002
PP 23-JUL-1999 JP 2000561364
PR RICHARD C HARVEY,PAUL S EASTMAN
PI C12Q1/68,C12N15/09,C12N15/00
PC Description of Artificial Sequence: Synthetic promoter primer
CC including T7
CC promoter sequence at residues 1-27
FH Key Location/Qualifiers
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FEATURES
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Best Local Similarity 85.2%; Pred. No. 8.8e-05;
Matches 23; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

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Db 27 ACTCAGACCTGAGGCTCAAAGTCAGA 1

RESULT 6
LOCUS BD222524 54 bp RNA linear PAT 17-JUL-2003
DEFINITION Methods for detecting and measuring spliced nucleic acids.
ACCESSION BD222524
VERSION BD222524.1 GI:33032294
KEYWORDS JP 2002521037-A/2.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 54)
AUTHORS Harvey,R.C. and Eastman,P.S.
TITLE Methods for detecting and measuring spliced nucleic acids
JOURNAL Patent: JP 2002521037-A 2 16-JUL-2002;
GEN PROBE INC
COMMENT OS Artificial Sequence
PN JP 2002521037-A/2

ORIGIN
Query Match      100.0%; Score 27; DB 6; Length 54;
Best Local Similarity 85.2%; Pred. No. 8.8e-05;
Matches 23; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACUCAGACCCUGAGGCUCAAAAGUCAGA 27
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Db 28 ACTCAGACCTGAGGCTCAAAGTCAGA 54

RESULT 7
LOCUS BD222525/c 54 bp DNA linear PAT 17-JUL-2003
DEFINITION Methods for detecting and measuring spliced nucleic acids.
ACCESSION BD222525
VERSION BD222525.1 GI:33032295
KEYWORDS JP 2002521037-A/3.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 54)
AUTHORS Harvey,R.C. and Eastman,P.S.
TITLE Methods for detecting and measuring spliced nucleic acids
JOURNAL Patent: JP 2002521037-A 3 16-JUL-2002;
GEN PROBE INC
COMMENT OS Artificial Sequence
PN JP 2002521037-A/3
PD 16-JUL-2002
PP 23-JUL-1999 JP 2000561364
PR RICHARD C HARVEY,PAUL S EASTMAN
PI C12Q1/68,C12N15/09,C12N15/00
PC Description of Artificial Sequence: Reverse complement of SEQ
CC ID NO:1
FH Key Location/Qualifiers
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Query Match      100.0%; Score 27; DB 6; Length 54;
Best Local Similarity 85.2%; Pred. No. 8.8e-05;
Matches 23; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACUCAGACCCUGAGGCUCAAAAGUCAGA 27
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Db 27 ACTCAGACCTGAGGCTCAAAGTCAGA 1

RESULT 8
LOCUS BD222526/c 54 bp RNA linear PAT 17-JUL-2003
DEFINITION Methods for detecting and measuring spliced nucleic acids.
ACCESSION BD222526
VERSION BD222526.1 GI:33032296
KEYWORDS JP 2002521037-A/2.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 54)
AUTHORS Harvey,R.C. and Eastman,P.S.
TITLE Methods for detecting and measuring spliced nucleic acids
JOURNAL Patent: JP 2002521037-A 2 16-JUL-2002;
GEN PROBE INC
COMMENT OS Artificial Sequence
PN JP 2002521037-A/2
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VERSION      BD22526.1  GI:33032296
KEYWORDS     JP 2002521037-A/4.
SOURCE       synthetic construct
ORGANISM     artificial sequences.
REFERENCE    1 (bases 1 to 54)
AUTHORS      Harvey,R.C. and Eastman,P.S.
TITLE        Methods for detecting and measuring spliced nucleic acids
JOURNAL      Patent: JP 2002521037-A 4 16-JUL-2002;
COMMENT      GEN PROBE INC
OS           Artificial Sequence
PN           JP 2002521037-A/4
PD           16-JUL-2002
PF           23-JUL-1999  JP 2000561364
PR           23-JUL-1998  US 09/121239
PI           RICHARD C HARVEY, PAUL S EASTMAN
PC           C12Q1/68,C12N15/09,C12N15/00
CC           Description of Artificial Sequence: RNA version of SEQ ID NO:3
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Best Local Similarity 85.2%; Pred. No. 8.8e-05;
Matches 23; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ACUCAGACCCUGAGGCUCAAGUCAGA 27
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Db 27 ACTCAGACCCGTGAGGCTCAAAGTCAGA 1

RESULT 9
HST922FU/c
LOCUS       Human ALL t(9;22)(q34;q11) mRNA for bcr-abl fusion protein (ALL =
DEFINITION acute lymphoblastic leukaemia).
VERSION     X07537.1  GI:36673
KEYWORDS    bcr gene; breakpoint cluster region gene; c-abl gene; cellular
SOURCE      Homo sapiens (human)
ORGANISM    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 102)
AUTHORS     ar-Rushdi,A., Negrini,M., Kurzrock,R., Huebner,K. and Croce,C.M.
TITLE       Fusion of the bcr and the c-abl genes in ph'-positive acute
            lymphocytic leukemia with no rearrangement in the breakpoint
            cluster region
JOURNAL     Oncogene 2 (4), 353-357 (1988)
MEDLINE     88202926
PUBMED      3283653
FEATURES     Location/Qualifiers
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              /db_xref="RENTREMBL:CAA30410"
              /translation="QIWPNDGEGAFHGDAELQRPVASFPEQGLSEA"
              misc_feature <1..46

misc_feature /note="bcr protein (1st exon region 1812)"
46..47
/note="site of fusion of bcr and abl"
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/note="abl protein (2nd exon region)"

ORIGIN
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Best Local Similarity 85.2%; Pred. No. 7.6e-05;
Matches 23; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ACUCAGACCCUGAGGCUCAAGUCAGA 27
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Db 96 ACTCAGACCCGTGAGGCTCAAAGTCAGA 70

RESULT 10
HUMABLB/c
LOCUS       Human abl mRNA containing alternative first exons.
DEFINITION M14754.1  GI:177947
ACCESSION   M14754
VERSION     c-myc proto-oncogene; protein kinase.
KEYWORDS    Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 153)
AUTHORS     Shtivelman,E., Lifshitz,B., Gale,R.P., Roe,B.A. and Canaani,E.
TITLE       Alternative splicing of RNAs transcribed from the human abl gene
            and from the bcr-abl fused gene
JOURNAL     Cell 47 (2), 277-284 (1986)
MEDLINE     87028219
PUBMED      3021337
COMMENT     Original source text: Human cDNA to mRNA, clone P18.
FEATURES     Location/Qualifiers
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              1..153
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              /mol_type="mRNA"
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Best Local Similarity 85.2%; Pred. No. 7e-05;
Matches 23; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

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Db 144 ACTCAGACCCGTGAGGCTCAAAGTCAGA 118

RESULT 11
HUMBCRA2/c
LOCUS       Human chronic myelocytic leukemia c-abl oncogene breakpoint cluster
DEFINITION region (bcr) DNA, exon al.
ACCESSION   M25948
VERSION     M25948.1  GI:179382
KEYWORDS    breakpoint cluster region; c-abl oncogene; chronic myelocytic
            leukemia.
SEGMENT     2 of 3
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SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 204)  
AUTHORS De Klein, A., Hermans, A., Bootsma, D., Grosveld, G., Heisterkamp, N., Stam, K. and Groffen, J.  
TITLE The role of the Philadelphia translocation in chronic myelocytic leukemia  
JOURNAL Ann. Clin. Res. 18 (5-6), 278-283 (1986)  
MEDLINE 87183193  
PUBMED 3471171  
COMMENT Original source text: Human fibroblast cell line K562, cDNA to mRNA, clone pVI-3.  
FEATURES  
source  
Location/Qualifiers  
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/organism="Homo sapiens"  
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Query Match 100.0%; Score 27; DB 9; Length 204;  
Best Local Similarity 85.2%; Pred. No. 6.5e-05;  
Matches 23; Conservative 4; Mismatches 0; Indels 0; Gaps 0;  
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Query Match 100.0%; Score 27; DB 9; Length 204;  
Best Local Similarity 85.2%; Pred. No. 6.5e-05;  
Matches 23; Conservative 4; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ACUCAGACCCUGAGGCUCAAAAGUCAGA 27  
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RESULT 12  
102402/c  
LOCUS I02402 Sequence 1 from Patent US 4874853 linear PAT 21-MAY-1993  
DEFINITION I02402  
ACCESSION I02402.1 GI:270541  
VERSION I02402.1  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 205)  
AUTHORS Rossi, J.J.  
TITLE Synthetic oligonucleotides useful in diagnosis of chronic myelogenous leukemia  
JOURNAL Patent: US 4874853-A 1 17-OCT-1989;  
City of Hope; Duarte, CA  
FEATURES  
source  
Location/Qualifiers  
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Best Local Similarity 85.2%; Pred. No. 6.5e-05;  
Matches 23; Conservative 4; Mismatches 0; Indels 0; Gaps 0;  
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Db 156 ACTCAGACCCCTGAGGCTCAAGTCAGA 130  
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RESULT 13  
HUMCABL1/c HUMCABL1 234 bp DNA linear PRI 04-MAY-2000  
LOCUS HUMCABL1  
DEFINITION Homo sapiens c-abl (ABL) gene, exon al.  
ACCESSION M13098  
VERSION M13098.1 GI:179747  
KEYWORDS  
SEGMENT 1 of 2  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 234)  
AUTHORS Grosveld, G., Verwoerd, T., van Aghoven, T., de Klein, A., Ranachandran, K.L., Heisterkamp, N., Stam, K. and Groffen, J.  
TITLE The chronic myelocytic cell line K562 contains a breakpoint in bcr and produces a chimeric bcr/c-abl transcript  
JOURNAL Mol. Cell. Biol. 6 (2), 607-616 (1986)  
MEDLINE 87064346  
PUBMED 3023859  
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Location/Qualifiers  
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Db 80 ACTCAGACCCCTGAGGCTCAAGTCAGA 54  
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RESULT 14  
158633/c  
LOCUS I58633 Sequence 1 from patent US 5652222. linear PAT 07-OCT-1997  
DEFINITION I58633  
ACCESSION I58633  
VERSION I58633.1 GI:2477871  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 257)  
AUTHORS Calabretta, B. and Gewirtz, A.M.  
TITLE Selective inhibition of leukemic cell proliferation by bcr-abl antisense oligonucleotides  
JOURNAL Patent: US 5652222-A 1 29-JUL-1997;  
Location/Qualifiers  
1..257  
/organism="unknown"  
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Best Local Similarity 85.2%; Pred. No. 6.2e-05;  
Matches 23; Conservative 4; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ACUCAGACCCUGAGGCUCAAAAGUCAGA 27  
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Db 81 ACTCAGACCCCTGAGGCTCAAGTCAGA 55  
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RESULT 15  
196199/c  
LOCUS I96199 Sequence 36 from patent US 5734039. linear PAT 01-DEC-1998  
DEFINITION I96199  
ACCESSION I96199  
VERSION I96199.1 GI:3940669  
KEYWORDS

SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 257)  
AUTHORS Calabretta, B. and Skorski, T.  
TITLE Antisense oligonucleotides targeting cooperating oncogenes  
JOURNAL Patent: US 5734039-A 36 31-MAR-1998;  
FEATURES Location/Qualifiers  
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Db 81 ACTCAGACCCCTGAGGCTCAAAAGTCAGA 55

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Job time : 574.63 secs



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OM nucleic - nucleic search, using sw model

Run on: May 26, 2004, 14:55:11 ; Search time 120.416 Seconds  
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Title: US-09-121-239-21

Perfect score: 27

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Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 3373863 seqs, 2124099041 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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4: Geneseqn2001as:\*  
5: Geneseqn2001bs:\*  
6: Geneseqn2002s:\*  
7: Geneseqn2003as:\*  
8: Geneseqn2003bs:\*  
9: Geneseqn2003cs:\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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C 1	27	100.0	27	3 AAZ60861	Aaz60861 Oligonucleotide
C 2	27	100.0	27	3 AAZ60862	Aaz60862 Oligonucleotide
C 3	27	100.0	27	3 AAZ60860	Aaz60860 Oligonucleotide
C 4	27	100.0	27	3 AAZ60859	Aaz60859 Oligonucleotide
C 5	27	100.0	54	3 AAZ60843	Aaz60843 Oligonucleotide
C 6	27	100.0	54	3 AAZ60841	Aaz60841 Oligonucleotide
C 7	27	100.0	54	3 AAZ60840	Aaz60840 Oligonucleotide
C 8	27	100.0	54	3 AAZ60842	Aaz60842 Oligonucleotide
C 9	27	100.0	205	1 AAN91666	Aan91666 Bcr-abl fusion
C 10	27	100.0	257	2 AAQ34625	Aaq34625 Human bcr
C 11	27	100.0	257	2 AAV20458	Aav20458 Human bcr
C 12	27	100.0	266	2 AAQ34628	Aaq34628 Human bcr
C 13	27	100.0	266	2 AAV20459	Aav20459 Human bcr
C 14	27	100.0	299	3 AAZ60864	Aaz60864 Region su
C 15	27	100.0	350	3 AAZ60863	Aaz60863 Region su
C 16	27	100.0	423	6 ABS73179	Abs73179 DNA encod
C 17	27	100.0	468	6 ABS73171	Abs73171 Human tra
C 18	27	100.0	549	6 ABS73314	Abs73314 DNA encod
C 19	27	100.0	679	6 ABS73172	Abs73172 DNA encod
C 20	27	100.0	854	6 ABS73170	Abs73170 DNA encod
C 21	27	100.0	921	5 AAS85025	Aas85025 DNA encod
C 22	27	100.0	922	6 ABS73180	Abs73180 DNA encod
C 23	27	100.0	997	6 ABS73173	Abs73173 DNA encod

C 24	27	100.0	1024	7 ABZ82900	Abz82900 Toxicolog
C 25	27	100.0	1079	5 AAS85026	Aas85026 DNA encod
C 26	27	100.0	1079	5 ABS73181	Abs73181 DNA encod
C 27	27	100.0	1097	2 AAT91764	Aat91764 Chimeric
C 28	27	100.0	1212	5 AAS85028	Aas85028 DNA encod
C 29	27	100.0	3323	7 ABZ18519	Abz18519 Group III
C 30	27	100.0	3380	7 ABZ18520	Abz18520 Group III
C 31	27	100.0	3393	7 ABX95815	Abx95815 cDNA enco
C 32	27	100.0	3623	2 AAV20457	Aav20457 Human c-a
C 33	27	100.0	3780	2 AAT61864	Aat61864 c-abl gen
C 34	27	100.0	3840	7 AAD52781	Aad52781 Human Abl
C 35	27	100.0	5434	6 ABV77964	Abv77964 Hypoxia-r
C 36	27	100.0	5520	2 AAT61865	Aat61865 c-abl gen
C 37	27	100.0	5527	6 ABN97215	Abn97215 Gene #371
C 38	27	100.0	84539	6 ABL64158	AbL64158 Stomach c
C 39	26	96.3	80	2 AAQ34631	Aaq34631 Human bcr
C 40	26	96.3	80	2 AAV20460	Aav20460 Human bcr
C 41	25	92.6	200	2 AAT88785	Aat88785 Leukaemic
C 42	24	88.9	50	2 AAQ86626	Aaq86626 CML chrom
C 43	24	88.9	50	2 AAT15571	Aat15571 CML-2 chr
C 44	24	88.9	50	2 AAT42417	Aat42417 CML chrom
C 45	24	88.9	50	2 AAV66349	Aav66349 CML-2 chr

## ALIGNMENTS

RESULT 1  
AAZ60861/c  
ID AAZ60861 standard; DNA; 27 BP.  
XX  
AC AAZ60861;  
XX  
DT 16-MAY-2000 (first entry)  
XX  
DE Oligonucleotide used to detect bcr b3-abl fusion transcripts.  
XX  
KW Fusion transcript; translocation; bcr b3 region; abl gene;  
KW amplification assay; detection assay; medical diagnosis;  
KW clinical monitoring; chimeric RNA; fusion RNA; condition marker;  
KW disease marker; cancer; leukemia; ss.  
XX  
OS Synthetic.  
XX  
PN WO200005418-A1.  
XX  
PD 03-FEB-2000.  
XX  
PF 23-JUL-1999; 99WO-US016832.  
XX  
PR 23-JUL-1998; 98US-00121239.  
XX  
PA (GENP-) GEN-PROBE INC.  
XX  
PI Harvey RC, Eastman PS;  
XX  
DR WPI; 2000-182730/16.  
XX  
PT Novel methods for preparing RNA from biological samples, used for the  
XX detection and measurement of nucleic acids and fusion nucleic acids.  
XX  
PS Claim 19; Page 43; 49pp; English.  
XX  
CC Oligonucleotides AAZ60840-62 and AAZ60865-66 are used in the method of  
CC the invention to detect fusion transcripts produced from a translocation  
CC between the bcr b3 region and the abl gene. The specification describes a  
CC method for detecting a fusion nucleic acid (particularly chimeric mRNA  
CC species), in a biological sample. The method comprises contacting a  
CC sample of fusion nucleic acid with primers, amplifying the hybridized  
CC fusion nucleic acid, and detecting the target hybrid. The method is used  
CC for the simple and rapid preparation of RNA from a biological sample,  
CC particularly from the cytoplasm of eukaryotic cells, which is suitable  
CC for use in an amplification and detection assay. The methods are used for

CC the analysis and detection of nucleic acids in biological samples. The  
CC methods are useful in the human medical and veterinary fields, for  
CC medical diagnoses and clinical monitoring of a patient's response to  
CC therapy where a disease or medical condition is associated with a  
CC particular type and/or level of mRNA present in the sample. The methods  
CC are also useful for detecting or quantifying fusion or chimeric RNA  
CC species, and for detecting a translocation as a marker for a given  
CC condition or disease, e.g. translocations associated with cancers,  
CC particularly forms of leukemia

XX Sequence 27 BP; 4 A; 6 C; 8 G; 9 T; 0 U; 0 Other;  
SQ Query Match 100.0%; Score 27; DB 3; Length 27;  
Best Local Similarity 85.2%; Pred. No. 3.9e-05;  
Matches 23; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACUCAGACCCUGAGGCUCAAAAGUCAGA 27  
Db 27 ACTCAGACCCGTGAGGCTCAAAGTCAGA 1  
||:|||||:|||||:|||||:|||||

RESULT 2  
AAZ60862/c  
ID AAZ60862 standard; RNA; 27 BP.  
XX  
AC AAZ60862;  
XX  
DT 16-MAY-2000 (first entry)  
DE Oligonucleotide used to detect bcr b3-abl fusion transcripts.  
XX  
KW Fusion transcript; translocation; bcr b3 region; abl gene;  
KW amplification assay; detection assay; medical diagnosis;  
KW clinical monitoring; chimeric RNA; fusion RNA; condition marker;  
KW disease marker; cancer; leukemia; ss.  
XX  
OS Synthetic.  
XX  
PN WO200005418-A1.  
XX  
PD 03-FEB-2000.  
XX  
PF 23-JUL-1999; 99WO-US016832.  
XX  
PR 23-JUL-1998; 98US-00121239.  
XX  
PA (GENP-) GEN-PROBE INC.  
XX  
PI Harvey RC, Eastman PS;  
XX  
DR WPI; 2000-182730/16.  
XX  
PS Claim 19; Page 44; 49pp; English.  
XX  
CC Oligonucleotides AAZ60840-62 and AAZ60865-66 are used in the method of  
CC the invention to detect fusion transcripts produced from a translocation  
CC between the bcr b3 region and the abl gene. The specification describes a  
CC method for detecting a fusion nucleic acid (particularly chimeric RNA  
CC species), in a biological sample. The method comprises contacting a  
CC sample of fusion nucleic acid with primers, amplifying the hybridized  
CC fusion nucleic acid, and detecting the target hybrid. The method is used  
CC for the simple and rapid preparation of RNA from a biological sample,  
CC particularly from the cytoplasm of eukaryotic cells, which is suitable  
CC for use in an amplification and detection assay. The methods are used for  
CC the analysis and detection of nucleic acids in biological samples. The  
CC methods are useful in the human medical and veterinary fields, for  
CC medical diagnoses and clinical monitoring of a patient's response to  
CC therapy where a disease or medical condition is associated with a  
CC particular type and/or level of mRNA present in the sample. The methods  
CC are also useful for detecting or quantifying fusion or chimeric RNA  
CC species, and for detecting a translocation as a marker for a given  
CC condition or disease, e.g. translocations associated with cancers,  
CC particularly forms of leukemia

CC species, and for detecting a translocation as a marker for a given  
CC condition or disease, e.g. translocations associated with cancers,  
CC particularly forms of leukemia

XX Sequence 27 BP; 4 A; 6 C; 8 G; 0 T; 9 U; 0 Other;  
SQ Query Match 100.0%; Score 27; DB 3; Length 27;  
Best Local Similarity 85.2%; Pred. No. 3.9e-05;  
Matches 23; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACUCAGACCCUGAGGCUCAAAAGUCAGA 27  
Db 27 ACTCAGACCCGTGAGGCTCAAAGTCAGA 1  
||:|||||:|||||:|||||:|||||

RESULT 3  
AAZ60860  
ID AAZ60860 standard; RNA; 27 BP.  
XX  
AC AAZ60860;  
XX  
DT 16-MAY-2000 (first entry)  
DE Oligonucleotide used to detect bcr b3-abl fusion transcripts.  
XX  
KW Fusion transcript; translocation; bcr b3 region; abl gene;  
KW amplification assay; detection assay; medical diagnosis;  
KW clinical monitoring; chimeric RNA; fusion RNA; condition marker;  
KW disease marker; cancer; leukemia; ss.  
XX  
OS Synthetic.  
XX  
PN WO200005418-A1.  
XX  
PD 03-FEB-2000.  
XX  
PF 23-JUL-1999; 99WO-US016832.  
XX  
PR 23-JUL-1998; 98US-00121239.  
XX  
PA (GENP-) GEN-PROBE INC.  
XX  
PI Harvey RC, Eastman PS;  
XX  
DR WPI; 2000-182730/16.  
XX  
PS Novel methods for preparing RNA from biological samples, used for the  
detection and measurement of nucleic acids and fusion nucleic acids.  
XX  
PS Claim 19; Page 43; 49pp; English.  
XX  
CC Oligonucleotides AAZ60840-62 and AAZ60865-66 are used in the method of  
CC the invention to detect fusion transcripts produced from a translocation  
CC between the bcr b3 region and the abl gene. The specification describes a  
CC method for detecting a fusion nucleic acid (particularly chimeric RNA  
CC species), in a biological sample. The method comprises contacting a  
CC sample of fusion nucleic acid with primers, amplifying the hybridized  
CC fusion nucleic acid, and detecting the target hybrid. The method is used  
CC for the simple and rapid preparation of RNA from a biological sample,  
CC particularly from the cytoplasm of eukaryotic cells, which is suitable  
CC for use in an amplification and detection assay. The methods are used for  
CC the analysis and detection of nucleic acids in biological samples. The  
CC methods are useful in the human medical and veterinary fields, for  
CC medical diagnoses and clinical monitoring of a patient's response to  
CC therapy where a disease or medical condition is associated with a  
CC particular type and/or level of mRNA present in the sample. The methods  
CC are also useful for detecting or quantifying fusion or chimeric RNA  
CC species, and for detecting a translocation as a marker for a given  
CC condition or disease, e.g. translocations associated with cancers,  
CC particularly forms of leukemia

XX Sequence 27 BP; 9 A; 8 C; 6 G; 0 T; 4 U; 0 Other;

Db 1 ACTCAGACCCCTGAGGCTCAAAGTCAGA 27

RESULT 5  
AAZ60843/C  
ID AAZ60843 standard; RNA; 54 BP.  
XX AC  
XX AAZ60843;  
XX 16-MAY-2000 (first entry)  
XX DE Oligonucleotide used to detect bcr b3-abl fusion transcripts.  
XX KW Fusion transcript; translocation; bcr b3 region; abl gene;  
KW amplification assay; detection assay; medical diagnosis;  
KW clinical monitoring; chimeric RNA; fusion RNA; condition marker;  
KW disease marker; cancer; leukemia; sg.  
XX OS Synthetic.  
OS WO200005418-A1.  
PN XX  
XX PD 03-FEB-2000.  
XX PF 23-JUL-1999; 99WO-US016832.  
XX PR 23-JUL-1998; 98US-00121239.  
XX PA (GENP-) GEN-PROBE INC.  
XX PI Harvey RC, Eastman PS;  
XX WPI; 2000-182730/16.  
XX DR  
XX PT Novel methods for preparing RNA from biological samples, used for the  
XX detection and measurement of nucleic acids and fusion nucleic acids.  
XX Claim 19; Page 40; 49pp; English.  
XX CC Oligonucleotides AAZ60840-62 and AAZ60865-66 are used in the method of  
CC the invention to detect fusion transcripts produced from a translocation a  
CC between the bcr b3 region and the abl gene. The specification describes a  
CC method for detecting a fusion nucleic acid (particularly chimeric mRNA  
CC species), in a biological sample. The method comprises contacting a  
CC sample of fusion nucleic acid with primers, amplifying the hybridized  
CC fusion nucleic acid, and detecting the target hybrid. The method is used  
CC for the simple and rapid preparation of RNA from a biological sample,  
CC particularly from the cytoplasm of eukaryotic cells, which is suitable  
CC for use in an amplification and detection assay. The methods are used for  
CC the analysis and detection of nucleic acids in biological samples. The  
CC methods are useful in the human medical and veterinary fields, for  
CC medical diagnoses and clinical monitoring of a patient's response to  
CC therapy where a disease or medical condition is associated with a  
CC particular type and/or level of mRNA present in the sample. The methods  
CC are also useful for detecting or quantifying fusion or chimeric RNA  
CC species, and for detecting a translocation as a marker for a given  
CC condition or disease, e.g. translocations associate with cancers,  
CC particularly forms of leukemia  
XX SQ Sequence 54 BP; 11 A; 11 C; 12 G; 0 T; 20 U; 0 Other;

Query Match 100.0%; Score 27; DB 3; Length 54;  
Best Local Similarity 85.2%; Pred. No. 3.8e-05;  
Matches 23; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACUCAGACCCUGAGGCUCAAAUGCAGA 27  
||:|||||:||:|||||:  
27 ACTCAGACCCCTGAGGCTCAAAGTCAGA 1

Db  
RESULT 6  
AAZ60841  
ID AAZ60841 standard; RNA; 54 BP.

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XX AC AAZ60841;
XX DT 16-MAY-2000 (first entry)
XX DE Oligonucleotide used to detect bcr b3-abl fusion transcripts.
XX DE Fusion transcript; translocation; bcr b3 region; abl gene;
XX KW amplification assay; detection assay; medical diagnosis;
XX KW clinical monitoring; chimeric RNA; fusion RNA; condition marker;
XX KW disease marker; cancer; leukemia; ss.
XX OS Synthetic.
XX PN WO200005418-A1.
XX PD 03-FEB-2000.
XX PF 23-JUL-1999; 99WO-US016832.
XX PR 23-JUL-1998; 98US-00121239.
XX PA (GENP-) GEN-PROBE INC.
XX PI Harvey RC, Eastman PS;
XX PI WPI; 2000-182730/16.
XX DR Novel methods for preparing RNA from biological samples, used for the
XX PT detection and measurement of nucleic acids and fusion nucleic acids.
XX PS Claim 19; Page 40; 49pp; English.
XX CC Oligonucleotides AAZ60840-62 and AAZ60865-66 are used in the method of
XX CC the invention to detect fusion transcripts produced from a translocation
XX CC between the bcr b3 region and the abl gene. The specification describes a
XX CC method for detecting a fusion nucleic acid (particularly chimeric mRNA
XX CC species), in a biological sample. The method comprises contacting a
XX CC sample of fusion nucleic acid with primers, amplifying the hybridized
XX CC fusion nucleic acid, and detecting the target hybrid. The method is used
XX CC for the simple and rapid preparation of RNA from a biological sample,
XX CC particularly from the cytoplasm of eukaryotic cells, which is suitable
XX CC for use in an amplification and detection assay. The methods are used for
XX CC the analysis and detection of nucleic acids in biological samples. The
XX CC methods are useful in the human medical and veterinary fields, for
XX CC medical diagnoses and clinical monitoring of a patient's response to
XX CC therapy where a disease or medical condition is associated with a
XX CC particular type and/or level of mRNA present in the sample. The methods
XX CC are also useful for detecting or quantifying fusion or chimeric RNA
XX CC species, and for detecting a translocation as a marker for a given
XX CC condition or disease, e.g. translocations associate with cancers,
XX CC particularly forms of leukemia
XX SQ Sequence 54 BP; 20 A; 12 C; 11 G; 0 T; 11 U; 0 Other;
Query Match 100.0%; Score 27; DB 3; Length 54;
Best Local Similarity 100.0%; Pred. No. 3.8e-05;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ACUCAGACCCUGAGGCUCAAAAGUCAGA 27
DB 28 ACUCAGACCCUGAGGCUCAAAAGUCAGA 54
|||||
RESULT 7
AAZ60840
ID AAZ60840 standard; DNA; 54 BP.
XX AC AAZ60840;
XX DT 16-MAY-2000 (first entry)
XX DE Oligonucleotide used to detect bcr b3-abl fusion transcripts.

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XX KW Fusion transcript; translocation; bcr b3 region; abl gene;
XX KW amplification assay; detection assay; medical diagnosis;
XX KW clinical monitoring; chimeric RNA; fusion RNA; condition marker;
XX KW disease marker; cancer; leukemia; ss.
XX OS Synthetic.
XX PN WO200005418-A1.
XX PD 03-FEB-2000.
XX PF 23-JUL-1999; 99WO-US016832.
XX PR 23-JUL-1998; 98US-00121239.
XX PA (GENP-) GEN-PROBE INC.
XX PI Harvey RC, Eastman PS;
XX PI WPI; 2000-182730/16.
XX DR Novel methods for preparing RNA from biological samples, used for the
XX PT detection and measurement of nucleic acids and fusion nucleic acids.
XX PS Claim 19; Page 39; 49pp; English.
XX CC Oligonucleotides AAZ60840-62 and AAZ60865-66 are used in the method of
XX CC the invention to detect fusion transcripts produced from a translocation
XX CC between the bcr b3 region and the abl gene. The specification describes a
XX CC method for detecting a fusion nucleic acid (particularly chimeric mRNA
XX CC species), in a biological sample. The method comprises contacting a
XX CC sample of fusion nucleic acid with primers, amplifying the hybridized
XX CC fusion nucleic acid, and detecting the target hybrid. The method is used
XX CC for the simple and rapid preparation of RNA from a biological sample,
XX CC particularly from the cytoplasm of eukaryotic cells, which is suitable
XX CC for use in an amplification and detection assay. The methods are used for
XX CC the analysis and detection of nucleic acids in biological samples. The
XX CC methods are useful in the human medical and veterinary fields, for
XX CC medical diagnoses and clinical monitoring of a patient's response to
XX CC therapy where a disease or medical condition is associated with a
XX CC particular type and/or level of mRNA present in the sample. The methods
XX CC are also useful for detecting or quantifying fusion or chimeric RNA
XX CC species, and for detecting a translocation as a marker for a given
XX CC condition or disease, e.g. translocations associate with cancers,
XX CC particularly forms of leukemia
XX SQ Sequence 54 BP; 20 A; 12 C; 11 G; 11 T; 0 U; 0 Other;
Query Match 100.0%; Score 27; DB 3; Length 54;
Best Local Similarity 85.2%; Pred. No. 3.8e-05;
Matches 23; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
QY 1 ACUCAGACCCUGAGGCUCAAAAGUCAGA 27
DB 28 ACTCAGACCTGAGGCTCAAAAGTCAGA 54
|||||
RESULT 8
AAZ60842/c
ID AAZ60842 standard; DNA; 54 BP.
XX AC AAZ60842;
XX DT 16-MAY-2000 (first entry)
XX DE Oligonucleotide used to detect bcr b3-abl fusion transcripts.
XX KW Fusion transcript; translocation; bcr b3 region; abl gene;
XX KW amplification assay; detection assay; medical diagnosis;
XX KW clinical monitoring; chimeric RNA; fusion RNA; condition marker;
XX KW disease marker; cancer; leukemia; ss.

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PA (UTEM ) UNIV TEMPLE.
XX Calabretta B, Gewirtz AM;
XX WPI; 1993-017893/02.
DR Treating Ph1-positive leukaemia(s) using bcr-abl anti-sense oligo-
PT nucleotide(s) - to selectively inhibit leukaemic cell proliferation
PT without adversely affecting normal haematopoiesis.
XX Disclosure; Fig 1; 74pp; English.
XX This is the sequence around the bcr-abl junction derived from a group of
CC five chronic myeloid leukaemia (CML) patients in blast crisis. It is the
CC L-6 type junction, formed by fusion of bcr exon 2 to c-abl exon 2.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX SQ Sequence 257 BP; 72 A; 62 C; 64 G; 59 T; 0 U; 0 Other;
Query Match 100.0%; Score 27; DB 2; Length 257;
Best Local Similarity 85.2%; Pred. No. 3.8e-05;
Matches 23; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
QY 1 ACUCAGACCCUGAGGCUCAAGUCAGA 27
DB 81 ACTCAGACCTGAGGCTCAAGTCAGA 55
RESULT 11
AAV20458/c
ID AAV20458 standard; DNA; 257 BP.
XX AC AAV20458;
XX 17-JUN-1998 (first entry)
XX Human bcr-abl oncogene b2a2 genotype.
XX Human; oncogene; proto-oncogene; neoplastic disease; anticancer; cancer;
XX antisense oligonucleotide; bcr-abl; ds.
XX Homo sapiens.
XX US5734039-A.
XX 31-MAR-1998.
XX 15-SEP-1994; 94US-00306691.
XX 15-SEP-1994; 94US-00306691.
XX (UYJE-) UNIV JEFFERSON THOMAS.
XX Calabretta B, Skorski T;
XX WPI; 1998-229882/20.
XX Anticancer composition comprising two anti-sense oligo:nucleotide(s) -
XX targeting cytoplasmic and nuclear oncogene(s).
XX Claim 1; Col 109-110; 92pp; English.
XX The present sequence represents an oncogene from the present invention.
XX The present invention describes a composition which comprises two
XX antisense oligonucleotides. The first oligonucleotide is specific for a
XX cytoplasmic oncogene or proto-oncogene selected from ras, raf, EGF-1, c-
XX fms, c-ros, c-kit, c-met, c-trk, c-src, c-abl, bcr-abl, c-fgr and c-yes.
XX The second oligonucleotide is specific for a nuclear oncogene or proto-
XX oncogene selected from myc, jun, c-ets, c-fos, c-myb, B-myb, c-rel, c-
XX vav, c-ski, c-spi, cyclin D1, PML/RAR alpha , AML1/MTG8, E2A/p1 and ALL-
XX 1/AF-4. The composition is used for treating cancer. The combination of
XX antisense oligonucleotides has synergistically enhanced ability to
XX inhibit growth of cancer cells
PA (UTEM ) UNIV TEMPLE.
XX Calabretta B, Gewirtz AM;
XX WPI; 1993-017893/02.
DR Treating Ph1-positive leukaemia(s) using bcr-abl anti-sense oligo-
PT nucleotide(s) - to selectively inhibit leukaemic cell proliferation
PT without adversely affecting normal haematopoiesis.
XX Disclosure; Fig 1; 74pp; English.
XX This is the sequence around the bcr-abl junction derived from two chronic
CC myeloid leukaemia (CML) patients in blast crisis. It is the K-28 type
CC junction, formed by fusion of bcr exon 3 to c-abl exon 2. (Updated on 25-
CC MAR-2003 to correct PN field.)
XX SQ Sequence 266 BP; 72 A; 64 C; 66 G; 64 T; 0 U; 0 Other;
Query Match 100.0%; Score 27; DB 2; Length 266;
Best Local Similarity 85.2%; Pred. No. 3.8e-05;
Matches 23; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
QY 1 ACUCAGACCCUGAGGCUCAAGUCAGA 27
DB 90 ACTCAGACCTGAGGCTCAAGTCAGA 64
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RESULT 13
AAV20459/c
ID AAV20459 standard; DNA; 266 BP.
XX
XX AAV20459;
AC
XX
XX 17-JUN-1998 (first entry)
DT
XX
XX Human bcr-abl oncogene b3a2 genotype.
DE
XX
XX Human; oncogene; proto-oncogene; neoplastic disease; anticancer; cancer;
KW antisense oligonucleotide; bcr-abl; ds.
XX
XX Homo sapiens.
OS
XX
XX US5734039-A.
PN
XX
XX 31-MAR-1998.
PD
XX
XX 15-SEP-1994; 94US-00306691.
PF
XX
XX 15-SEP-1994; 94US-00306691.
PR
XX
XX (UYJE-) UNIV JEFFERSON THOMAS.
PA
XX
XX Calabretta B, Skorski T;
PI
XX
XX WPI; 1998-229882/20.
DR
XX
XX Anticancer composition comprising two anti-sense oligo-nucleotide(s) -
PT targeting cytoplasmic and nuclear oncogene(s).
PT
XX
XX Claim 1; Col 109-110; 92pp; English.
PS
XX
XX The present sequence represents an oncogene from the present invention.
CC
XX
XX The present invention describes a composition which comprises two
CC antisense oligonucleotides. The first oligonucleotide is specific for a
CC cytoplasmic oncogene or proto-oncogene selected from ras, raf, EGF-1, c-
CC fms, c-ros, c-kit, c-trk, c-src, c-abl, bcr-abl, c-fgr and c-yes.
CC The second oligonucleotide is specific for a nuclear oncogene or proto-
CC oncogene selected from myc, jun, c-ets, c-fos, c-myc, B-myb, c-rel, c-
CC vav, c-ski, c-spi, cyclin D1, PML/RAR alpha, AML1/MTG8, E2A/p12 and ALL-
CC 1/AF-4. The composition is used for treating cancer. The combination of
CC antisense oligonucleotides has synergistically enhanced ability to
CC inhibit growth of cancer cells
XX
XX Sequence 266 BP; 72 A; 64 C; 66 G; 64 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 27; DB 2; Length 266;
Best Local Similarity 85.2%; Pred. No. 3.8e-05;
Matches 23; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACUCAGACCCUGAGGCUCAAGUCAGA 27
||:|||||:||||:||||:||||:||||
Db 90 ACTCAGACCCUGAGGCTCAAGTCAGA 64

RESULT 14
AAZ60864/c
ID AAZ60864 standard; DNA; 299 BP.
XX
XX AAZ60864;
AC
XX
XX 16-MAY-2000 (first entry)
DT
XX
XX Region surrounding a splice junction in a normal abl transcript.
DE
XX
XX Fusion transcript; translocation; bcr b3 region; abl gene;
KW amplification assay; detection assay; medical diagnosis;
KW clinical monitoring; chimeric RNA; fusion RNA; condition marker;
KW disease marker; cancer; leukemia; ss.
XX

RESULT 15
AAZ60863/c
ID AAZ60863 standard; DNA; 350 BP.
XX
XX AAZ60863;
AC
XX
XX 16-MAY-2000 (first entry)
DT
XX
XX Region surrounding a bcr-able splice junction.
DE
XX
XX Fusion transcript; translocation; bcr b3 region; abl gene;
KW amplification assay; detection assay; medical diagnosis;
KW clinical monitoring; chimeric RNA; fusion RNA; condition marker;
KW disease marker; cancer; leukemia; ss.
XX
XX Unidentified.
OS
XX
XX WO200005418-A1.
PN
XX
XX 03-FEB-2000.
PD
XX
XX 23-JUL-1999; 99WO-US016832.
PF
XX
XX 23-JUL-1998; 98US-00121239.
PR
XX
XX (GENP-) GEN-PROBE INC.
PA
XX
XX Harvey RC, Eastman PS;
PI
XX
XX WPI; 2000-182730/16.
DR
XX
XX Novel methods for preparing RNA from biological samples, used for the
PT detection and measurement of nucleic acids and fusion nucleic acids.
PT
XX
XX Disclosure; Fig 3; 49pp; English.
PS
XX
XX The present sequence represents a region surrounding a potential splice
CC junction in a normal abl transcript. The specification describes
CC oligonucleotides which are used to detect fusion transcripts produced
CC from a translocation between the bcr b3 region and the abl gene. The
CC specification also describes a method for detecting a fusion nucleic acid
CC (particularly chimeric mRNA species), in a biological sample. The method
CC comprises contacting a sample of fusion nucleic acid with primers,
CC amplifying the hybridized fusion nucleic acid, and detecting the target
CC hybrid. The method is used for the simple and rapid preparation of RNA
CC from a biological sample, particularly from the cytoplasm of eukaryotic
CC cells, which is suitable for use in an amplification and detection assay.
CC The methods are used for the analysis and detection of nucleic acids in
CC biological samples. The methods are useful in the human medical and
CC veterinary fields, for medical diagnoses and clinical monitoring of a
CC patients response to therapy where a disease or medical condition is
CC associated with a particular type and/or level of mRNA present in the
CC sample. The methods are also useful for detecting or quantifying fusion
CC or chimeric RNA species, and for detecting a translocation as a marker
CC for a given condition or disease, e.g. translocations associate with
CC cancers, particularly forms of leukemia
XX
XX Sequence 299 BP; 77 A; 70 C; 81 G; 71 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 27; DB 3; Length 299;
Best Local Similarity 85.2%; Pred. No. 3.8e-05;
Matches 23; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACUCAGACCCUGAGGCUCAAGUCAGA 27
||:|||||:||||:||||:||||:||||
Db 201 ACTCAGACCCUGAGGCTCAAGTCAGA 175

RESULT 16
AAZ60863/c
ID AAZ60863 standard; DNA; 350 BP.
XX
XX AAZ60863;
AC
XX
XX 16-MAY-2000 (first entry)
DT
XX
XX Region surrounding a bcr-able splice junction.
DE
XX
XX Fusion transcript; translocation; bcr b3 region; abl gene;
KW amplification assay; detection assay; medical diagnosis;
KW clinical monitoring; chimeric RNA; fusion RNA; condition marker;
KW disease marker; cancer; leukemia; ss.
XX
XX Unidentified.
OS
XX
XX WO200005418-A1.
PN
XX
XX 03-FEB-2000.
PD

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XX 23-JUL-1999; 99WO-US016832.  
 XX PF  
 XX 23-JUL-1998; 98US-00121239.  
 XX PR  
 XX (GENP-) GEN-PROBE INC.  
 XX PA  
 XX Harvey RC, Eastman PS;  
 XX PI  
 XX WPI; 2000-182730/16.  
 XX DR  
 XX Novel methods for preparing RNA from biological samples, used for the  
 PT detection and measurement of nucleic acids and fusion nucleic acids.  
 PT  
 XX Disclosure; Fig 2; 49pp; English.  
 XX  
 CC The present sequence represents a region surrounding a bcr-able splice  
 CC junction. The specification describes oligonucleotides which are used to  
 CC detect fusion transcripts produced from a translocation between the bcr  
 CC b3 region and the abl gene. The specification also describes a method for  
 CC detecting a fusion nucleic acid (particularly chimeric mRNA species), in  
 CC a biological sample. The method comprises contacting a sample of fusion  
 CC nucleic acid with primers, amplifying the hybridized fusion nucleic acid,  
 CC and detecting the target hybrid. The method is used for the simple and  
 CC rapid preparation of RNA from a biological sample, particularly from the  
 CC cytoplasm of eukaryotic cells, which is suitable for use in an  
 CC amplification and detection assay. The methods are used for the analysis  
 CC and detection of nucleic acids in biological samples. The methods are  
 CC useful in the human medical and veterinary fields, for medical diagnoses  
 CC and clinical monitoring of a patient's response to therapy where a disease  
 CC or medical condition is associated with a particular type and/or level of  
 CC mRNA present in the sample. The methods are also useful for detecting or  
 CC quantifying fusion or chimeric RNA species, and for detecting a  
 CC translocation as a marker for a given condition or disease, e.g.  
 CC translocations associate with cancers, particularly forms of leukemia  
 XX  
 SQ Sequence 350 BP; 85 A; 92 C; 89 G; 84 T; 0 U; 0 Other;

Query Match 100.0%; Score 27; DB 3; Length 350;  
 Best Local Similarity 85.2%; Pred. No. 3.8e-05;  
 Matches 23; Conservative 4; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 ACUCAGACCCUGAGGUCUAAAGUCAGA 27  
 ||:|||||:|||||:|||||:|||||  
 Db 251 ACTCAGACCCCTGAGGCTCAAGTCAGA 225

Search completed: May 26, 2004, 16:52:25  
 Job time : 120.416 secs



GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: May 26, 2004, 16:02:51 ; Search time 22.7559 Seconds  
(without alignments)  
658.454 Million cell updates/sec

Title: US-09-121-239-21

Perfect score: 27

Sequence: 1 ACUCAGACCCUGAGGCUCAAAGUCAGA 27

Scoring table: OLIGO\_NUC

Gapop 60.0 , Gapext 60.0

Searched: 682709 seqs, 277475446 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents NA.\*

- 1: /cgn2\_6/prodata/2/ina/5A COMB.seq.\*
- 2: /cgn2\_6/prodata/2/ina/5B COMB.seq.\*
- 3: /cgn2\_6/prodata/2/ina/6A COMB.seq.\*
- 4: /cgn2\_6/prodata/2/ina/6B COMB.seq.\*
- 5: /cgn2\_6/prodata/2/ina/PCTUS COMB.seq.\*
- 6: /cgn2\_6/prodata/2/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	27	100.0	204	5	PCT-US93-06251-5
C 2	27	100.0	257	1	US-08-152-621-1
C 3	27	100.0	257	1	US-08-306-691B-36
C 4	27	100.0	257	5	PCT-US92-05035-1
C 5	27	100.0	266	1	US-08-152-621-4
C 6	27	100.0	266	1	US-08-306-691B-37
C 7	27	100.0	266	5	PCT-US92-05035-4
C 8	27	100.0	1078	4	US-09-310-842-1
C 9	27	100.0	3623	1	US-08-306-691B-35
C 10	26	96.3	80	1	US-08-152-621-7
C 11	26	96.3	80	1	US-08-306-691B-38
C 12	26	96.3	80	5	PCT-US92-05035-7
C 13	24	88.9	50	4	US-09-168-947-45
C 14	22	81.5	22	1	US-08-013-419-1
C 15	22	81.5	22	1	US-08-122-795B-10
C 16	22	81.5	22	1	US-08-525-818-1
C 17	22	81.5	22	2	US-09-028-184-1
C 18	22	81.5	22	5	PCT-US94-00680-1
C 19	22	81.5	22	5	PCT-US94-00963A-10
C 20	17	63.0	56	1	US-07-340-652-19
C 21	17	63.0	56	1	US-08-355-553-19
C 22	16	59.3	2992	2	US-08-841-349-10
C 23	16	59.3	2992	4	US-09-431-184A-10
C 24	15	55.6	20	1	US-08-761-131-7
C 25	15	55.6	21	3	US-07-784-222-2
C 26	15	55.6	21	4	US-09-502-954-2
C 27	15	55.6	40	1	US-08-761-131-1

C 28	15	55.6	40	1	US-08-761-131-2	Sequence 2, Appli
C 29	15	55.6	818	4	US-09-599-360B-37	Sequence 37, Appli
C 30	15	55.6	822	4	US-09-621-976-1361	Sequence 1361, Ap
C 31	15	55.6	2214	4	US-09-489-847-113	Sequence 113, App
C 32	15	55.6	2227	4	US-09-489-847-30	Sequence 30, Appl
C 33	15	55.6	7052	4	US-09-526-193A-22	Sequence 22, Appl
C 34	14	51.9	426	4	US-09-621-976-18309	Sequence 18309, A
C 35	14	51.9	474	4	US-09-615-192A-264	Sequence 264, App
C 36	14	51.9	888	4	US-09-171-209-7	Sequence 7, Appli
C 37	14	51.9	973	4	US-09-599-360B-71	Sequence 71, Appl
C 38	14	51.9	1910	2	US-08-808-931-17	Sequence 17, Appl
C 39	14	51.9	1910	3	US-08-808-931-17	Sequence 17, Appl
C 40	14	51.9	1910	3	US-09-050-603A-17	Sequence 17, Appl
C 41	14	51.9	1910	3	US-09-102-420B-17	Sequence 17, Appl
C 42	14	51.9	1910	4	US-09-497-698-17	Sequence 17, Appl
C 43	14	51.9	2050	4	US-09-620-312D-761	Sequence 761, App
C 44	14	51.9	2150	2	US-08-318-837-1	Sequence 1, Appli
C 45	14	51.9	2606	2	US-08-808-931-26	Sequence 26, Appl

## ALIGNMENTS

RESULT 1  
PCT-US93-06251-5/c  
; Sequence 5, Application PC/TUS9306251  
; GENERAL INFORMATION:  
; APPLICANT: Wickstrom, Eric and Rife, Jason P.  
; TITLE OF INVENTION: Trivalent Synthesis of Oligonucleotides Containing  
; TITLE OF INVENTION: Stereospecific Alkylphosphonates and Arylphosphonates  
; NUMBER OF SEQUENCES: 93  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER  
; STREET: 400 Garden City Plaza  
; CITY: Garden City  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 11530  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US93/06251  
; FILING DATE: 19930630  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Digiglio, Frank S.  
; REGISTRATION NUMBER: 31,346  
; REFERENCE/DOCKET NUMBER: 8586  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 516-742-4343  
; TELEFAX: 516-742-4366  
; TELEX: 230 901 SANS UR  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 204 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
PCT-US93-06251-5

Query Match 100.0%; Score 27; DB 5; Length 204;  
Best Local Similarity 85.2%; Pred. No. 1.2e-06;  
Matches 23; Conservative 4; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ACUCAGACCCUGAGGCUCAAAGUCAGA 27  
DB 65 ACTCAGACCCUGAGGCTCAAGTCAGA 39

## RESULT 2

US-08-152-621-1/c  
; Sequence 1, Application US/08152621  
; Patent No. 5652222  
; GENERAL INFORMATION:  
; APPLICANT: Calabretta, Bruno  
; APPLICANT: Gewirtz, Alan M.  
; TITLE OF INVENTION: Selective Inhibition of  
; TITLE OF INVENTION: Leukemic Cell Proliferation by bcr-abl  
; TITLE OF INVENTION: Antisense Oligonucleotides  
; NUMBER OF SEQUENCES: 34  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SEIDEL, GONDA, LAVORGNA  
; ADDRESSEE: & MONACO, P.C.  
; STREET: 1800 Two Penn Center  
; CITY: Philadelphia  
; STATE: Pennsylvania  
; COUNTRY: U.S.A.  
; ZIP: 19102  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb  
; COMPUTER: IBM PS/2  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: WordPerfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/152,621  
; FILING DATE: No. 5652222ember 15, 1993  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/718,302  
; FILING DATE: June 18, 1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Monaco, Daniel A.  
; REGISTRATION NUMBER: 30,480  
; REFERENCE/DOCKET NUMBER: 6056-120 (CT.) 1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (215) 568-8383  
; TELEFAX: (215) 568-5549  
; TELEX: No. 565222e  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 257 Nucleotides  
; TYPE: nucleic acid  
; STRANDEDNESS: single stranded  
; TOPOLOGY: linear  
US-08-152-621-1

Query Match 100.0%; Score 27; DB 1; Length 257;  
Best Local Similarity 85.2%; Pred. No. 1.2e-06;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ACUCAGACCCUGAGGCUCAAGUCAGA 27  
Db 81 ACTCAGACCTGAGGCTCAAAGTCAGA 55

## RESULT 3

US-08-306-691B-36/c  
; Sequence 36, Application US/08306691B  
; Patent No. 5734039  
; GENERAL INFORMATION:  
; APPLICANT: Calabretta, Bruno  
; APPLICANT: Skorski, Tomasz  
; TITLE OF INVENTION: ANTISENSE  
; TITLE OF INVENTION: OLIGONUCLEOTIDES TARGETING COOPERATING ONCOGENES  
; NUMBER OF SEQUENCES: 55  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Seidel, Gonda, Lavorgna & Monaco, P.C.  
; STREET: Two Penn Center, Suite 1800  
; CITY: Philadelphia  
; STATE: Pennsylvania  
; COUNTRY: U.S.A.  
; ZIP: 19102

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb  
; COMPUTER: IBM PS/2  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: WordPerfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/306,691B  
; FILING DATE: September 15, 1994  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Monaco, Daniel A.  
; REGISTRATION NUMBER: 30,480  
; REFERENCE/DOCKET NUMBER: 8321-8  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (215) 568-8383  
; TELEFAX: (215) 568-5549  
; TELEX: No. 5734039e  
; INFORMATION FOR SEQ ID NO: 36:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 257 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-306-691B-36

Query Match 100.0%; Score 27; DB 1; Length 257;  
Best Local Similarity 85.2%; Pred. No. 1.2e-06;  
Matches 23; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

OY 1 ACUCAGACCCUGAGGCUCAAGUCAGA 27  
Db 81 ACTCAGACCTGAGGCTCAAAGTCAGA 55

## RESULT 4

PCT-US92-05035-1/c  
; Sequence 1, Application PC/TUS9205035  
; GENERAL INFORMATION:  
; APPLICANT: Calabretta, Bruno  
; APPLICANT: Gewirtz, Alan M.  
; TITLE OF INVENTION: Selective Inhibition of  
; TITLE OF INVENTION: Leukemic Cell Proliferation by bcr-abl  
; TITLE OF INVENTION: Antisense Oligonucleotides  
; NUMBER OF SEQUENCES: 34  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Temple University - Of The Common-  
; ADDRESSEE: wealth System of Higher Education  
; STREET: 406 University Services Building  
; CITY: Philadelphia  
; STATE: Pennsylvania  
; COUNTRY: U.S.A.  
; ZIP: 19122  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb  
; COMPUTER: IBM PS/2  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: WordPerfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US92/05035  
; FILING DATE: 19920615  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/718,302  
; FILING DATE: June 18, 1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/869,911  
; FILING DATE: April 14, 1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Monaco, Daniel A.  
; REGISTRATION NUMBER: 30,480

; REFERENCE/DOCKET NUMBER: 6056-120 (CIP) 1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (215) 568-8383  
; TELEFAX: (215) 568-5549  
; TELEX: None  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 257 Nucleotides  
; TYPE: NUCLEIC ACID  
; STRANDEDNESS: single stranded  
; TOPOLOGY: linear  
PCT-US92-05035-1

Query Match 100.0%; Score 27; DB 5; Length 257;  
Best Local Similarity 85.2%; Pred. No. 1.2e-06;  
Matches 23; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACUCAGACCCUGAGGCUCAAGUCAGA 27  
||:|||||:||||:||||:||||:||||  
Db 81 ACTCAGACCCUGAGGCTCAAGTCAGA 55

RESULT 5  
US-08-152-621-4/c  
; Sequence 4, Application US/08152621  
; Patent No. 5652222  
; GENERAL INFORMATION:  
; APPLICANT: Calabretta, Bruno  
; APPLICANT: Gewirtz, Alan M.  
; TITLE OF INVENTION: Selective Inhibition of  
; TITLE OF INVENTION: Leukemic Cell Proliferation by bcr-abl  
; TITLE OF INVENTION: Antisense Oligonucleotides  
; NUMBER OF SEQUENCES: 34  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SEIDEL, GONDA, LAVORNA  
; ADDRESSEE: & MONACO, P.C.  
; STREET: 1800 Two Penn Center  
; CITY: Philadelphia  
; STATE: Pennsylvania  
; COUNTRY: U.S.A.  
; ZIP: 19102

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb  
; COMPUTER: IBM PS/2  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: WordPerfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/152,621  
; FILING DATE: No. 5652222ember 15, 1993  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/718,302  
; FILING DATE: June 18, 1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Monaco, Daniel A.  
; REGISTRATION NUMBER: 30,480  
; REFERENCE/DOCKET NUMBER: 6056-120 (CT.) 1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (215) 568-8383  
; TELEFAX: (215) 568-5549  
; TELEX: No. 5652222e  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 266 Nucleotides  
; TYPE: nucleic acid  
; STRANDEDNESS: single stranded  
; TOPOLOGY: linear  
US-08-152-621-4

Query Match 100.0%; Score 27; DB 1; Length 266;  
Best Local Similarity 85.2%; Pred. No. 1.2e-06;  
Matches 23; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACUCAGACCCUGAGGCUCAAGUCAGA 27  
||:|||||:||||:||||:||||:||||  
Db 90 ACTCAGACCCUGAGGCTCAAGTCAGA 64

RESULT 6  
US-08-306-691B-37/c  
; Sequence 37, Application US/08306691B  
; Patent No. 5734039  
; GENERAL INFORMATION:  
; APPLICANT: Calabretta, Bruno  
; APPLICANT: Skorski, Tomasz  
; TITLE OF INVENTION: ANTISENSE  
; TITLE OF INVENTION: OLIGONUCLEOTIDES TARGETING COOPERATING ONCOGENES  
; NUMBER OF SEQUENCES: 55  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Seidel, Gonda, Lavoigna & Monaco, P.C.  
; STREET: Two Penn Center, Suite 1800  
; CITY: Philadelphia  
; STATE: Pennsylvania  
; COUNTRY: U.S.A.  
; ZIP: 19102

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb  
; COMPUTER: IBM PS/2  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: WordPerfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/306,691B  
; FILING DATE: September 15, 1994  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Monaco, Daniel A.  
; REGISTRATION NUMBER: 30,480  
; REFERENCE/DOCKET NUMBER: 8321-8  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (215) 568-8383  
; TELEFAX: (215) 568-5549  
; TELEX: No. 5734039e  
; INFORMATION FOR SEQ ID NO: 37:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 266 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-306-691B-37

Query Match 100.0%; Score 27; DB 1; Length 266;  
Best Local Similarity 85.2%; Pred. No. 1.2e-06;  
Matches 23; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACUCAGACCCUGAGGCUCAAGUCAGA 27  
||:|||||:||||:||||:||||:||||  
Db 90 ACTCAGACCCUGAGGCTCAAGTCAGA 64

RESULT 7  
PCT-US92-05035-4/c  
; Sequence 4, Application PC/TUS9205035  
; GENERAL INFORMATION:  
; APPLICANT: Calabretta, Bruno  
; APPLICANT: Gewirtz, Alan M.  
; TITLE OF INVENTION: Selective Inhibition of  
; TITLE OF INVENTION: Leukemic Cell Proliferation by bcr-abl  
; TITLE OF INVENTION: Antisense Oligonucleotides  
; NUMBER OF SEQUENCES: 34  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Temple University - Of The Common-  
; ADDRESSEE: wealth System of Higher Education  
; STREET: 406 University Services Building

```
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: U.S.A.
; ZIP: 19122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/05035
; FILING DATE: 19920615
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/718,302
; FILING DATE: June 18, 1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/869,911
; FILING DATE: April 14, 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Monaco, Daniel A.
; REGISTRATION NUMBER: 30,480
; REFERENCE/DOCKET NUMBER: 6056-120 (CIP) 1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-8383
; TELEFAX: (215) 568-5549
; TELEX: None
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 266 Nucleotides
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single stranded
; TOPOLOGY: linear
; PCT-US92-05035-4

Query Match 100.0%; Score 27; DB 5; Length 266;
Best Local Similarity 85.2%; Pred. No. 1.2e-06;
Matches 23; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACUCAGACCCUGAGGCUCAAAAGUCAGA 27
Db 90 ACTCAGACCCGTGAGGCTCAAAGTCAGA 64

RESULT 8
US-09-310-842-1/c
; Sequence 1, Application US/09310842A
; Patent No. 6451593
; GENERAL INFORMATION:
; APPLICANT: Wittig, Prof. Burghardt
; APPLICANT: Jungmans, Claas
; TITLE OF INVENTION: Design Principle for Constructing Expression Constructs for Gene
; TITLE OF INVENTION: Therapy
; FILE REFERENCE: XI 597/99
; CURRENT APPLICATION NUMBER: US/09/310,842A
; CURRENT FILING DATE: 1999-05-12
; EARLIER APPLICATION NUMBER: DE 196 48 625.4
; EARLIER FILING DATE: 1996-11-13
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1078
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: gene
; LOCATION: (1)..(1078)
; OTHER INFORMATION: bcr3=abl2; Oligo DNA Dumbbell
; FEATURE:
; NAME/KEY: misc binding
; LOCATION: (1)..(2)
; OTHER INFORMATION: intramolecular binding site; the T-nucleotides at position 1 to
; OTHER INFORMATION: 2 can be modified with amino or caroxy features
```

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; FEATURE:
; NAME/KEY: misc binding
; LOCATION: (1077)..(1078)
; OTHER INFORMATION: intramolecular binding site; the T-nucleotides at position 1077
; OTHER INFORMATION: to 1078 can be modified with amino or caroxy features
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Strandness: both; nucleic
; OTHER INFORMATION: acid (linear), hypothetical: No. 6451593 anti-sense: NO
US-09-310-842-1
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Query Match 100.0%; Score 27; DB 4; Length 1078;
Best Local Similarity 85.2%; Pred. No. 1.2e-06;
Matches 23; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
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QY 1 ACUCAGACCCUGAGGCUCAAAAGUCAGA 27
Db 824 ACTCAGACCCGTGAGGCTCAAAGTCAGA 798
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RESULT 9
US-08-306-691B-35/c
; Sequence 35, Application US/08306691B
; Patent No. 5734039
; GENERAL INFORMATION:
; APPLICANT: Calabretta, Bruno
; APPLICANT: Skorski, Tomasz
; TITLE OF INVENTION: ANTISENSE
; TITLE OF INVENTION: OLIGONUCLEOTIDES TARGETING COOPERATING ONCOGENES
; NUMBER OF SEQUENCES: 55
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seidel, Gonda, Lavorina & Monaco, P.C.
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: U.S.A.
; ZIP: 19102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/306,691B
; FILING DATE: September 15, 1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Monaco, Daniel A.
; REGISTRATION NUMBER: 30,480
; REFERENCE/DOCKET NUMBER: 8321-8
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-8383
; TELEFAX: (215) 568-5549
; TELEX: No. 5734039e
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3623 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; US-08-306-691B-35
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Query Match 100.0%; Score 27; DB 1; Length 3623;
Best Local Similarity 85.2%; Pred. No. 1.3e-06;
Matches 23; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
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QY 1 ACUCAGACCCUGAGGCUCAAAAGUCAGA 27
Db 276 ACTCAGACCCGTGAGGCTCAAAGTCAGA 250
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RESULT 10  
US-08-152-621-7/c  
; Sequence 7, Application US/08152621  
; Patent No. 5652222  
; GENERAL INFORMATION:  
; APPLICANT: Calabretta, Bruno  
; APPLICANT: Gewirtz, Alan M.  
; TITLE OF INVENTION: Selective Inhibition of  
; TITLE OF INVENTION: Leukemic Cell Proliferation by bcr-abl  
; TITLE OF INVENTION: Antisense Oligonucleotides  
; NUMBER OF SEQUENCES: 34  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SEIDEL, GONDA, LAVORGNA  
; ADDRESSEE: & MONACO, P.C.  
; STREET: 1800 Two Penn Center  
; CITY: Philadelphia  
; STATE: Pennsylvania  
; COUNTRY: U.S.A.  
; ZIP: 19102  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb  
; COMPUTER: IBM PS/2  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: WordPerfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/152,621  
; FILING DATE: June 18, 1991  
; CLASSIFICATION: 514  
; PRIORITY INFORMATION:  
; PRIORITY NUMBER: 07/718,302  
; FILING DATE: June 18, 1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Monaco, Daniel A.  
; REGISTRATION NUMBER: 30,480  
; REFERENCE/DOCKET NUMBER: 6056-120 (CT.) 1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (215) 568-8383  
; TELEFAX: (215) 568-5549  
; TELEX: No. 5652222e  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 80 Nucleotides  
; TYPE: nucleic acid  
; STRANDEDNESS: single stranded  
; TOPOLOGY: linear  
US-08-152-621-7

Query Match 96.3%; Score 26; DB 1; Length 80;  
Best Local Similarity 84.6%; Pred. No. 4.3e-06;  
Matches 22; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 2 CUCAGACCCUGAGGCUCAAGUCAGA-27  
Db 80 CTCAGACCCCTGAGGCTCAAGTCAGA 55

RESULT 11  
US-08-306-691B-38/c  
; Sequence 38, Application US/08306691B  
; Patent No. 5734039  
; GENERAL INFORMATION:  
; APPLICANT: Calabretta, Bruno  
; APPLICANT: Skorski, Tomasz  
; TITLE OF INVENTION: ANTISENSE  
; TITLE OF INVENTION: OLIGONUCLEOTIDES TARGETING COOPERATING ONCOGENES  
; NUMBER OF SEQUENCES: 55  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Seidel, Gonda, Lavorgna & Monaco, P.C.  
; STREET: Two Penn Center, Suite 1800  
; CITY: Philadelphia  
; STATE: Pennsylvania  
; COUNTRY: U.S.A.  
; ZIP: 19102

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb  
COMPUTER: IBM PS/2  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: WordPerfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/306,691B  
FILING DATE: September 15, 1994  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Monaco, Daniel A.  
REGISTRATION NUMBER: 30,480  
REFERENCE/DOCKET NUMBER: 8321-8  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (215) 568-8383  
TELEFAX: (215) 568-5549  
TELEX: No. 5734039e  
INFORMATION FOR SEQ ID NO: 38:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 80 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-306-691B-38

Query Match 96.3%; Score 26; DB 1; Length 80;  
Best Local Similarity 84.6%; Pred. No. 4.3e-06;  
Matches 22; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 2 CUCAGACCCUGAGGCUCAAGUCAGA 27  
Db 80 CTCAGACCCCTGAGGCTCAAGTCAGA 55

RESULT 12  
PCT-US92-05035-7/c  
; Sequence 7, Application PC/TUS9205035  
; GENERAL INFORMATION:  
; APPLICANT: Calabretta, Bruno  
; APPLICANT: Gewirtz, Alan M.  
; TITLE OF INVENTION: Selective Inhibition of  
; TITLE OF INVENTION: Leukemic Cell Proliferation by bcr-abl  
; TITLE OF INVENTION: Antisense Oligonucleotides  
; NUMBER OF SEQUENCES: 34  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Temple University - Of The Common-  
; ADDRESSEE: wealth System of Higher Education  
; STREET: 406 University Services Building  
; CITY: Philadelphia  
; STATE: Pennsylvania  
; COUNTRY: U.S.A.  
; ZIP: 19122  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb  
; COMPUTER: IBM PS/2  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: WordPerfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US92/05035  
; FILING DATE: 19920615  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; PRIOR APPLICATION NUMBER: 07/718,302  
; FILING DATE: June 18, 1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/869,911  
; FILING DATE: April 14, 1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Monaco, Daniel A.  
; REGISTRATION NUMBER: 30,480

/ REFERENCE/DOCKET NUMBER: 6056-120 (CIP) 1  
/ TELECOMMUNICATION INFORMATION:  
/ TELEPHONE: (215) 568-8383  
/ TELEFAX: (215) 568-5549  
/ TELEX: None  
/ INFORMATION FOR SEQ ID NO: 7:  
/ SEQUENCE CHARACTERISTICS:  
/ LENGTH: 80 Nucleotides  
/ TYPE: NUCLEIC ACID  
/ STRANDEDNESS: single stranded  
/ TOPOLOGY: linear  
PCT-US92-05035-7

Query Match 96.3%; Score 26; DB 5; Length 80;  
Best Local Similarity 84.6%; Pred. No. 4.3e-06;  
Matches 22; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 2 CUCAGACCCUGAGGCUCAAGUCAGA-27  
|:|||||:|||||:|||||:|||||:  
Db 80 CTCAGACCCCTGAGGCTCAAAGTCAGA 55

## RESULT 13

US-09-168-947-45  
/ Sequence 45, Application US/09168947  
/ Patent No. 6589734  
/ GENERAL INFORMATION:  
/ APPLICANT: KACIAN, DANIEL L.  
/ APPLICANT: FUJITA, TIMOTHY J.  
/ APPLICANT: MCDONOUGH, SHERROL H.  
/ TITLE OF INVENTION: DETECTION OF HIV  
/ FILE REFERENCE: 218/130  
/ CURRENT APPLICATION NUMBER: US/09/168,947  
/ CURRENT FILING DATE: 1998-10-08  
/ EARLIER APPLICATION NUMBER: 08/469,067  
/ EARLIER FILING DATE: 1995-06-06  
/ EARLIER APPLICATION NUMBER: 07/550,837  
/ EARLIER FILING DATE: 1990-07-10  
/ NUMBER OF SEQ ID NOS: 46  
/ SOFTWARE: FastSeq for Windows Version 3.0  
/ SEQ ID NO 45  
/ LENGTH: 50  
/ TYPE: DNA  
/ ORGANISM: Artificial Sequence  
/ FEATURE:  
/ OTHER INFORMATION: Synthesized nucleic acid molecule  
US-09-168-947-45

Query Match 88.9%; Score 24; DB 4; Length 50;  
Best Local Similarity 83.3%; Pred. No. 5.7e-05;  
Matches 20; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACUCAGACCCUGAGGCUCAAGUC 24  
|:|||||:|||||:|||||:|||||:  
Db 27 ACTCAGACCCCTGAGGCTCAAAGTC 50

## RESULT 14

US-08-013-419-1  
/ Sequence 1, Application US/08013419  
/ Patent No. 5300635  
/ GENERAL INFORMATION:  
/ APPLICANT: Macfarlane, Donald E.  
/ TITLE OF INVENTION: Product and Process for Isolating RNA  
/ NUMBER OF SEQUENCES: 2  
/ CORRESPONDENCE ADDRESS:  
/ ADDRESSEE: Howson and Howson  
/ STREET: Spring House Corporate Center, P.O. Box 457  
/ CITY: Spring House  
/ STATE: Pennsylvania  
/ COUNTRY: USA  
/ ZIP: 19477  
/ COMPUTER READABLE FORM:

/ MEDIUM TYPE: Floppy disk  
/ COMPUTER: IBM PC compatible  
/ OPERATING SYSTEM: PC-DOS/MS-DOS  
/ SOFTWARE: PatentIn Release #1.0, Version #1.25  
/ CURRENT APPLICATION DATA:  
/ APPLICATION NUMBER: US/08/013,419  
/ FILING DATE: 19930201  
/ CLASSIFICATION: 435  
/ ATTORNEY/AGENT INFORMATION:  
/ NAME: Bak, Mary E.  
/ REGISTRATION NUMBER: 31,215  
/ REFERENCE/DOCKET NUMBER: URIF1USA  
/ TELECOMMUNICATION INFORMATION:  
/ TELEPHONE: 215-540-9206  
/ TELEFAX: 215-540-5818  
/ INFORMATION FOR SEQ ID NO: 1:  
/ SEQUENCE CHARACTERISTICS:  
/ LENGTH: 22 base pairs  
/ TYPE: NUCLEIC ACID  
/ STRANDEDNESS: unknown  
/ TOPOLOGY: unknown  
/ MOLECULE TYPE: DNA (genomic)  
US-08-013-419-1

Query Match 81.5%; Score 22; DB 1; Length 22;  
Best Local Similarity 81.8%; Pred. No. 0.00077;  
Matches 18; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 3 UCAGACCCUGAGGCUCAAGUC 24  
:|||||:|||||:|||||:|||||:  
Db 1 TCAGACCCCTGAGGCTCAAAGTC 22

## RESULT 15

US-08-122-795B-10  
/ Sequence 10, Application US/08122795B  
/ Patent No. 5635385  
/ GENERAL INFORMATION:  
/ APPLICANT: Lance H. Leopold  
/ APPLICANT: Scott K. Shore  
/ APPLICANT: Moolle V. R. Reddy  
/ APPLICANT: E. Premkumar Reddy  
/ TITLE OF INVENTION: MULTI-UNIT RIBOZYME  
/ INHIBITION OF ONCOGENE EXPRESSION  
/ NUMBER OF SEQUENCES: 11  
/ CORRESPONDENCE ADDRESS:  
/ ADDRESSEE: Seidel, Gonda, Lavorigna  
/ ADDRESSEE: & Monaco, P.C.  
/ STREET: Two Penn Center Plaza, Suite 1800  
/ CITY: Philadelphia  
/ STATE: Pennsylvania  
/ COUNTRY: U.S.A.  
/ ZIP: 19102  
/ COMPUTER READABLE FORM:  
/ MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb  
/ COMPUTER: IBM PS/2  
/ OPERATING SYSTEM: MS-DOS  
/ SOFTWARE: Wordperfect 5.1  
/ CURRENT APPLICATION DATA:  
/ APPLICATION NUMBER: US/08/122,795B  
/ FILING DATE:  
/ CLASSIFICATION: 514  
/ PRIOR APPLICATION DATA:  
/ APPLICATION NUMBER: 122,795  
/ FILING DATE: 15 September 1993  
/ ATTORNEY/AGENT INFORMATION:  
/ NAME: Monaco, Daniel A.  
/ REGISTRATION NUMBER: 30,480  
/ REFERENCE/DOCKET NUMBER: 6056-192  
/ TELECOMMUNICATION INFORMATION:  
/ TELEPHONE: (215) 568-8383  
/ TELEFAX: (215) 568-5549  
/ TELEX: NO. 5635385e

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; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 22 Nucleotides
;   TYPE: nucleic acid
;   STRANDEDNESS: single stranded
;   TOPOLOGY: linear
; US-08-122-795B-10
Query Match      81.5%; Score 22; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 0.00077;
Matches 18; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
QY      3 UCAGACCCUGAGGCUCAAGUC 24
Db       1 TCAGACCCUGAGGCTCAAGTC 22

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Job time : 22.7559 secs

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: May 27, 2004, 11:30:47 ; Search time 142.089 Seconds  
(without alignments)  
864.392 Million cell updates/sec

Title: US-09-121-239-21

Perfect score: 27

Sequence: 1 ACUCAGCCUGAGGCUCAAGUCAGA 27

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 2960401 seqs, 2274450654 residues

Word size : 0

Total number of hits satisfying chosen parameters: 5920802

Minimum DB seq length: 0

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Post-processing: Listing first 45 summaries

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- 3: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq:
- 4: /cgn2\_6/ptodata/2/pubpna/US06\_PUBCOMB.seq:
- 5: /cgn2\_6/ptodata/2/pubpna/US07\_NEW\_PUB.seq:
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- 10: /cgn2\_6/ptodata/2/pubpna/US09B\_PUBCOMB.seq:
- 11: /cgn2\_6/ptodata/2/pubpna/US09C\_PUBCOMB.seq:
- 12: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq:
- 13: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq:
- 14: /cgn2\_6/ptodata/2/pubpna/US10A\_PUBCOMB.seq:
- 15: /cgn2\_6/ptodata/2/pubpna/US10B\_PUBCOMB.seq:
- 16: /cgn2\_6/ptodata/2/pubpna/US10C\_PUBCOMB.seq:
- 17: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq:
- 18: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq:
- 19: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	27	100.0	1078	15	US-10-228-811-1
C 2	27	100.0	3393	15	US-10-263-480-1
C 3	27	100.0	3450	16	US-10-457-954-5
C 4	27	100.0	3840	15	US-10-204-041-3
C 5	27	100.0	5434	13	US-10-170-385-182
C 6	27	100.0	5527	9	US-09-880-107-3710
C 7	27	100.0	5744	16	US-10-439-703-5
C 8	27	100.0	84539	15	US-09-962-436-36
C 9	24	88.9	50	15	US-10-244-490-45
C 10	22	81.5	22	9	US-09-995-912-4
C 11	22	81.5	22	9	US-09-747-165-3
C 12	21	77.8	21	13	US-10-382-634-20
C 13	21	77.8	21	15	US-10-349-320-19
C 14	16	59.3	468	10	US-09-918-995-19841

15	59.3	639	13	US-10-027-632-163921	Sequence 163921,
16	59.3	639	13	US-10-027-632-163922	Sequence 163922,
17	59.3	639	16	US-10-027-632-163921	Sequence 163921,
18	59.3	639	16	US-10-027-632-163922	Sequence 163922,
19	59.3	118502	13	US-10-087-192-397	Sequence 397, Appli
20	55.6	21	15	US-10-236-880-2	Sequence 2, Appli
C 21	55.6	403	10	US-09-918-995-24908	Sequence 24908, A
C 22	55.6	442	10	US-09-918-995-8048	Sequence 8048, Ap
C 23	55.6	487	13	US-10-027-632-67648	Sequence 67648, A
C 24	55.6	487	16	US-10-027-632-67648	Sequence 67648, A
C 25	55.6	554	9	US-09-864-761-9446	Sequence 9446, Ap
C 26	55.6	562	10	US-09-918-995-27376	Sequence 27376, A
C 27	55.6	566	15	US-10-029-386-5976	Sequence 5976, Ap
C 28	55.6	598	13	US-10-027-632-15713	Sequence 15713, A
C 29	55.6	598	16	US-10-027-632-15713	Sequence 15713, A
C 30	55.6	610	15	US-10-101-464A-186	Sequence 186, App
C 31	55.6	637	13	US-10-027-632-210218	Sequence 210218,
C 32	55.6	637	15	US-10-027-632-210218	Sequence 210218,
C 33	55.6	649	13	US-10-027-632-37896	Sequence 37896, A
C 34	55.6	649	16	US-10-027-632-37896	Sequence 37896, A
C 35	55.6	681	13	US-10-027-632-152558	Sequence 152558,
C 36	55.6	681	13	US-10-027-632-152558	Sequence 152558,
C 37	55.6	681	16	US-10-027-632-152558	Sequence 152558,
C 38	55.6	681	15	US-10-027-632-152559	Sequence 152559,
C 39	55.6	818	13	US-10-315-664-37	Sequence 37, Appli
C 40	55.6	820	15	US-10-181-611-1	Sequence 1, Appli
C 41	55.6	825	13	US-10-424-599-93197	Sequence 93197, A
C 42	55.6	950	9	US-09-978-295A-220	Sequence 220, App
C 43	55.6	950	9	US-09-978-697-220	Sequence 220, App
C 44	55.6	950	9	US-09-978-192A-220	Sequence 220, App
C 45	55.6	950	9	US-09-999-832A-220	Sequence 220, App

## ALIGNMENTS

### RESULT 1

US-10-228-811-1/c  
; Sequence 1, Application US/10228811  
; Publication No. US20030054392A1  
; GENERAL INFORMATION:  
; APPLICANT: Wittig, Prof. Burghardt  
; APPLICANT: Jungmans, Claas  
; TITLE OF INVENTION: Design Principle for Constructing Expression Constructs for Gene  
; TITLE OF INVENTION: Therapy  
; FILE REFERENCE: XI 597/99  
; CURRENT APPLICATION NUMBER: US/10/238,811  
; CURRENT FILING DATE: 2002-08-27  
; PRIOR APPLICATION NUMBER: DE 196 48 625.4  
; PRIOR FILING DATE: 1996-11-13  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 1078  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; NAME/KEY: gene  
; LOCATION: (1)..(1078)  
; OTHER INFORMATION: bcr3=abl2; Oligo DNA Dumbbell  
; FEATURE:  
; NAME/KEY: misc\_binding  
; LOCATION: (1)..(2)  
; OTHER INFORMATION: intramolecular binding site; the T-nucleotides at position 1 to  
; OTHER INFORMATION: 2 can be modified with amino or caroxy features  
; FEATURE:  
; NAME/KEY: misc\_binding  
; LOCATION: (1077)..(1078)  
; OTHER INFORMATION: intramolecular binding site; the T-nucleotides at position 1077  
; OTHER INFORMATION: to 1078 can be modified with amino or caroxy features  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Strandness: both; nucleic  
; OTHER INFORMATION: acid (linear), hypothetical: No. US20030054392A1 anti-sense: No

US-10-228-811-1

Query Match 100.0%; Score 27; DB 15; Length 1078;  
 Best Local Similarity 85.2%; Pred. No. 5.7e-06;  
 Matches 23; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACUCAGACCCUGAGGCUCAAGUCAGA 27  
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 Db 824 ACTCAGACCCUGAGGCTCAAAGTCAGA 798

RESULT 2

US-10-263-480-1/c  
 ; Sequence 1, Application US/10263480  
 ; Publication No. US20030170851A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: No. US20030170851A1artis AG  
 ; TITLE OF INVENTION: Organic Compounds  
 ; FILE REFERENCE: Case 4-32175P1/PROV  
 ; CURRENT APPLICATION NUMBER: US/10/263,480  
 ; CURRENT FILING DATE: 2002-10-03  
 ; NUMBER OF SEQ ID NOS: 2  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 1  
 ; LENGTH: 3393  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: (1)..(3393)  
 US-10-263-480-1

Query Match 100.0%; Score 27; DB 15; Length 3393;  
 Best Local Similarity 85.2%; Pred. No. 5e-06;  
 Matches 23; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACUCAGACCCUGAGGCUCAAGUCAGA 27  
 ||:|||||:|||||:|||||:|||||:|||||  
 Db 129 ACTCAGACCCUGAGGCTCAAAGTCAGA 103

RESULT 3

US-10-457-954-5/c  
 ; Sequence 5, Application US/10457954  
 ; Publication No. US20040005623A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Longley, B. Jack  
 ; TITLE OF INVENTION: Method of determining tumor sensitivities to therapeutic drugs  
 ; FILE REFERENCE: 960296.98890  
 ; CURRENT APPLICATION NUMBER: US/10/457,954  
 ; CURRENT FILING DATE: 2003-06-10  
 ; PRIOR APPLICATION NUMBER: 60/387,370  
 ; PRIOR FILING DATE: 2002-06-10  
 ; PRIOR APPLICATION NUMBER: 60/387,406  
 ; PRIOR FILING DATE: 2002-06-10  
 ; NUMBER OF SEQ ID NOS: 8  
 ; SOFTWARE: PatentIn version 3.2  
 ; SEQ ID NO 5  
 ; LENGTH: 3450  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: (1)..(3447)  
 ; FEATURE:  
 ; NAME/KEY: misc\_structure  
 ; LOCATION: (730)..(765)  
 ; OTHER INFORMATION: encode amino acids 244-255 for forming the sides of the enzymatic  
 ; FEATURE:  
 ; NAME/KEY: misc\_structure  
 ; LOCATION: (931)..(1077)  
 ; OTHER INFORMATION: encode amino acids 311-359 for forming the sides of the enzymatic

OTHER INFORMATION: pocket

FEATURE:  
 NAME/KEY: misc\_structure  
 LOCATION: (1141)..(1206)  
 ; OTHER INFORMATION: encode amino acids 381-402 for forming the enzymatic pocket's  
 ; OTHER INFORMATION: activation loop  
 US-10-457-954-5

Query Match 100.0%; Score 27; DB 16; Length 3450;  
 Best Local Similarity 85.2%; Pred. No. 5e-06;  
 Matches 23; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACUCAGACCCUGAGGCUCAAGUCAGA 27  
 ||:|||||:|||||:|||||:|||||:|||||  
 Db 186 ACTCAGACCCUGAGGCTCAAAGTCAGA 160

RESULT 4

US-10-204-041-3/c  
 ; Sequence 3, Application US/10204041  
 ; Publication No. US20030176443A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: STEIN-GERLACH, MATTHIAS  
 ; APPLICANT: SALASSIDIS, KONSTADINOS  
 ; APPLICANT: BACHER, GERALD  
 ; APPLICANT: MULLER, STEFAN  
 ; TITLE OF INVENTION: Pyridylpyrimidine Derivatives as Effective Compounds Against Prion  
 ; TITLE OF INVENTION: Infections and Prion Diseases  
 ; FILE REFERENCE: AXM-007.1P US  
 ; CURRENT APPLICATION NUMBER: US/10/204,041  
 ; CURRENT FILING DATE: 2002-08-16  
 ; PRIOR APPLICATION NUMBER: EP 0111858.5  
 ; PRIOR FILING DATE: 2001-05-16  
 ; PRIOR APPLICATION NUMBER: PCT/EP02/05420  
 ; PRIOR FILING DATE: 2002-05-16  
 ; NUMBER OF SEQ ID NOS: 20  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 3  
 ; LENGTH: 3840  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-10-204-041-3

Query Match 100.0%; Score 27; DB 15; Length 3840;  
 Best Local Similarity 85.2%; Pred. No. 4.9e-06;  
 Matches 23; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACUCAGACCCUGAGGCUCAAGUCAGA 27  
 ||:|||||:|||||:|||||:|||||:|||||  
 Db 493 ACTCAGACCCUGAGGCTCAAAGTCAGA 467

RESULT 5

US-10-170-385-182/c  
 ; Sequence 182, Application US/10170385  
 ; Publication No. US20030203372A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ward, Neil Raymond  
 ; APPLICANT: Mundy, Christopher Robert  
 ; APPLICANT: Kan, On  
 ; APPLICANT: Harris, Robert Alan  
 ; APPLICANT: White, Jonathan  
 ; APPLICANT: Binley, Katie Mary  
 ; APPLICANT: Rayner, William Nigel  
 ; APPLICANT: Naylor, Stuart  
 ; APPLICANT: Kingsman, Susan Mary  
 ; APPLICANT: Krige, David  
 ; TITLE OF INVENTION: ANALYSIS METHOD  
 ; FILE REFERENCE: 53268200100  
 ; CURRENT APPLICATION NUMBER: US/10/170,385  
 ; CURRENT FILING DATE: 2002-06-12  
 ; PRIOR APPLICATION NUMBER: PCT/GB02/01662  
 ; PRIOR FILING DATE: 2002-04-08

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; PRIOR APPLICATION NUMBER: PCT/GB01/05458
; PRIOR FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 549
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 182
; LENGTH: 5434
; TYPE: DNA
; ORGANISM: Homo Sapiens
; US-10-170-385-182

Query Match      100.0%; Score 27; DB 13; Length 5434;
Best Local Similarity 85.2%; Pred. No. 4.7e-06;
Matches 23; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACUCAGACCCUGAGGCUCAAAAGUCAGA 27
Db 183 ACTCAGACCTGAGGCTCAAAGTCAGA 157

RESULT 6
US-09-880-107-3710/c
; Sequence 3710, Application US/09880107
; Patent No. US20020142981A1
; GENERAL INFORMATION:
; APPLICANT: Horne, Darci T.
; APPLICANT: Vockley, Joseph G.
; APPLICANT: Scherf, Uwe
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
; FILE REFERENCE: 44921-5028-WO
; CURRENT APPLICATION NUMBER: US/09/880,107
; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: US 60/211,379
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: US 60/237,054
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 3950
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3710
; LENGTH: 5527
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20020142981A1 X16416
US-09-880-107-3710

Query Match      100.0%; Score 27; DB 9; Length 5527;
Best Local Similarity 85.2%; Pred. No. 4.7e-06;
Matches 23; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACUCAGACCCUGAGGCUCAAAAGUCAGA 27
Db 276 ACTCAGACCTGAGGCTCAAAGTCAGA 250

RESULT 7
US-10-439-703-5/c
; Sequence 5, Application US/10439703
; Publication No. US20040018527A1
; GENERAL INFORMATION:
; APPLICANT: Chang, Jenny
; APPLICANT: O'Connell, Peter
; TITLE OF INVENTION: Differential Patterns of Gene Expression that Predict for Docetax
; FILE OF INVENTION: Chemoresensitivity and Chemoresistance
; FILE REFERENCE: HO-P2482US/10205813
; CURRENT APPLICATION NUMBER: US/10/439,703
; CURRENT FILING DATE: 2003-05-16
; PRIOR APPLICATION NUMBER: US 60/381,141
; PRIOR FILING DATE: 2002-05-17
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 5744
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; TYPE: DNA
; ORGANISM: Human
; US-10-439-703-5

Query Match      100.0%; Score 27; DB 16; Length 5744;
Best Local Similarity 85.2%; Pred. No. 4.7e-06;
Matches 23; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACUCAGACCCUGAGGCUCAAAAGUCAGA 27
Db 493 ACTCAGACCTGAGGCTCAAAGTCAGA 467

RESULT 8
US-09-962-436-36/c
; Sequence 36, Application US/09962436
; Patent No. US20020081301A1
; GENERAL INFORMATION:
; APPLICANT: Soppet, Daniel
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu
; FILE OF INVENTION: Sets
; FILE REFERENCE: 689290-75
; CURRENT APPLICATION NUMBER: US/09/962,436
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/60/235,082
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/234,924
; PRIOR FILING DATE: 2000-09-25
; NUMBER OF SEQ ID NOS: 568
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 36
; LENGTH: 84539
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-962-436-36

Query Match      100.0%; Score 27; DB 9; Length 84539;
Best Local Similarity 85.2%; Pred. No. 3.4e-06;
Matches 23; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACUCAGACCCUGAGGCUCAAAAGUCAGA 27
Db 49938 ACTCAGACCTGAGGCTCAAAGTCAGA 49912

RESULT 9
US-10-244-490-45
; Sequence 45, Application US/10244490
; Publication No. US20030152916A1
; GENERAL INFORMATION:
; APPLICANT: KACIAN, DANIEL L.
; APPLICANT: FULTZ, TIMOTHY J.
; APPLICANT: MCDONOUGH, SHERROL H.
; TITLE OF INVENTION: DETECTION OF HIV
; FILE REFERENCE: 218/130
; CURRENT APPLICATION NUMBER: US/10/244,490
; CURRENT FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: US/09/168,947
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 08/469,067
; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: 07/550,837
; PRIOR FILING DATE: 1990-07-10
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 45
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthesized nucleic acid molecule
US-10-244-490-45
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Query Match 88.9%; Score 24; DB 15; Length 50;  
Best Local Similarity 83.3%; Pred. No. 0.00042;  
Matches 20; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACUCAGACCCUGAGGCUCAAGUC 24  
DB 27 ACTCAGACCCUGAGGCTCAAGTC 50

## RESULT 10

US-09-995-912-4  
; Sequence 4, Application US/09995912  
; Patent No. US20020137076A1  
; GENERAL INFORMATION:  
; APPLICANT: Shultz, John W.  
; APPLICANT: Lewis, Martin K.  
; APPLICANT: Andrews, Christine  
; TITLE OF INVENTION: RNA Polymers and Uses Thereof  
; FILE REFERENCE: PRMG-06684  
; CURRENT APPLICATION NUMBER: US/09/995,912  
; CURRENT FILING DATE: 2001-11-28  
; PRIOR APPLICATION NUMBER: 60/253,451  
; PRIOR FILING DATE: 2000-11-28  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 4  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic  
US-09-995-912-4

Query Match 81.5%; Score 22; DB 9; Length 22;  
Best Local Similarity 81.8%; Pred. No. 0.0065;  
Matches 18; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 3 UCAGACCCUGAGGCUCAAGUC 24  
DB 1 TCAGACCCUGAGGCTCAAGTC 22

## RESULT 11

US-09-747-165-3  
; Sequence 3, Application US/09747165  
; Publication No. US20020192645A1  
; GENERAL INFORMATION:  
; APPLICANT: TSENG, RICHARD W.  
; APPLICANT: SAMOSZUK, MICHAEL K.  
; TITLE OF INVENTION: BCR-ABL GENE REARRANGEMENT ASSAY METHOD  
; FILE REFERENCE: 034827/0302  
; CURRENT APPLICATION NUMBER: US/09/747,165  
; CURRENT FILING DATE: 2001-09-24  
; PRIOR APPLICATION NUMBER: 60/173,050  
; PRIOR FILING DATE: 1999-12-24  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 3  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Primer  
US-09-747-165-3

Query Match 81.5%; Score 22; DB 9; Length 22;  
Best Local Similarity 81.8%; Pred. No. 0.0065;  
Matches 18; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 3 UCAGACCCUGAGGCUCAAGUC 24  
DB 1 TCAGACCCUGAGGCTCAAGTC 22

## RESULT 12

US-10-382-634-20  
; Sequence 20, Application US/10382634  
; Publication No. US20040038921A1  
; GENERAL INFORMATION:  
; APPLICANT: Kreutzer, Roalnd  
; TITLE OF INVENTION: Composition and Method for Inhibiting Expression of a Target Gene  
; FILE REFERENCE: 20200/2062  
; CURRENT APPLICATION NUMBER: US/10/382,634  
; CURRENT FILING DATE: 2003-03-07  
; PRIOR APPLICATION NUMBER: DE 101 55 280.7  
; PRIOR FILING DATE: 2001-10-26  
; PRIOR APPLICATION NUMBER: DE 101 58 411.3  
; PRIOR FILING DATE: 2001-11-29  
; PRIOR APPLICATION NUMBER: DE 101 60 151.4  
; PRIOR FILING DATE: 2001-12-07  
; PRIOR APPLICATION NUMBER: DE 102 30 996.5  
; PRIOR FILING DATE: 2002-07-09  
; PRIOR APPLICATION NUMBER: PCT/EP02/00152  
; PRIOR FILING DATE: 2002-01-09  
; PRIOR APPLICATION NUMBER: PCT/EP02/00151  
; PRIOR FILING DATE: 2002-01-09  
; PRIOR APPLICATION NUMBER: PCT/EP02/11971  
; PRIOR FILING DATE: 2002-10-25  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 20  
; LENGTH: 21  
; TYPE: DNA  
; ORGANISM: artificial sequence  
; FEATURE:  
; OTHER INFORMATION: PRIMER  
US-10-382-634-20

Query Match 77.8%; Score 21; DB 13; Length 21;  
Best Local Similarity 81.0%; Pred. No. 0.024;  
Matches 17; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 3 UCAGACCCUGAGGCUCAAGU 23  
DB 1 TCAGACCCUGAGGCTCAAGT 21

## RESULT 13

US-10-349-320-19  
; Sequence 19, Application US/10349320  
; Publication No. US20030190654A1  
; GENERAL INFORMATION:  
; APPLICANT: Heidenreich, Olaf  
; TITLE OF INVENTION: DOUBLE-STRANDED RNA (dsRNA) AND METHOD OF USE  
; FILE REFERENCE: 20200/2112  
; CURRENT APPLICATION NUMBER: US/10/349,320  
; CURRENT FILING DATE: 2003-01-22  
; PRIOR APPLICATION NUMBER: DE 102 02 419.7  
; PRIOR FILING DATE: 2002-01-22  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 19  
; LENGTH: 21  
; TYPE: DNA  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: primer  
US-10-349-320-19

Query Match 77.8%; Score 21; DB 15; Length 21;  
Best Local Similarity 81.0%; Pred. No. 0.024;  
Matches 17; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 3 UCAGACCCUGAGGCUCAAGU 23  
DB 1 TCAGACCCUGAGGCTCAAGT 21

RESULT 14

US-09-918-995-19841/c  
 ; Sequence 19841, Application US/09918995  
 ; Publication No. US20030073623A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Hyseq, Inc.  
 ; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED  
 ; FILE REFERENCE: 20411-756  
 ; CURRENT APPLICATION NUMBER: US/09/918,995  
 ; CURRENT FILING DATE: 2001-07-30  
 ; PRIOR APPLICATION NUMBER: US/09/235,076  
 ; PRIOR FILING DATE: 1999-01-20  
 ; NUMBER OF SEQ ID NOS: 38054  
 ; SOFTWARE: FastSEQ for Windows Version 3.0  
 ; SEQ ID NO 19841  
 ; LENGTH: 468  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: misc feature  
 ; LOCATION: (1)-(468)  
 ; OTHER INFORMATION: n = A,T,C or G  
 US-09-918-995-19841

Query Match 59.3%; Score 16; DB 10; Length 468;  
 Best Local Similarity 81.2%; Pred. No. 12;  
 Matches 13; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 10 CUGAGGCUCAAGUCA 25  
 DB 331 CTGAGGCTCAAGTCA 316

RESULT 15

US-10-027-632-163921  
 ; Sequence 163921, Application US/10027632  
 ; Publication No. US20020198371A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Wang, David G.  
 ; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
 ; FILE REFERENCE: 108827.129  
 ; CURRENT APPLICATION NUMBER: US/10/027,632  
 ; CURRENT FILING DATE: 2002-04-30  
 ; PRIOR APPLICATION NUMBER: US 60/218,006  
 ; PRIOR FILING DATE: 2000-07-12  
 ; PRIOR APPLICATION NUMBER: US 60/198,676  
 ; PRIOR FILING DATE: 2000-04-20  
 ; PRIOR APPLICATION NUMBER: US 60/193,483  
 ; PRIOR FILING DATE: 2000-03-29  
 ; PRIOR APPLICATION NUMBER: US 60/185,218  
 ; PRIOR FILING DATE: 2000-02-24  
 ; PRIOR APPLICATION NUMBER: US 60/167,363  
 ; PRIOR FILING DATE: 1999-11-23  
 ; PRIOR APPLICATION NUMBER: US 60/156,358  
 ; PRIOR FILING DATE: 1999-09-28  
 ; PRIOR APPLICATION NUMBER: US 60/146,002  
 ; PRIOR FILING DATE: 1999-08-09  
 ; NUMBER OF SEQ ID NOS: 325720  
 ; SOFTWARE: FastSEQ for Windows Version 4.0  
 ; SEQ ID NO 163921  
 ; LENGTH: 639  
 ; TYPE: DNA  
 ; ORGANISM: Human  
 US-10-027-632-163921

Query Match 59.3%; Score 16; DB 13; Length 639;  
 Best Local Similarity 87.5%; Pred. No. 12;  
 Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 CAGACCCUGAGGCUCA 19  
 DB 522 CAGACCCUGAGGCTCA 537

Search completed: May 27, 2004, 14:58:32  
 Job time : 142.089 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 26, 2004, 15:22:41 ; Search time 953.308 Seconds  
(without alignments)  
845.770 Million cell updates/sec

Title: US-09-121-239-21

Perfect score: 27

Sequence: 1 ACUCAGCCUGAGGCUCAAUCACAGA 27

Scoring table: OLIGO\_NUC  
Gapop\_60.0 , Gapext 60.0

Searched: 27513289 seqs, 14931090276 residues

Word size : 0

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

EST:\*

1: em\_estba:\*

2: em\_esthum:\*

3: em\_estin:\*

4: em\_estmu:\*

5: em\_estov:\*

6: em\_estpl:\*

7: em\_estro:\*

8: em\_htc:\*

9: gb\_est1:\*

10: gb\_est2:\*

11: gb\_htc:\*

12: gb\_est3:\*

13: gb\_est4:\*

14: gb\_est5:\*

15: em\_estfun:\*

16: em\_estom:\*

17: em\_gss\_hum:\*

18: em\_gss\_inv:\*

19: em\_gss\_pin:\*

20: em\_gss\_vrt:\*

21: em\_gss\_fun:\*

22: em\_gss\_mam:\*

23: em\_gss\_mus:\*

24: em\_gss\_pro:\*

25: em\_gss\_rod:\*

26: em\_gss\_pbg:\*

27: em\_gss\_vrl:\*

28: gb\_gsl:\*

29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	27	100.0	157	10	AW386252 CM4-PT001
2	27	100.0	404	14	H81820 YS8609.rl
C 3	27	100.0	421	12	BM832613 K-EST0107
4	27	100.0	781	13	BX097261 BX097261

5	19	70.4	181	10	BE927145
6	19	70.4	875	10	BE973844
C 7	18	66.7	686	12	BI332596
C 8	18	66.7	851	10	BF531871
C 9	17	63.0	539	29	CE192426
C 10	17	63.0	542	29	CE536813
C 11	17	63.0	714	29	CE270642
C 12	17	63.0	778	29	CNS072JP
C 13	17	63.0	780	28	BG206281
C 14	17	63.0	788	28	BZ865134
C 15	17	63.0	824	12	BI246488
C 16	17	63.0	874	29	AG160977
C 17	16	59.3	129	14	CF250190
C 18	16	59.3	174	10	BF782656
C 19	16	59.3	192	10	BE522588
C 20	16	59.3	206	12	BI740150
C 21	16	59.3	210	9	AV222166
C 22	16	59.3	238	10	BE525308
C 23	16	59.3	240	10	BE525590
C 24	16	59.3	241	10	BE525578
C 25	16	59.3	241	10	BE530312
C 26	16	59.3	243	10	BB439432
C 27	16	59.3	244	10	BE525566
C 28	16	59.3	247	10	BE525452
C 29	16	59.3	250	10	BE529949
C 30	16	59.3	259	10	BE528577
C 31	16	59.3	265	9	AV140149
C 32	16	59.3	284	9	AV364585
C 33	16	59.3	290	10	BB441430
C 34	16	59.3	297	10	BE522587
C 35	16	59.3	300	10	BB248616
C 36	16	59.3	305	10	BB731714
C 37	16	59.3	306	10	BE524258
C 38	16	59.3	312	13	BY415640
C 39	16	59.3	321	10	BB043130
C 40	16	59.3	321	10	BE523402
C 41	16	59.3	324	9	AI482323
C 42	16	59.3	330	10	BE525407
C 43	16	59.3	331	10	BE525064
C 44	16	59.3	341	9	AJ444339
C 45	16	59.3	341	10	BE525372

#### ALIGNMENTS

RESULT 1  
AW386252/c 157 bp mRNA linear EST 04-FEB-2000  
LOCUS CM4-PT0015-071299-057-d10 PT0015 Homo sapiens cDNA, mRNA sequence.  
DEFINITION AW386252  
ACCESSION AW386252.1 GI:6890976  
VERSION EST.  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 157)  
HCGP <http://www.ludwig.org.br/ORESTES>.  
AUTHORS The FAPESP/LICR Human Cancer Genome Project  
TITLE Unpublished (1999)  
JOURNAL Contact: Simpson A.J.G.  
COMMENT Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: [asimpson@ludwig.org.br](mailto:asimpson@ludwig.org.br)  
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL  
(<http://www.ludwig.org.br/scripts/gethtml2.pl?ti=CM4&t2=CM4-PT0015-071299-057-d10&t3=1999-12-07&t4=1>)

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Seq primer: puc 18 forward
High quality sequence start: 2
High quality sequence stop: 157.
FEATURES
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            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /dev_stage="Adult"
            /clone_lib="PT0015"
            /note="Organ: pnet; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORSTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
ORIGIN
    Query Match      100.0%; Score 27; DB 10; Length 157;
    Best Local Similarity 85.2%; Pred. No. 6.8e-05;
    Matches 23; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
QY      1 ACUCAGACCCUGAGGCGCUAAAGUCAGA 27
Db      117 ACTCAGACCCUGAGGCTCAAGTCAGA 91
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RESULT 2
H81820
LOCUS      H81820          404 bp      mRNA      linear      EST 09-NOV-1995
DEFINITION Ys68e09.r1 Soares retina N2b4HR Homo sapiens cDNA clone
IMAGE:219976 5' similar to gb:M14752 PROTO-ONCOGENE
TYROSINE-PROTEIN KINASE ABL (HUMAN);, mRNA sequence.
ACCESSION H81820.1 GI:1059909
VERSION    H81820.1
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
REFERENCE  1 (bases 1 to 404)
AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevasakis,E., Waterston,R., Williamson,A., Wohlmann,P. and Wilson,R.
TITLE      The WashU-Merck EST Project
JOURNAL    Unpublished (1995)
COMMENT    Contact: Wilson RK
           4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
           Tel: 314 286 1800
           Fax: 314 286 1810
           Email: est@watson.wustl.edu
           High quality sequence stops: 382
           Source: IMAGE Consortium LNL
           This clone is available royalty-free through LNL; contact the
           IMAGE Consortium (info@image.lnl.gov) for further information.
           Insert Length: 1427 Std Error: 0.00
           Seq primer: M13RP1
           High quality sequence stop: 382.
FEATURES
    source
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            /organism="Homo sapiens"
            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /db_xref="GDB:3847969"
            /clone="IMAGE:219976"
            /sex="male"
            /tissue_type="retina"
            /dev_stage="55 year old"
            /lab_host="DH10B (ampicillin resistant)"

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/clone lib="Soares retina N2b4HR"
/note="Organ: eye; Vector: pT7T3D (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5', TGTTACCAATCTGAAGTGGAGCGCGCGCTTTTCTTTTCTTTT 3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). The retinas were obtained from a 55 year old Caucasian and total cellular poly(A)+ RNA was extracted 6 hrs after their removal. The retina RNA was kindly provided by Roderick R. McInnes M.D. Ph.D. from the University of Toronto. Library constructed by Bento Soares and M.Fatima Bonaudo."
ORIGIN
    Query Match      100.0%; Score 27; DB 14; Length 404;
    Best Local Similarity 85.2%; Pred. No. 8.8e-05;
    Matches 23; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
QY      1 ACUCAGACCCUGAGGCGCUAAAGUCAGA 27
Db      75 ACTCAGACCCUGAGGCTCAAGTCAGA 101
        ||:|||||:||||:||||:||||:||||
RESULT 3
BM832613/c
LOCUS      BM832613          421 bp      mRNA      linear      EST 06-MAR-2002
DEFINITION K-EST0107122 S11SNU1 Homo sapiens cDNA clone S11SNU1-47-E02 5',
            mRNA sequence.
ACCESSION BM832613
VERSION    BM832613.1 GI:19189022
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
REFERENCE  1 (bases 1 to 421)
AUTHORS   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
           Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Kim,Y.S.
           21C Frontier Korean EST Project 2001
           Unpublished (2002)
           Contact: Kim YS
           Genome Research Center
           Korea Research Institute of Bioscience & Biotechnology
           52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea
           Tel: +82-42-860-4470
           Fax: +82-42-860-4409
           Email: yongsung@mail.kribb.re.kr
           Plate: 47 row: E column: 02
           High quality sequence stop: 421.
FEATURES
    source
        1..421
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            /mol_type="mRNA"
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            /cell_type="Lymphoblast-like"
            /cell_line="SNU-1"
            /lab_host="Top10F"
            /clone_lib="S11SNU1"
            /note="Organ: Stomach; Vector: pME18-FL3; Site_1: XhoI; Site_2: XhoI; The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tabacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including SfiI site by treatment of T4 RNA ligase and the first strand cDNA was synthesized with Superscript II using SfiI oligo-dT primer. After first strand synthesis, RNA was degraded by NaOH treatment and cDNA was amplified by PCR

```



reaction. The PCR products were digested with SfiI and cloned into DraIII- digested pME18S-FL3 vector. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10p' by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."

## ORIGIN

Query Match 100.0%; Score 27; DB 12; Length 421;  
Best Local Similarity 85.2%; Pred. No. 8.9e-05;  
Matches 23; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACUCAGACCCUGAGGCUCAAGUCAGA 27  
||:|||||:||||:||||:||||:||||:  
DB 306 ACTCAGACCCCTGAGGCTCAAAGTCAGA 280

## RESULT 4

BX097261

LOCUS

DEFINITION BX097261 Soares retina N2b4HR Homo sapiens cDNA clone  
IMAGE:998C17436 ; IMAGE:219976, mRNA sequence.

ACCESSION

BX097261

VERSION

BX097261.1

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 781)

AUTHORS

Ebert, L., Heil, O., Hennig, S., Neubert, P., Partsch, E., Peters, M.,

Radehof, U., Schneider, D. and Korn, B.

TITLE

Human Unigeneset - RZPD3

JOURNAL

Unpublished (2003)

COMMENT

Contact: Ina Rolfs

RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH

Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany

RZPD; IMAGp998C17436.

RZPDLIB; I.M.A.G.E. cDNA Clone Collection;

Human Unigeneset - RZPD3 (RZPDLIB No.972)

http://www.rzpd.de/CloneCards/cgi-

bin/showLib.pl.cgi/response?libNo=972 Contact: Ina Rolfs

RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH

Heubnerweg 6, D-14059 Berlin, Germany

Tel: +49 30 32639 101

Fax: +49 30 32639 111

www.rzpd.de

This clone is available royalty-free from RZPD;

contact RZPD (clone@rzpd.de) for further information. Seq primer:

M13r, Primer sequence: TTTCACAGGAAACAGCTATGAC.

Location/Qualifiers

1. .781

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGp998C17436 ; IMAGE:219976"

/sex="male"

/tissue\_type="retina"

/lab\_host="PH10B (ampicillin resistant)"

/note="Organ: eye; Vector: p773D (Pharmacia) with a

modified polylinker; Site 1: Not 1; Site 2: Eco RI; 1st

strand cDNA was primed with a Not I - oligo(dT) primer [5'

TGTTACCATCTGAGTGGAGCGCGCTTTTCTTTTCTTTT 3'].

double-stranded cDNA was size selected, ligated to Eco RI

adapters (Pharmacia), digested with Not I and cloned into

the Not I and Eco RI sites of a modified p773 vector

(Pharmacia). The retinas were obtained from a 55 year old

Caucasian and total cellular poly(A)+ RNA was extracted 6

hrs after their removal. The retina RNA was kindly

provided by Roderick R. McInnes M.D. Ph.D. from the

University of Toronto. Library constructed by Bento

## ORIGIN

Query Match 100.0%; Score 27; DB 13; Length 781;  
Best Local Similarity 85.2%; Pred. No. 0.0011;  
Matches 23; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACUCAGACCCUGAGGCUCAAGUCAGA 27  
||:|||||:||||:||||:||||:||||:  
DB 55 ACTCAGACCCCTGAGGCTCAAAGTCAGA 81

## RESULT 5

BE927145

LOCUS

DEFINITION

BE927145

ACCESSION

BE927145.1

VERSION

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 181)

AUTHORS

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,

Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,

Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,

Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V.,

O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and

Simpson, A.J.

TITLE

Shotgun sequencing of the human transcriptome with ORF expressed

sequence tags

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

20020663

10737800

COMMENT

Contact: Simpson A.J.G.

Laboratory of Cancer Genetics

Ludwig Institute for Cancer Research

Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,

Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome

Project. This entry can be seen in the following URL

(http://www.ludwig.org.br/scripts/gethtml2.pl?cl=4&amp;t=1&amp;f=1)

900-015-e08&amp;t3=2000-09-01&amp;t4=1)

Seq primer: puc 18 forward

High quality sequence start: 57

High quality sequence stop: 130.

Location/Qualifiers

1. .181

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/dev\_stage="Adult"

/clone\_lib="CN0007"

/note="Organ: colon normal; Vector: puc18; Site 1: SmaI;

Site 2: SmaI; A mini-library was made by cloning products

derived from ORESTES PCR (U.S. Letters Patent application

No. 196,716 - Ludwig Institute for Cancer Research)

profiles into the pUC 18 vector. Reverse transcription of

tissue mRNA and cDNA amplification were performed under

low stringency conditions."

## ORIGIN

Query Match 70.4%; Score 19; DB 10; Length 181;  
Best Local Similarity 84.2%; Pred. No. 2.2;  
Matches 16; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACUCAGACCCUGAGGCUCA 19  
||:|||||:||||:||||:||||:||||:  
DB 91 ACTCAGACCCCTGAGGCTCA 109

```
RESULT 6
BF973844/c
LOCUS
DEFINITION
602241947F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4330571 5',
mRNA sequence.
ACCESSION
BF973844
VERSION
BF973844.1 GI:12341059
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 875)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM193 row: n column: 12
High quality sequence stop: 772.
Location/Qualifiers
1..875
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue="leiomysarcoma cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 46"
/notes="Organ: uterus; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGGAG(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
Library."
ORIGIN
Query Match 70.4%; Score 19; DB 10; Length 875;
Best Local Similarity 84.2%; Pred. No. 3.4;
Matches 16; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 CUCAGACCCUGAGGCUCAA 20
|:|||||:|||||:|
Db 783 CTCAGACCTGAGGCTCAA 765

RESULT 7
BI332596/c
LOCUS
DEFINITION
602980736F1 NCI_CGAP_Li9 Mus musculus cDNA clone IMAGE:5133728 5',
mRNA sequence.
ACCESSION
BI332596
VERSION
BI332596.1 GI:15017253
KEYWORDS
EST.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 686)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9776 row: j column: 02
High quality sequence stop: 652.
Location/Qualifiers
1..851
/organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:4209889"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NCI_CGAP_Li9"
/notes="Organ: liver; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.9 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
ORIGIN
Query Match 66.7%; Score 18; DB 12; Length 686;
Best Local Similarity 88.9%; Pred. No. 12;
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 AGACCCUGAGGCUCAAAG 22
|||||:|||||:|
Db 566 AGACCTGAGGCTCAAAG 549

RESULT 8
BF531871/c
LOCUS
DEFINITION
602072805F1 NCI_CGAP_Li9 Mus musculus cDNA clone IMAGE:4209889 5',
mRNA sequence.
ACCESSION
BF531871
VERSION
BF531871.1 GI:11619234
KEYWORDS
EST.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 851)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9776 row: j column: 02
High quality sequence stop: 652.
Location/Qualifiers
1..851
/organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:4209889"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NCI_CGAP_Li9"
/notes="Organ: liver; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.9 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
ORIGIN
Query Match 66.7%; Score 18; DB 12; Length 686;
Best Local Similarity 88.9%; Pred. No. 12;
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 AGACCCUGAGGCUCAAAG 22
|||||:|||||:|
Db 566 AGACCTGAGGCTCAAAG 549

JOURNAL COMMENT
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11328 row: g column: 09
High quality sequence stop: 677.
Location/Qualifiers
1..686
/organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:5133728"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NCI_CGAP_Li9"
/notes="Organ: liver; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.9 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
ORIGIN
Query Match 66.7%; Score 18; DB 12; Length 686;
Best Local Similarity 88.9%; Pred. No. 12;
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 AGACCCUGAGGCUCAAAG 22
|||||:|||||:|
Db 566 AGACCTGAGGCTCAAAG 549

JOURNAL COMMENT
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9776 row: j column: 02
High quality sequence stop: 652.
Location/Qualifiers
1..851
/organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:4209889"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NCI_CGAP_Li9"
/notes="Organ: liver; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.9 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
ORIGIN
Query Match 66.7%; Score 18; DB 12; Length 686;
Best Local Similarity 88.9%; Pred. No. 12;
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 AGACCCUGAGGCUCAAAG 22
|||||:|||||:|
Db 566 AGACCTGAGGCTCAAAG 549

JOURNAL COMMENT
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9776 row: j column: 02
High quality sequence stop: 652.
Location/Qualifiers
1..851
/organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:4209889"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NCI_CGAP_Li9"
/notes="Organ: liver; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.9 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
ORIGIN
Query Match 66.7%; Score 18; DB 12; Length 686;
Best Local Similarity 88.9%; Pred. No. 12;
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 AGACCCUGAGGCUCAAAG 22
|||||:|||||:|
Db 566 AGACCTGAGGCTCAAAG 549
```



peripheral blood"

/evidence=not\_experimental

## ORIGIN

Query Match 63.0%; Score 17; DB 29; Length 714;  
 Best Local Similarity 82.4%; Pred. No. 43;  
 Matches 14; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 UCAGACCCUGAGGCUCA 19  
 :|||||:|||||:  
 Db 469 TCAGACCTGAGGCTCA 485

## RESULT 12

CNS072JP/c  
 LOCUS 778 bp DNA linear GSS 07-JUL-2001  
 DEFINITION clone BA0AB012A05 of library BA0AB from strain CLIB 210 of Kluyveromyces lactis, genomic survey sequence.  
 ACCESSION AL426299  
 VERSION AL426299.1 GI:12209493  
 KEYWORDS GSS.  
 SOURCE Kluyveromyces lactis  
 ORGANISM Kluyveromyces lactis

REFERENCE 1 (bases 1 to 778)  
 AUTHORS Souciet,J.L., Aigle,M., Artiguenave,F., Blandin,G., Bolotin-Fukuhara,M., Bon,E., Brottier,P., Casaregola,S., de-Montigny,J., Dujon,B., Durrens,P., Lepingle,A., Llorente,B., Malpertuy,A., Neuveglise,C., Ozier-Kalogeropoulos,O., Potier,S., Saurin,W., Tekala,F., Toffano-Nioche,C., Wesolowski-Louvel,M., Wincker,P. and Weissenbach,J.

TITLE Genomic exploration of the hemiascomycetous yeasts: 1. A set of yeast species for molecular evolution studies  
 JOURNAL FEBS Lett. 487 (1), 3-12 (2000)  
 MEDLINE 20584711  
 PUBMED 11152876

REFERENCE 2 (bases 1 to 778)  
 AUTHORS Bolotin-Fukuhara,M., Toffano-Nioche,C., Artiguenave,F., Duchateau-Nguyen,G., Lemaire,M., Marmeisse,R., Montrocher,R., Robert,C., Ternier,M., Wincker,P. and Wesolowski-Louvel,M.  
 TITLE Genomic exploration of the hemiascomycetous yeasts: 11.

JOURNAL FEBS Lett. 487 (1), 66-70 (2000)  
 MEDLINE 20584721  
 PUBMED 11152886

REFERENCE 3 (bases 1 to 778)  
 AUTHORS Direct Submission

TITLE Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage, 2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)  
 COMMENT This GSS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii, Kluyveromyces Kluyveri, Kluyveromyces thermotolerans, Kluyveromyces lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila, Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.

## FEATURES

source  
 1..778  
 /organism="Kluyveromyces lactis"  
 /mol\_type="genomic DNA"  
 /strain="CLIB 210"  
 /variety="lactis"  
 /db\_xref="taxon:28985"  
 /clone="BA0AB012A05"  
 /clone\_lib="BA0AB"

## misc\_feature

<1..>378  
 /note="similar to Saccharomyces cerevisiae ORF YGR120c [ SEC35 ; required for ER to golgi vesicle docking ]"

## ORIGIN

Query Match 63.0%; Score 17; DB 29; Length 778;  
 Best Local Similarity 82.4%; Pred. No. 44;  
 Matches 14; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 11 UGAGGCUCAAGUCAGA 27  
 :|||||:|||||:  
 Db 534 TCAGGCTCAAGTCAGA 518

## RESULT 13

BG206281/c  
 LOCUS 780 bp mRNA linear EST 21-APR-2001  
 DEFINITION RST575726 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.  
 ACCESSION BG206281  
 VERSION BG206281.1 GI:13727968  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 780)  
 AUTHORS Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R., Cain,S., Leventhal,C., Thornton,M., Ramachandran,R., Whittington,J., Lerner,L., Costanzo,D., McElligott,K., Booser,S., Mays,R., Smith,E., Veloso,N., Klika,A., Hess,J., Cothren,K., Lo,K., Offenbacher,J., Danzig,J. and Ducar,M.  
 TITLE Creation of genome-wide protein expression libraries using random activation of gene expression  
 JOURNAL Nat. Biotechnol. 19 (5), 440-445 (2001)  
 MEDLINE 21227151  
 PUBMED 11329013

COMMENT Contact: Scott J. Cain  
 Athersys, Inc.  
 3201 Carnegie Ave, Cleveland, OH 44115, USA  
 Tel: 216 431 9900  
 Fax: 216 361 9596  
 Email: scain@athersys.com  
 High quality sequence stop: 425.  
 Location/Qualifiers  
 1..780  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /cell\_line="HT1080"  
 /clone\_lib="Athersys RAGE Library"  
 /note="See 'Creation of Genome-wide Protein Expression Libraries using Random Activation of Gene Expression', Nature Biotechnology, in press. Note that even though the cell type indicated is HT1080, since a random activation method was used, these sequence tags are not necessarily expressed in HT1080 under normal circumstances."

## FEATURES

## source

1..780  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /cell\_line="HT1080"  
 /clone\_lib="Athersys RAGE Library"  
 /note="See 'Creation of Genome-wide Protein Expression Libraries using Random Activation of Gene Expression', Nature Biotechnology, in press. Note that even though the cell type indicated is HT1080, since a random activation method was used, these sequence tags are not necessarily expressed in HT1080 under normal circumstances."

## ORIGIN

Query Match 63.0%; Score 17; DB 12; Length 780;  
 Best Local Similarity 82.4%; Pred. No. 44;  
 Matches 14; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 UCAGACCCUGAGGCUCA 19  
 :|||||:|||||:  
 Db 76 TCAGACCTGAGGCTCA 60

## RESULT 14

BZ865134/c  
 LOCUS 788 bp DNA linear GSS 18-MAR-2003  
 DEFINITION CH240\_235MB.TJ CHORI-240 Bos taurus genomic clone CH240\_235MB, genomic survey sequence.  
 ACCESSION BZ865134  
 VERSION BZ865134.1 GI:29092539  
 KEYWORDS GSS.

**SOURCE** Bos taurus (cow)  
**ORGANISM** Bos taurus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bovinae; Bos.  
**REFERENCE** 1 (bases 1 to 788)  
**AUTHORS** Zhao, S., Shetty, J., Shatman, S., Tsengaye, G., Geer, K., Shvartsbeyn, A., Gebregorgis, E., Chen, D., Riggs, F., de Jong, P., Crawford, A. M. and McSwan, J. C.  
**TITLE** Bovine BAC End Sequences from Library CHORI-240  
**JOURNAL** Unpublished (2003)  
**COMMENT** Department of Eukaryotic Genomics  
 The Institute for Genomic Research  
 9712 Medical Center Dr., Rockville, MD 20850, USA  
 Tel: 301 838 0200  
 Fax: 301 838 0208  
 Email: szhao@tigr.org  
 Clones are derived from the bovine BAC library CHORI-240 (<http://www.chori.org/bacpac/bovine240.htm>). For BAC library availability, please contact Pieter de Jong ([pdejong@mail.choi.org](mailto:pdejong@mail.choi.org)). Clones may be purchased from BACPAC Resources (<http://www.chori.org/bacpac/ordering/information.htm>). This work was undertaken as part of the International Bovine BAC Mapping Consortium (IBBMC) by AgResearch Ltd., New Zealand and The Institute of Genomic Research (TIGR), USA.  
 Plate: 235 row: M column: 8  
 Seq primer: SP6  
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 /db\_xref="taxon:9913"  
 /clone="CH240\_235M8"  
 /sex="Male"  
 /cell\_type="Blood"  
 /clone\_lib="CHORI-240"  
 /notes="Vector: pTARBAC1.3; Site 1: MboI; Site 2: MboI; Hereford bull Li Domino 99375; CHORI-240 Bovine BAC library (Male) produced by Pieter de Jong"

## ORIGIN

Query Match 63.0%; Score 17; DB 28; Length 788;  
 Best Local Similarity 88.2%; Pred. No. 44;  
 Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 AGACCCUGAGGCUCAAA 21

Db 293 AGACCCUGAGGCTCAAA 277

**RESULT 15**  
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 LOCUS 824 bp mRNA linear EST 17-JUL-2001  
**DEFINITION** G02958537F1 NCI\_CGAP\_Li9 Mus musculus cDNA clone IMAGE:5124201 5', mRNA sequence.  
**ACCESSION** BI246488  
**VERSION** BI246488.1 GI:14790501  
**KEYWORDS** EST.  
**SOURCE** Mus musculus (house mouse)  
**ORGANISM** Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 824)  
**REFERENCE** NIH-MGC <http://mgc.nci.nih.gov/>.  
**AUTHORS** National Institutes of Health, Mammalian Gene Collection (MGC)  
**JOURNAL** Unpublished (1999)  
**COMMENT** Contact: Robert Strausberg, Ph.D.  
 Email: cgabs-i@mail.nih.gov  
 Tissue Procurement: Jeffrey E. Green, M.D.  
 cDNA Library Preparation: Life Technologies, Inc.

**FEATURES** Location/Qualifiers  
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 /mol\_type="mRNA"  
 /strain="FVB/N"  
 /db\_xref="taxon:10090"  
 /clone="IMAGE:5124201"  
 /lab\_host="DH10B (T1 phage-resistant)"  
 /clone\_lib="NCI CGAP Li9"  
 /note="Organ: liver; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: Sall; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.9 kb. Constructed by Life Technologies. Note: this is a NCI\_CGAP Library."

## ORIGIN

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 Best Local Similarity 88.2%; Pred. No. 45;  
 Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 6 GACCCUGAGGCUCAAAAG 22

Db 567 GACCCUGAGGCTCAAAAG 551

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 Job time : 954.308 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 27, 2004, 02:16:55 ; Search time 715.838 Seconds  
(without alignments)  
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Scoring table: OLIGO\_NUC  
Gapop\_60.0 , Gapext 60.0

Searched: 3470272 seqs, 21671516995 residues

Word size : 0  
Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0  
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- 33: em\_hgt\_mus:
- 34: em\_hgt\_pln:
- 35: em\_hgt\_rod:
- 36: em\_hgt\_mam:
- 37: em\_hgt\_vrt:
- 38: em\_sy:
- 39: em\_hgt\_hum:
- 40: em\_hgt\_mus:
- 41: em\_hgt\_other:

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

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C 2	27	100.0	27	6	BD222543	BD222543 Methods f
C 3	27	100.0	27	6	BD222544	BD222544 Methods f
C 4	27	100.0	27	6	BD222545	BD222545 Methods f
C 5	27	100.0	54	6	BD222523	BD222523 Methods f
C 6	27	100.0	54	6	BD222524	BD222524 Methods f
C 7	27	100.0	54	6	BD222525	BD222525 Methods f
C 8	27	100.0	54	6	BD222526	BD222526 Methods f
C 9	27	100.0	102	9	HST922FU	X07537 Human ALL t
C 10	27	100.0	153	9	HUMABLB	M14754 Human abl m
C 11	27	100.0	204	9	HUMBCRA2	M25948 Human chron
C 12	27	100.0	205	6	I02402	I02402 Sequence 1
C 13	27	100.0	234	9	HUMCABL1	M13098 Homo sapien
C 14	27	100.0	257	6	I58633	I58633 Sequence 1
C 15	27	100.0	257	6	I96199	I96199 Sequence 36
C 16	27	100.0	266	6	I58636	I58636 Sequence 4
C 17	27	100.0	266	6	I96200	I96200 Sequence 37
C 18	27	100.0	299	6	BD222547	BD222547 Methods f
C 19	27	100.0	350	6	BD222546	BD222546 Methods f
C 20	27	100.0	423	9	AB069693	AB069693 Homo sapi
C 21	27	100.0	468	9	HUMCMICABL	M25946 Human chron
C 22	27	100.0	468	9	HUMMK562A	M13096 Human chime
C 23	27	100.0	491	9	HUMALIBCR	M19730 Human acute
C 24	27	100.0	494	9	HUMABLC	M30833 Human abl p
C 25	27	100.0	532	9	HUMABLEA	M14753 Human abl m
C 26	27	100.0	549	9	HSREAKP3	Z35761 Homo sapien
C 27	27	100.0	679	9	HUMABLB	M30832 Human bcr/a
C 28	27	100.0	854	9	HUMABLD	M30829 Human bcr/a
C 29	27	100.0	922	9	HSAL131467	AJ131467 Homo sapi
C 30	27	100.0	997	9	HSAL131466	AJ131466 Homo sapi
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C 32	27	100.0	1078	6	AR230688	AR230688 Sequence
C 33	27	100.0	1079	9	AF113911	AF113911 Homo sapi
C 34	27	100.0	3393	6	AX743957	AX743957 Sequence
C 35	27	100.0	3623	6	I96198	I96198 Sequence 35
C 36	27	100.0	3840	6	AX601393	AX601393 Sequence
C 37	27	100.0	3840	9	HUMABLA	M14752 Human c-abl
C 38	27	100.0	5527	6	AX411066	AX411066 Sequence
C 39	27	100.0	5527	9	HSABL	X16416 Human c-abl
C 40	27	100.0	5744	6	AX779943	AX779943 Sequence
C 41	27	100.0	84539	6	AX331986	AX331986 Sequence
C 42	27	100.0	84539	9	HSABLGR3	U07563 Human proto
C 43	27	100.0	176466	9	AL161733	AL161733 Human DNA
C 44	26	96.3	80	6	I58639	I58639 Sequence 7
C 45	26	96.3	80	6	I96201	I96201 Sequence 38

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LOCUS BD222542 27 bp DNA linear PAT 17-JUL-2003  
DEFINITION Methods for detecting and measuring spliced nucleic acids.  
ACCESSION BD222542  
VERSION BD222542.1 GI:33032312  
KEYWORDS JP 2002521037-A/20.  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1 (bases 1 to 27)  
AUTHORS Harvey, R.C. and Eastman, P.S.  
TITLE Methods for detecting and measuring spliced nucleic acids  
JOURNAL Patent: JP 2002521037-A 20 16-JUL-2002;  
GEN PROBE INC





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Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 TCTGACTTTGAGCCTCAGGGTCTGAGT 27

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LOCUS          54 bp DNA linear PAT 17-JUL-2003
DEFINITION    Methods for detecting and measuring spliced nucleic acids.
ACCESSION     BD222523
VERSION       BD222523.1 GI:33032293
KEYWORDS      JP 2002521037-A/1.
SOURCE        synthetic construct
ORGANISM      artificial sequences.
REFERENCE     1 (bases 1 to 54)
AUTHORS       Harvey,R.C. and Eastman,P.S.
TITLE         Methods for detecting and measuring spliced nucleic acids
JOURNAL       Patent: JP 2002521037-A 1 16-JUL-2002;
              GEN PROBE INC
COMMENT       OS Artificial Sequence
              PN JP 2002521037-A/1
              PD 16-JUL-2002
              PF 23-JUL-1999 JP 2000561364
              PR 23-JUL-1998 US 09/121239
              PI RICHARD C HARVEY,PAUL S EASTMAN
              PC C12Q1/68,C12N15/09,C12N15/00
              CC Description of Artificial Sequence: Synthetic promoter primer
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Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 54 TCTGACTTTGAGCCTCAGGGTCTGAGT 28

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DEFINITION    Methods for detecting and measuring spliced nucleic acids.
ACCESSION     BD222525
VERSION       BD222525.1 GI:33032295
KEYWORDS      JP 2002521037-A/3.
SOURCE        synthetic construct
ORGANISM      artificial sequences.
REFERENCE     1 (bases 1 to 54)
AUTHORS       Harvey,R.C. and Eastman,P.S.
TITLE         Methods for detecting and measuring spliced nucleic acids
JOURNAL       Patent: JP 2002521037-A 3 16-JUL-2002;
              GEN PROBE INC
COMMENT       OS Artificial Sequence
              PN JP 2002521037-A/3
              PD 16-JUL-2002
              PF 23-JUL-1999 JP 2000561364
              PR 23-JUL-1998 US 09/121239
              PI RICHARD C HARVEY,PAUL S EASTMAN
              PC C12Q1/68,C12N15/09,C12N15/00
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LOCUS          54 bp RNA linear PAT 17-JUL-2003
DEFINITION    Methods for detecting and measuring spliced nucleic acids.
ACCESSION     BD222526
VERSION       BD222526.1 GI:33032294
KEYWORDS      JP 2002521037-A/2.
SOURCE        synthetic construct
ORGANISM      artificial sequences.
REFERENCE     1 (bases 1 to 54)
AUTHORS       Harvey,R.C. and Eastman,P.S.
TITLE         Methods for detecting and measuring spliced nucleic acids
JOURNAL       Patent: JP 2002521037-A 2 16-JUL-2002;
              GEN PROBE INC
COMMENT       OS Artificial Sequence
              PN JP 2002521037-A/2
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SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 204)  
 AUTHORS De Klein, A., Hermans, A., Bootsma, D., Grosveld, G., Heisterkamp, N., Stam, K. and Groffen, J.  
 TITLE The role of the Philadelphia translocation in chronic myelocytic leukemia  
 JOURNAL Ann. Clin. Res. 18 (5-6), 278-283 (1986)  
 MEDLINE 87183193  
 PUBMED 3471171  
 COMMENT Original source text: Human fibroblast cell line K562, cDNA to mRNA, clone pvi-3.  
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 Db 39 TCTGACTTTGAGCCTCAGGCTCTGAGT 65  
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 LOCUS I02402 205 bp ss-DNA linear PAT 21-MAY-1993  
 DEFINITION Sequence 1 from Patent US 4874853.  
 ACCESSION I02402  
 VERSION I02402.1 GI:270541  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCE 1 (bases 1 to 205)  
 AUTHORS Rossi, J.J.  
 TITLE Synthetic oligonucleotides useful in diagnosis of chronic myelogenous leukemia  
 JOURNAL Patent: US 4874853-A 1 17-OCT-1989;  
 City of Hope; Duarte, CA  
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 Db 130 TCTGACTTTGAGCCTCAGGCTCTGAGT 156  
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 HUMCABL1  
 LOCUS HUMCABL1 234 bp DNA linear PRI 04-MAY-2000  
 DEFINITION Homo sapiens c-abl (ABL1) gene, exon al.  
 ACCESSION M13098  
 VERSION M13098.1 GI:179747  
 KEYWORDS  
 SEGMENT 1 of 2  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 234)  
 AUTHORS Grosveld, G., Verwoerd, T., van Agthoven, T., de Klein, A., Ranachandran, K.L., Heisterkamp, N., Stam, K. and Groffen, J.  
 TITLE The chronic myelocytic cell line K562 contains a breakpoint in bcr and produces a chimeric bcr/c-abl transcript  
 JOURNAL Mol. Cell. Biol. 6 (2), 607-616 (1986)  
 MEDLINE 87064346  
 PUBMED 3023859  
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 I58633  
 LOCUS I58633 257 bp DNA linear PAT 07-OCT-1997  
 DEFINITION Sequence 1 from patent US 5652222.  
 ACCESSION I58633  
 VERSION I58633.1 GI:2477871  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCE 1 (bases 1 to 257)  
 AUTHORS Calabretta, B. and Gewirtz, A.M.  
 TITLE Selective inhibition of leukemic cell proliferation by bcr-abl antisense oligonucleotides  
 JOURNAL Patent: US 5652222-A 1 29-JUL-1997;  
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 I96199  
 LOCUS I96199 257 bp DNA linear PAT 01-DEC-1998  
 DEFINITION Sequence 36 from patent US 5734039.  
 ACCESSION I96199  
 VERSION I96199.1 GI:3940669  
 KEYWORDS

SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 257)  
AUTHORS Calabretta,B. and Skorski,T.  
TITLE Antisense oligonucleotides targeting cooperating oncogenes  
JOURNAL Patent: US 5734039-A 36 31-MAR-1998;  
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Search completed: May 27, 2004, 12:06:10  
Job time : 715.838 secs

GenCore version 5.1.1.6  
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OM nucleic - nucleic search, using sw model

Run on: May 26, 2004, 16:52:28 ; Search time 166.387 Seconds  
(without alignments)  
689.363 Million cell updates/sec

Title: US-09-121-239-22

Perfect score: 27

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Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 3373863 seqs, 2124099041 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

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5: Geneseqn2001bs:\*  
6: Geneseqn2002s:\*  
7: Geneseqn2003as:\*  
8: Geneseqn2003bs:\*  
9: Geneseqn2003cs:\*  
10: Geneseqn2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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C 7	27	100.0	54	3	Aaz60840 Oligonucl
8	27	100.0	54	3	Aaz60842 Oligonucl
9	27	100.0	205	1	Aan91666 Bcr-abl f
10	27	100.0	257	2	Aaq34625 Human bcr
11	27	100.0	257	2	Aav20458 Human bcr
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13	27	100.0	266	2	Aav20459 Human bcr
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17	27	100.0	468	6	Abst73171 Human tra
18	27	100.0	549	6	Abst73314 DNA encod
19	27	100.0	679	6	Abst73172 DNA encod
20	27	100.0	854	6	Abst73170 DNA encod
21	27	100.0	921	5	Aas85025 DNA encod
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24	27	100.0	1024	7	Abz82900 Toxicolog
25	27	100.0	1079	5	Aas85026 DNA encod
26	27	100.0	1079	6	Abst73181 DNA encod
27	27	100.0	1097	2	Aat91764 Chimeric
28	27	100.0	1212	5	Aas85028 DNA encod
29	27	100.0	3323	7	Abz18519 Group III
30	27	100.0	3380	7	Abz18520 Group III
31	27	100.0	3393	7	Abx95815 cDNA enco
32	27	100.0	3623	2	Aav20457 Human c-a
33	27	100.0	3780	2	Aat61864 c-abl gen
34	27	100.0	3840	7	Aad52781 Human Abl
35	27	100.0	5434	6	Abv77964 Hypoxia-r
36	27	100.0	5520	2	Aat61865 c-abl gen
37	27	100.0	5527	6	Abn97215 Gene #371
38	27	100.0	84539	6	AbL64158 Stomach c
40	26	96.3	80	2	Aaq34631 Human Phi
41	25	92.6	200	2	Aat88785 Human bcr
C 42	24	88.9	50	2	Aat88785 Leukaemic
C 43	24	88.9	50	2	Aaq86626 CML chrom
C 44	24	88.9	50	2	Aat15571 CML-2 chr
C 45	24	88.9	50	2	Aat42417 CML chrom
					Aav66349 CML-2 chr

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AC AAZ60861;  
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DT 16-MAY-2000 (first entry)  
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DE Oligonucleotide used to detect bcr b3-abl fusion transcripts.  
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KW Fusion transcript; translocation; bcr b3 region; abl gene;  
KW amplification assay; detection assay; medical diagnosis;  
KW clinical monitoring; chimeric RNA; fusion RNA; condition marker;  
KW disease marker; cancer; leukemia; ss.  
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OS Synthetic.  
XX  
FN WO200005418-A1.  
XX  
PD 03-FEB-2000.  
XX  
PF 23-JUL-1999; 99WO-US016832.  
XX  
PR 23-JUL-1998; 98US-00121239.  
PA (GENP-) GEN-PROBE INC.  
PI Harvey RC, Eastman PS;  
XX  
DR WPI; 2000-182730/16.  
XX  
PT Novel methods for preparing RNA from biological samples, used for the  
XX detection and measurement of nucleic acids and fusion nucleic acids.  
XX  
XX Claim 19; Page 43; 49pp; English.

Oligonucleotides AAZ60840-62 and AAZ60865-66 are used in the method of the invention to detect fusion transcripts produced from a translocation between the bcr b3 region and the abl gene. The specification describes a method for detecting a fusion nucleic acid (particularly chimeric mRNA species), in a biological sample. The method comprises contacting a sample of fusion nucleic acid with primers, amplifying the hybridized fusion nucleic acid, and detecting the target hybrid. The method is used for the simple and rapid preparation of RNA from a biological sample, particularly from the cytoplasm of eukaryotic cells, which is suitable for use in an amplification and detection assay. The methods are used for

CC the analysis and detection of nucleic acids in biological samples. The  
CC methods are useful in the human medical and veterinary fields, for  
CC medical diagnoses and clinical monitoring of a patient's response to  
CC therapy where a disease or medical condition is associated with a  
CC particular type and/or level of mRNA present in the sample. The methods  
CC are also useful for detecting or quantifying fusion or chimeric RNA  
CC species, and for detecting a translocation as a marker for a given  
CC condition or disease, e.g. translocations associate with cancers,  
CC particularly forms of leukemia

XX Sequence 27 BP; 4 A; 6 C; 8 G; 9 T; 0 U; 0 Other;  
SQ Query Match 100.0%; Score 27; DB 3; Length 27;  
Best Local Similarity 100.0%; Pred. No. 3.9e-05;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCTGACTTTGAGCCTCAGGCTCTGAGT 27  
Db 1 TCTGACTTTGAGCCTCAGGCTCTGAGT 27

RESULT 2  
AAZ60862  
ID AAZ60862 standard; RNA; 27 BP.  
XX  
AC AAZ60862;  
XX  
DT 16-MAY-2000 (first entry)  
XX  
DE Oligonucleotide used to detect bcr b3-abl fusion transcripts.  
XX Fusion transcript; translocation; bcr b3 region; abl gene;  
KW amplification assay; detection assay; medical diagnosis;  
KW clinical monitoring; chimeric RNA; fusion RNA; condition marker;  
KW disease marker; cancer; leukemia; ss.  
XX  
OS Synthetic.  
XX  
PN WO200005418-A1.  
XX  
PD 03-FEB-2000.  
XX  
PF 23-JUL-1999; 99WO-US016832.  
XX  
PR 23-JUL-1998; 98US-00121239.  
XX  
PA (GENP-) GEN-PROBE INC.  
XX  
PI Harvey RC, Eastman PS;  
XX  
DR WPI; 2000-182730/16.  
XX  
PT Novel methods for preparing RNA from biological samples, used for the  
PT detection and measurement of nucleic acids and fusion nucleic acids.  
XX  
PS Claim 19; Page 44; 49pp; English.  
XX  
CC Oligonucleotides AAZ60840-62 and AAZ60865-66 are used in the method of  
CC the invention to detect fusion transcripts produced from a translocation  
CC between the bcr b3 region and the abl gene. The specification describes a  
CC method for detecting a fusion nucleic acid (particularly chimeric mRNA  
CC species), in a biological sample. The method comprises contacting a  
CC sample of fusion nucleic acid with primers, amplifying the hybridized  
CC fusion nucleic acid, and detecting the target hybrid. The method is used  
CC for the simple and rapid preparation of RNA from a biological sample,  
CC particularly from the cytoplasm of eukaryotic cells, which is suitable  
CC for use in an amplification and detection assay. The methods are used for  
CC the analysis and detection of nucleic acids in biological samples. The  
CC methods are useful in the human medical and veterinary fields, for  
CC medical diagnoses and clinical monitoring of a patient's response to  
CC therapy where a disease or medical condition is associated with a  
CC particular type and/or level of mRNA present in the sample. The methods  
CC are also useful for detecting or quantifying fusion or chimeric RNA  
CC species, and for detecting a translocation as a marker for a given  
CC condition or disease, e.g. translocations associate with cancers,  
CC particularly forms of leukemia

CC species, and for detecting a translocation as a marker for a given  
CC condition or disease, e.g. translocations associate with cancers,  
CC particularly forms of leukemia

XX Sequence 27 BP; 4 A; 6 C; 8 G; 0 T; 9 U; 0 Other;  
SQ Query Match 100.0%; Score 27; DB 3; Length 27;  
Best Local Similarity 66.7%; Pred. No. 3.9e-05;  
Matches 18; Conservative 9; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCTGACTTTGAGCCTCAGGCTCTGAGT 27  
Db 1 UCUGACUUGAGCCUCAGGGUCUGAGU 27

RESULT 3  
AAZ60860/c  
ID AAZ60860 standard; RNA; 27 BP.  
XX  
AC AAZ60860;  
XX  
DT 16-MAY-2000 (first entry)  
XX  
DE Oligonucleotide used to detect bcr b3-abl fusion transcripts.  
XX Fusion transcript; translocation; bcr b3 region; abl gene;  
KW amplification assay; detection assay; medical diagnosis;  
KW clinical monitoring; chimeric RNA; fusion RNA; condition marker;  
KW disease marker; cancer; leukemia; ss.  
XX  
OS Synthetic.  
XX  
PN WO200005418-A1.  
XX  
PD 03-FEB-2000.  
XX  
PF 23-JUL-1999; 99WO-US016832.  
XX  
PR 23-JUL-1998; 98US-00121239.  
XX  
PA (GENP-) GEN-PROBE INC.  
XX  
PI Harvey RC, Eastman PS;  
XX  
DR WPI; 2000-182730/16.  
XX  
PT Novel methods for preparing RNA from biological samples, used for the  
PT detection and measurement of nucleic acids and fusion nucleic acids.  
XX  
PS Claim 19; Page 43; 49pp; English.  
XX  
CC Oligonucleotides AAZ60840-62 and AAZ60865-66 are used in the method of  
CC the invention to detect fusion transcripts produced from a translocation  
CC between the bcr b3 region and the abl gene. The specification describes a  
CC method for detecting a fusion nucleic acid (particularly chimeric mRNA  
CC species), in a biological sample. The method comprises contacting a  
CC sample of fusion nucleic acid with primers, amplifying the hybridized  
CC fusion nucleic acid, and detecting the target hybrid. The method is used  
CC for the simple and rapid preparation of RNA from a biological sample,  
CC particularly from the cytoplasm of eukaryotic cells, which is suitable  
CC for use in an amplification and detection assay. The methods are used for  
CC the analysis and detection of nucleic acids in biological samples. The  
CC methods are useful in the human medical and veterinary fields, for  
CC medical diagnoses and clinical monitoring of a patient's response to  
CC therapy where a disease or medical condition is associated with a  
CC particular type and/or level of mRNA present in the sample. The methods  
CC are also useful for detecting or quantifying fusion or chimeric RNA  
CC species, and for detecting a translocation as a marker for a given  
CC condition or disease, e.g. translocations associate with cancers,  
CC particularly forms of leukemia

XX Sequence 27 BP; 9 A; 8 C; 6 G; 0 T; 4 U; 0 Other;

Qy 1 TCTGACTTTGAGCCTCAGGGTCTGAGT 27

XX  
AC AAZ60841;  
XX  
DT 16-MAY-2000 (first entry)  
XX  
DE Oligonucleotide used to detect bcr b3-abl fusion transcripts.  
XX  
DE  
XX Fusion transcript; translocation; bcr b3 region; abl gene;  
KW amplification assay; detection assay; medical diagnosis;  
KW clinical monitoring; chimeric RNA; fusion RNA; condition marker;  
KW disease marker; cancer; leukemia; ss.  
XX  
OS Synthetic.  
XX  
XX WO200005418-A1.  
PN  
XX  
XX 03-FEB-2000.  
PD  
XX  
XX 23-JUL-1999; 99WO-US016832.  
PF  
XX  
XX 23-JUL-1998; 98US-00121239.  
PR  
XX  
XX (GENP-) GEN-PROBE INC.  
PA  
PI Harvey RC, Eastman PS;  
XX  
XX WPI; 2000-182730/16.  
DR  
XX  
XX Novel methods for preparing RNA from biological samples, used for the  
PT detection and measurement of nucleic acids and fusion nucleic acids.  
PT  
XX  
PS Claim 19; Page 40; 49pp; English.  
XX  
XX Oligonucleotides AAZ60840-62 and AAZ60865-66 are used in the method of  
CC the invention to detect fusion transcripts produced from a translocation  
CC between the bcr b3 region and the abl gene. The specification describes a  
CC method for detecting a fusion nucleic acid (particularly chimeric mRNA  
CC species), in a biological sample. The method comprises contacting a  
CC sample of fusion nucleic acid with primers, amplifying the hybridized  
CC fusion nucleic acid, and detecting the target hybrid. The method is used  
CC for the simple and rapid preparation of RNA from a biological sample,  
CC particularly from the cytoplasm of eukaryotic cells, which is suitable  
CC for use in an amplification and detection assay. The methods are used for  
CC the analysis and detection of nucleic acids in biological samples. The  
CC methods are useful in the human medical and veterinary fields, for  
CC medical diagnoses and clinical monitoring of a patient's response to  
CC therapy where a disease or medical condition is associated with a  
CC particular type and/or level of mRNA present in the sample. The methods  
CC are also useful for detecting or quantifying fusion or chimeric RNA  
CC species, and for detecting a translocation as a marker for a given  
CC condition or disease, e.g. translocations associate with cancers,  
CC particularly forms of leukemia  
XX  
SQ Sequence 54 BP; 20 A; 12 C; 11 G; 0 T; 11 U; 0 Other;  
Query Match 100.0%; Score 27; DB 3; Length 54;  
Best Local Similarity 100.0%; Pred. No. 3.8e-05;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TCTGACTTTGAGCCTCAGGCTCTGAGT 27  
DB 54 TCTGACTTTGAGCCTCAGGCTCTGAGT 28  
RESULT 7  
AAZ60840/c  
ID AAZ60840 standard; DNA; 54 BP.  
XX  
XX AAZ60840;  
XX  
XX 16-MAY-2000 (first entry)  
XX  
DE Oligonucleotide used to detect bcr b3-abl fusion transcripts.

XX  
KW Fusion transcript; translocation; bcr b3 region; abl gene;  
KW amplification assay; detection assay; medical diagnosis;  
KW clinical monitoring; chimeric RNA; fusion RNA; condition marker;  
KW disease marker; cancer; leukemia; ss.  
XX  
OS Synthetic.  
XX  
XX WO200005418-A1.  
PN  
XX  
XX 03-FEB-2000.  
PD  
XX  
XX 23-JUL-1999; 99WO-US016832.  
PF  
XX  
XX 23-JUL-1998; 98US-00121239.  
PR  
XX  
XX (GENP-) GEN-PROBE INC.  
PA  
PI Harvey RC, Eastman PS;  
XX  
XX WPI; 2000-182730/16.  
DR  
XX  
XX Novel methods for preparing RNA from biological samples, used for the  
PT detection and measurement of nucleic acids and fusion nucleic acids.  
PT  
XX  
PS Claim 19; Page 39; 49pp; English.  
XX  
XX Oligonucleotides AAZ60840-62 and AAZ60865-66 are used in the method of  
CC the invention to detect fusion transcripts produced from a translocation  
CC between the bcr b3 region and the abl gene. The specification describes a  
CC method for detecting a fusion nucleic acid (particularly chimeric mRNA  
CC species), in a biological sample. The method comprises contacting a  
CC sample of fusion nucleic acid with primers, amplifying the hybridized  
CC fusion nucleic acid, and detecting the target hybrid. The method is used  
CC for the simple and rapid preparation of RNA from a biological sample,  
CC particularly from the cytoplasm of eukaryotic cells, which is suitable  
CC for use in an amplification and detection assay. The methods are used for  
CC the analysis and detection of nucleic acids in biological samples. The  
CC methods are useful in the human medical and veterinary fields, for  
CC medical diagnoses and clinical monitoring of a patient's response to  
CC therapy where a disease or medical condition is associated with a  
CC particular type and/or level of mRNA present in the sample. The methods  
CC are also useful for detecting or quantifying fusion or chimeric RNA  
CC species, and for detecting a translocation as a marker for a given  
CC condition or disease, e.g. translocations associate with cancers,  
CC particularly forms of leukemia  
XX  
SQ Sequence 54 BP; 20 A; 12 C; 11 G; 11 T; 0 U; 0 Other;  
Query Match 100.0%; Score 27; DB 3; Length 54;  
Best Local Similarity 100.0%; Pred. No. 3.8e-05;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TCTGACTTTGAGCCTCAGGCTCTGAGT 27  
DB 54 TCTGACTTTGAGCCTCAGGCTCTGAGT 28  
RESULT 8  
AAZ60842  
ID AAZ60842 standard; DNA; 54 BP.  
XX  
XX AAZ60842;  
XX  
XX 16-MAY-2000 (first entry)  
XX  
XX Oligonucleotide used to detect bcr b3-abl fusion transcripts.  
XX  
XX Fusion transcript; translocation; bcr b3 region; abl gene;  
KW amplification assay; detection assay; medical diagnosis;  
KW clinical monitoring; chimeric RNA; fusion RNA; condition marker;  
KW disease marker; cancer; leukemia; ss.  
XX



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OS Synthetic.
XX WO200005418-A1.
XX
XX
XX 03-FEB-2000.
XX
XX 23-JUL-1999; 99WO-US016832.
XX
XX 23-JUL-1998; 98US-00121239.
XX
XX (GENP-) GEN-PROBE INC.
XX
XX Harvey RC, Eastman PS;
XX
XX WPI; 2000-182730/16.
XX
XX Novel methods for preparing RNA from biological samples, used for the
XX detection and measurement of nucleic acids and fusion nucleic acids.
XX
XX Claim 19; Page 40; 49pp; English.
XX
XX Oligonucleotides AAZ60840-62 and AAZ60865-66 are used in the method of
XX the invention to detect fusion transcripts produced from a translocation
XX between the bcr b3 region and the abl gene. The specification describes a
XX method for detecting a fusion nucleic acid (particularly chimeric mRNA
XX species), in a biological sample. The method comprises contacting a
XX sample of fusion nucleic acid with primers, amplifying the hybridized
XX fusion nucleic acid, and detecting the target hybrid. The method is used
XX for the simple and rapid preparation of RNA from a biological sample,
XX particularly from the cytoplasm of eukaryotic cells, which is suitable
XX for use in an amplification and detection assay. The methods are used for
XX the analysis and detection of nucleic acids in biological samples. The
XX methods are useful in the human medical and veterinary fields, for
XX medical diagnoses and clinical monitoring of a patient's response to
XX therapy where a disease or medical condition is associated with a
XX particular type and/or level of mRNA present in the sample. The methods
XX are also useful for detecting or quantifying fusion or chimeric RNA
XX species, and for detecting a translocation as a marker for a given
XX condition or disease, e.g. translocations associate with cancers,
XX particularly forms of leukemia
XX
XX Sequence 54 BP; 11 A; 11 C; 12 G; 20 T; 0 U; 0 Other;

Query Match 100.0%; Score 27; DB 3; Length 54;
Best Local Similarity 100.0%; Pred. No. 3.8e-05;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCTGACTTTGAGCCTCAGGCTCTGAGT 27
DB 1 TCTGACTTTGAGCCTCAGGCTCTGAGT 27

RESULT 9
AA91666
ID AA91666 standard; DNA; 205 BP.
XX
XX AA91666;
XX
XX 14-MAR-1990 (first entry)
XX
XX Bcr-abl fusion message for leukaemia.
XX
XX Reciprocal translocation.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX FT exon 1..31
XX FT /tag= a
XX FT /note= "bcr exon 2"
XX FT exon 32..106
XX FT /tag= b
XX FT /note= "bcr exon 3"

Query Match 100.0%; Score 27; DB 3; Length 54;
Best Local Similarity 100.0%; Pred. No. 3.8e-05;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCTGACTTTGAGCCTCAGGCTCTGAGT 27
DB 1 TCTGACTTTGAGCCTCAGGCTCTGAGT 27

RESULT 10
AAQ34625
ID AAQ34625 standard; cDNA; 257 BP.
XX
XX AAQ34625;
XX
XX 25-MAR-2003 (revised)
XX
XX 10-MAY-1993 (first entry)
XX
XX Human bcr-abl junction.
XX
XX Leukaemia; treatment; blast crisis; specific; CML; translocation;
XX Philadelphia chromosome; chronic myeloid; chronic myelogenous; leukemia;
XX ss.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX FT misc_feature 23..40
XX FT /tag= b
XX FT /note= "breakpoint junction target sequence"
XX FT misc_feature 31..32
XX FT /tag= a
XX FT /note= "bcr-abl breakpoint"
XX
XX WO9222303-A1.
XX
XX 23-DEC-1992.
XX
XX 15-JUN-1992; 92WO-US005035.
XX
XX 18-JUN-1991; 91US-00718302.
XX
XX 14-APR-1992; 92US-00869911.
XX

FT exon 106..205
FT /tag= b
FT /note= "abl exon 2"
XX
XX EP338713-A.
XX
XX 25-OCT-1989.
XX
XX 11-APR-1989; 89EP-00303538.
XX
XX 18-APR-1988; 88US-00182434.
XX
XX (CITY ) CITY OF HOPE.
XX
XX Rossi JJ;
XX
XX WPI; 1989-311152/43.
XX
XX New synthetic oligo:nucleotide probes - used for detection of BCR-ABL RNA
XX from blood or bone marrow or chronic myelogenous leukaemia patients.
XX
XX Disclosure; Page 3; 4pp; English.
XX
XX Part of 8 kb RNA transcript, showing the fusion of abl and bcr. The abl
XX gene is from human chromosome 9, and this is spliced to a region on
XX chromosome 22 called the breakpoint cluster region (bcr). CML has
XX reciprocal translocation of human chromosomes 9 and 22
XX
XX Sequence 205 BP; 50 A; 55 C; 52 G; 48 T; 0 U; 0 Other;

Query Match 100.0%; Score 27; DB 1; Length 205;
Best Local Similarity 100.0%; Pred. No. 3.8e-05;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCTGACTTTGAGCCTCAGGCTCTGAGT 27
DB 130 TCTGACTTTGAGCCTCAGGCTCTGAGT 156

RESULT 10
AAQ34625
ID AAQ34625 standard; cDNA; 257 BP.
XX
XX AAQ34625;
XX
XX 25-MAR-2003 (revised)
XX
XX 10-MAY-1993 (first entry)
XX
XX Human bcr-abl junction.
XX
XX Leukaemia; treatment; blast crisis; specific; CML; translocation;
XX Philadelphia chromosome; chronic myeloid; chronic myelogenous; leukemia;
XX ss.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX FT misc_feature 23..40
XX FT /tag= b
XX FT /note= "breakpoint junction target sequence"
XX FT misc_feature 31..32
XX FT /tag= a
XX FT /note= "bcr-abl breakpoint"
XX
XX WO9222303-A1.
XX
XX 23-DEC-1992.
XX
XX 15-JUN-1992; 92WO-US005035.
XX
XX 18-JUN-1991; 91US-00718302.
XX
XX 14-APR-1992; 92US-00869911.
XX
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RESULT 13
AAV20459
ID AAV20459 standard; DNA; 266 BP.
XX
XX AAV20459;
XX
XX 17-JUN-1998 (first entry)
XX
XX Human bcr-abl oncogene b3a2 genotype.
XX
XX Human; oncogene; proto-oncogene; neoplastic disease; anticancer; cancer;
XX antisense oligonucleotide; bcr-abl; ds.
XX
XX Homo sapiens.
XX
XX US5734039-A.
XX
XX 31-MAR-1998.
XX
XX 15-SEP-1994; 94US-00306691.
XX
XX 15-SEP-1994; 94US-00306691.
XX
XX (UYJE-) UNIV JEFFERSON THOMAS.
XX
XX Calabretta B, Skorski T;
XX
XX WPI; 1998-229882/20.
XX
XX Anticancer composition comprising two anti-sense oligo:nucleotide(s) -
XX targeting cytoplasmic and nuclear oncogene(s).
XX
XX Claim 1; Col 109-110; 92pp; English.
XX
XX The present sequence represents an oncogene from the present invention.
XX
XX The present invention describes a composition which comprises two
XX antisense oligonucleotides. The first oligonucleotide is specific for a
XX cytoplasmic oncogene or proto-oncogene selected from ras, raf, EGF-1, c-
XX fms, c-kit, c-met, c-trk, c-src, c-abl, bcr-abl, c-fgr and c-yes.
XX
XX The second oligonucleotide is specific for a nuclear oncogene or proto-
XX oncogene selected from myc, jun, c-ets, c-fos, c-myc, B-mvb, c-rel, c-
XX vav, c-ski, c-spi, cyclin D1, FHL/RAR alpha, AML1/MTG8, E2A/p1 and ALL-
XX 1/AF-4. The composition is used for treating cancer. The combination of
XX antisense oligonucleotides has synergistically enhanced ability to
XX inhibit growth of cancer cells
XX
XX Sequence 266 BP; 72 A; 64 C; 66 G; 64 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 27; DB 2; Length 266;
XX Best Local Similarity 100.0%; Pred. No. 3.8e-05;
XX Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TCTGACTTTGAGCCTCAGGGTCTGAGT 27
DB 64 TCTGACTTTGAGCCTCAGGGTCTGAGT 90

RESULT 14
AAZ60864
ID AAZ60864 standard; DNA; 299 BP.
XX
XX AAZ60864;
XX
XX 16-MAY-2000 (first entry)
XX
XX Region surrounding a splice junction in a normal abl transcript.
XX
XX Fusion transcript; translocation; bcr b3 region; abl gene;
XX amplification assay; detection assay; medical diagnosis;
XX clinical monitoring; chimeric RNA; fusion RNA; condition marker;
XX disease marker; cancer; leukemia; ss.
XX

OS Unidentified.
XX WO200005418-A1.
XX
XX 03-FEB-2000.
XX
XX 23-JUL-1999; 99WO-US016832.
XX
XX 23-JUL-1999; 98US-00121239.
XX
XX (GENP-) GEN-PROBE INC.
XX
XX Harvey RC, Eastman PS;
XX
XX WPI; 2000-182730/16.
XX
XX Novel methods for preparing RNA from biological samples, used for the
XX detection and measurement of nucleic acids and fusion nucleic acids.
XX
XX Disclosure; Fig 3; 49pp; English.
XX
XX The present sequence represents a region surrounding a potential splice
XX junction in a normal abl transcript. The specification describes
XX oligonucleotides which are used to detect fusion transcripts produced
XX from a translocation between the bcr b3 region and the abl gene. The
XX specification also describes a method for detecting a fusion nucleic acid
XX (particularly chimeric mRNA species), in a biological sample. The method
XX comprises contacting a sample of fusion nucleic acid with primers,
XX amplifying the hybridized fusion nucleic acid, and detecting the target
XX hybrid. The method is used for the simple and rapid preparation of RNA
XX from a biological sample, particularly from the cytoplasm of eukaryotic
XX cells, which is suitable for use in an amplification and detection assay.
XX
XX The methods are used for the analysis and detection of nucleic acids in
XX biological samples. The methods are useful in the human medical and
XX veterinary fields, for medical diagnoses and clinical monitoring of a
XX patient's response to therapy where a disease or medical condition is
XX associated with a particular type and/or level of mRNA present in the
XX sample. The methods are also useful for detecting or quantifying fusion
XX or chimeric RNA species, and for detecting a translocation as a marker
XX for a given condition or disease, e.g. translocations associate with
XX cancers, particularly forms of leukemia
XX
XX Sequence 299 BP; 77 A; 70 C; 81 G; 71 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 27; DB 3; Length 299;
XX Best Local Similarity 100.0%; Pred. No. 3.8e-05;
XX Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TCTGACTTTGAGCCTCAGGGTCTGAGT 27
DB 175 TCTGACTTTGAGCCTCAGGGTCTGAGT 201

RESULT 15
AAZ60863
ID AAZ60863 standard; DNA; 350 BP.
XX
XX AAZ60863;
XX
XX 16-MAY-2000 (first entry)
XX
XX Region surrounding a bcr-able splice junction.
XX
XX Fusion transcript; translocation; bcr b3 region; abl gene;
XX amplification assay; detection assay; medical diagnosis;
XX clinical monitoring; chimeric RNA; fusion RNA; condition marker;
XX disease marker; cancer; leukemia; ss.
XX
XX Unidentified.
XX
XX WO200005418-A1.
XX
XX 03-FEB-2000.

```

XX 23-JUL-1999; 99WO-US016832.  
 XX  
 PR 23-JUL-1998; 98US-00121239.  
 XX  
 PA (GENP-) GEN-PROBE INC.  
 XX  
 XX Harvey RC, Eastman PS;  
 XX  
 DR WPI; 2000-182730/16.  
 XX  
 PT Novel methods for preparing RNA from biological samples, used for the  
 PT detection and measurement of nucleic acids and fusion nucleic acids.  
 XX  
 PS Disclosure; Fig 2; 49pp; English.  
 XX  
 CC The present sequence represents a region surrounding a bcr-able splice  
 CC junction. The specification describes oligonucleotides which are used to  
 CC detect fusion transcripts produced from a translocation between the bcr  
 CC b3 region and the abl gene. The specification also describes a method for  
 CC detecting a fusion nucleic acid (particularly chimeric mRNA species), in  
 CC a biological sample. The method comprises contacting a sample of fusion  
 CC nucleic acid with primers, amplifying the hybridized fusion nucleic acid,  
 CC and detecting the target hybrid. The method is used for the simple and  
 CC rapid preparation of RNA from a biological sample, particularly from the  
 CC cytoplasm of eukaryotic cells, which is suitable for use in an  
 CC amplification and detection assay. The methods are used for the analysis  
 CC and detection of nucleic acids in biological samples. The methods are  
 CC useful in the human medical and veterinary fields, for medical diagnoses  
 CC and clinical monitoring of a patient's response to therapy where a disease  
 CC or medical condition is associated with a particular type and/or level of  
 CC mRNA present in the sample. The methods are also useful for detecting or  
 CC quantifying fusion or chimeric RNA species, and for detecting a  
 CC translocation as a marker for a given condition or disease, e.g.  
 CC translocations associate with cancers, particularly forms of leukemia  
 XX  
 SQ Sequence 350 BP; 85 A; 92 C; 89 G; 84 T; 0 U; 0 Other;

Query Match 100.0%; Score 27; DB 3; Length 350;  
 Best Local Similarity 100.0%; Pred. No. 3.8e-05;  
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 TCTGACTTTGAGCCTCAGGCTCTCAGT 27  
 |||||  
 Db 225 TCTGACTTTGAGCCTCAGGCTCTCAGT 251

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 Job time : 167.387 secs

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OM nucleic - nucleic search, using sw model

Run on: May 27, 2004, 02:25:18 ; Search time 34.425 Seconds  
(without alignments)  
435.256 Million cell updates/sec

Title: US-09-121-239-22

Perfect score: 27  
Sequence: 1 TCTGACTTTGAGCCTCAGGCTCTGAGT 27

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Gapop\_60.0 , Gapext 60.0

Searched: 682709 seqs, 277475446 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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3: /cgn2\_6/prodata/2/ina/6A COMB.seq.\*  
4: /cgn2\_6/prodata/2/ina/6B COMB.seq.\*  
5: /cgn2\_6/prodata/2/ina/PCTUS COMB.seq.\*  
6: /cgn2\_6/prodata/2/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	27	100.0	204	5	PCT-US93-06251-5
2	27	100.0	257	1	US-08-152-621-1
3	27	100.0	257	1	US-08-306-691B-36
4	27	100.0	257	5	PCT-US92-05035-1
5	27	100.0	266	1	US-08-152-621-4
6	27	100.0	266	1	US-08-306-691B-37
7	27	100.0	266	5	PCT-US92-05035-4
8	27	100.0	1078	4	US-09-310-842-1
9	27	100.0	3623	1	US-08-306-691B-35
10	26	96.3	80	1	US-08-152-621-7
11	26	96.3	80	1	US-08-306-691B-38
12	26	96.3	80	5	PCT-US92-05035-7
13	24	88.9	50	4	US-09-168-947-45
14	24	81.5	22	1	US-08-013-419-1
15	22	81.5	22	1	US-08-122-795B-10
16	22	81.5	22	2	US-08-525-818-1
17	22	81.5	22	1	US-09-028-184-1
18	22	81.5	22	5	PCT-US94-00680-1
19	22	81.5	22	5	PCT-US94-09963A-10
20	17	63.0	56	1	US-07-940-652-19
21	17	63.0	56	1	US-08-355-553-19
22	16	59.3	2992	2	US-08-841-349-10
23	16	59.3	2992	4	US-09-431-184A-10
24	15	55.6	20	1	US-08-761-131-7
25	15	55.6	21	3	US-07-784-222-2
26	15	55.6	21	4	US-09-502-954-2
27	15	55.6	40	1	US-08-761-131-1

28	15	55.6	40	1	US-08-761-131-2	Sequence 2, Appli
29	15	55.6	818	4	US-09-599-360B-37	Sequence 37, Appli
30	15	55.6	822	4	US-09-621-976-1361	Sequence 1361, Ap
31	15	55.6	2214	4	US-09-489-847-113	Sequence 113, App
32	15	55.6	2227	4	US-09-489-847-30	Sequence 30, Appl
33	15	55.6	7052	4	US-09-526-193A-22	Sequence 22, Appl
34	14	51.9	426	4	US-09-621-976-18309	Sequence 18309, A
35	14	51.9	474	4	US-09-615-192A-264	Sequence 264, App
36	14	51.9	888	4	US-09-171-209-7	Sequence 7, Appli
37	14	51.9	973	4	US-09-599-360B-71	Sequence 71, Appl
38	14	51.9	1910	2	US-08-808-931-17	Sequence 17, Appl
39	14	51.9	1910	3	US-08-808-323-17	Sequence 17, Appl
40	14	51.9	1910	3	US-09-050-603A-17	Sequence 17, Appl
41	14	51.9	1910	3	US-09-102-420B-17	Sequence 17, Appl
42	14	51.9	1910	4	US-09-497-698-17	Sequence 17, Appl
43	14	51.9	2050	4	US-09-620-312D-761	Sequence 761, App
44	14	51.9	2150	2	US-08-318-837-1	Sequence 1, Appli
45	14	51.9	2606	2	US-08-808-931-26	Sequence 26, Appl

## ALIGNMENTS

RESULT 1  
PCT-US93-06251-5  
; Sequence 5, Application PC/TUS9306251  
; GENERAL INFORMATION:  
; APPLICANT: Wickstrom, Eric and Rife, Jason P.  
; TITLE OF INVENTION: Trivalent Synthesis of Oligonucleotides Containing  
; TITLE OF INVENTION: Stereospecific Alkylphosphonates and Arylphosphonates  
; NUMBER OF SEQUENCES: 93  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER  
; STREET: 400 Garden City Plaza  
; CITY: Garden City  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 11530  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US93/06251  
; FILING DATE: 19930630  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Digiglio, Frank S.  
; REGISTRATION NUMBER: 31,346  
; REFERENCE/DOCKET NUMBER: 8586  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 516-742-4343  
; TELEFAX: 516-742-4366  
; TELEX: 230 901 SANS UR  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 204 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
PCT-US93-06251-5

Query Match 100.0%; Score 27; DB 5; Length 204;

Best Local Similarity 100.0%; Pred. No. 1.2e-06; Indels 0; Caps 0;  
Matches 27; Conservative 0; Mismatches 0;

QY 1 TCTGACTTTGAGCCTCAGGCTCTGAGT 27

Db 39 TCTGACTTTGAGCCTCAGGCTCTGAGT 65

```
RESULT 2
US-08-152-621-1
; Sequence 1, Application US/08152621
; Patent No. 5652222
; GENERAL INFORMATION:
; APPLICANT: Calabretta, Bruno
; APPLICANT: Gewirtz, Alan M.
; TITLE OF INVENTION: Selective Inhibition of
; TITLE OF INVENTION: Leukemic Cell Proliferation by bcr-abl
; TITLE OF INVENTION: Antisense Oligonucleotides
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEIDEL, GONDA, LAVORGNA
; ADDRESSEE: & MONACO, P.C.
; STREET: 1800 Two Penn Center
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: U.S.A.
; ZIP: 19102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/152,621
; FILING DATE: No. 5652222ember 15, 1993
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 30,480
; REGISTRATION/DOCKET NUMBER: 07/718,302
; FILING DATE: June 18, 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Monaco, Daniel A.
; REGISTRATION/DOCKET NUMBER: 6056-120 (CT.) 1
; REFERENCE/DOCKET NUMBER: 6056-120 (CT.) 1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-8383
; TELEFAX: (215) 568-5549
; TELEX: No. 5652222e
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 Nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single stranded
; TOPOLOGY: linear
US-08-152-621-1
Query Match 100.0%; Score 27; DB 1; Length 257;
Best Local Similarity 100.0%; Pred. No. 1.2e-06;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TCTGACTTTGAGCCTCAGGCTCTGAGT 27
Db 55 TCTGACTTTGAGCCTCAGGCTCTGAGT 81

RESULT 3
US-08-306-691B-36
; Sequence 36, Application US/08306691B
; Patent No. 5734039
; GENERAL INFORMATION:
; APPLICANT: Calabretta, Bruno
; APPLICANT: Skorski, Tomasz
; TITLE OF INVENTION: ANTISENSE
; TITLE OF INVENTION: OLIGONUCLEOTIDES TARGETING COOPERATING ONCOGENES
; NUMBER OF SEQUENCES: 55
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seidel, Gonda, Lavorgna & Monaco, P.C.
; STREET: Two Penn Center, Suite 1800
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: U.S.A.
; ZIP: 19102
```

```
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/306,691B
FILING DATE: September 15, 1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Monaco, Daniel A.
REGISTRATION/DOCKET NUMBER: 8321-8
REFERENCE/DOCKET NUMBER: 8321-8
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-8383
TELEFAX: (215) 568-5549
TELEX: No. 5734039e
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 257 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-306-691B-36
Query Match 100.0%; Score 27; DB 1; Length 257;
Best Local Similarity 100.0%; Pred. No. 1.2e-06;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TCTGACTTTGAGCCTCAGGCTCTGAGT 27
Db 55 TCTGACTTTGAGCCTCAGGCTCTGAGT 81

RESULT 4
PCT-US92-05035-1
; Sequence 1, Application PC/TUS9205035
; GENERAL INFORMATION:
; APPLICANT: Calabretta, Bruno
; APPLICANT: Gewirtz, Alan M.
; TITLE OF INVENTION: Selective Inhibition of
; TITLE OF INVENTION: Leukemic Cell Proliferation by bcr-abl
; TITLE OF INVENTION: Antisense Oligonucleotides
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Temple University - Of The Common-
; ADDRESSEE: wealth System of Higher Education
; STREET: 406 University Services Building
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: U.S.A.
; ZIP: 19122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/05035
; FILING DATE: 19920615
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/718,302
; FILING DATE: June 18, 1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/869,911
; FILING DATE: April 14, 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Monaco, Daniel A.
; REGISTRATION NUMBER: 30,480
```

REFERENCE/DOCKET NUMBER: 6056-120 (CIP) 1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (215) 568-8383  
TELEFAX: (215) 568-5549  
TELEX: None  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 257 Nucleotides  
TYPE: NUCLEIC ACID  
STRANDEDNESS: single stranded  
TOPOLOGY: linear  
PCT-US92-05035-1

Query Match 100.0%; Score 27; DB 5; Length 257;  
Best Local Similarity 100.0%; Pred. No. 1.2e-06;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCTGACTTTGAGCCTCAGGGTCTGAGT 27  
Db 55 TCTGACTTTGAGCCTCAGGGTCTGAGT 81

## RESULT 5

US-08-152-621-4  
Sequence 4, Application US/08152621  
Patent No. 5652222  
GENERAL INFORMATION:  
APPLICANT: Calabretta, Bruno  
APPLICANT: Gewirtz, Alan M.  
TITLE OF INVENTION: Selective Inhibition of  
TITLE OF INVENTION: Leukemic Cell Proliferation by bcr-abl  
TITLE OF INVENTION: Antisense Oligonucleotides  
NUMBER OF SEQUENCES: 34  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SEIDEL, GONDA, LAVORNA  
ADDRESSEE: & MONACO, P.C.  
STREET: 1800 Two Penn Center  
CITY: Philadelphia  
STATE: Pennsylvania  
COUNTRY: U.S.A.  
ZIP: 19102

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb  
COMPUTER: IBM PS/2  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: WordPerfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/152,621  
FILING DATE: June 18, 1991  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/718,302  
FILING DATE: June 18, 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Monaco, Daniel A.  
REGISTRATION NUMBER: 30,480  
REFERENCE/DOCKET NUMBER: 6056-120 (CT.) 1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (215) 568-8383  
TELEFAX: (215) 568-5549  
TELEX: No. 5652222e  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 266 Nucleotides  
TYPE: nucleic acid  
STRANDEDNESS: single stranded  
TOPOLOGY: linear

Query Match 100.0%; Score 27; DB 1; Length 266;  
Best Local Similarity 100.0%; Pred. No. 1.2e-06;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCTGACTTTGAGCCTCAGGGTCTGAGT 27  
Db 64 TCTGACTTTGAGCCTCAGGGTCTGAGT 90

## RESULT 6

US-08-306-691B-37  
Sequence 37, Application US/08306691B  
Patent No. 5734039  
GENERAL INFORMATION:  
APPLICANT: Calabretta, Bruno  
APPLICANT: Skorski, Tomasz  
TITLE OF INVENTION: ANTISENSE  
TITLE OF INVENTION: OLIGONUCLEOTIDES TARGETING COOPERATING ONCOGENES  
NUMBER OF SEQUENCES: 55  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Seidel, Gonda, LAVORNA & Monaco, P.C.  
STREET: Two Penn Center, Suite 1800  
CITY: Philadelphia  
STATE: Pennsylvania  
COUNTRY: U.S.A.  
ZIP: 19102

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb  
COMPUTER: IBM PS/2  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: WordPerfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/306,691B  
FILING DATE: September 15, 1994  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Monaco, Daniel A.  
REGISTRATION NUMBER: 30,480  
REFERENCE/DOCKET NUMBER: 8321-8  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (215) 568-8383  
TELEFAX: (215) 568-5549  
TELEX: No. 5734039e  
INFORMATION FOR SEQ ID NO: 37:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 266 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-306-691B-37

Query Match 100.0%; Score 27; DB 1; Length 266;  
Best Local Similarity 100.0%; Pred. No. 1.2e-06;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCTGACTTTGAGCCTCAGGGTCTGAGT 27  
Db 64 TCTGACTTTGAGCCTCAGGGTCTGAGT 90

## RESULT 7

PCT-US92-05035-4  
Sequence 4, Application PC/TUS9205035  
GENERAL INFORMATION:  
APPLICANT: Calabretta, Bruno  
APPLICANT: Gewirtz, Alan M.  
TITLE OF INVENTION: Selective Inhibition of  
TITLE OF INVENTION: Leukemic Cell Proliferation by bcr-abl  
TITLE OF INVENTION: Antisense Oligonucleotides  
NUMBER OF SEQUENCES: 34  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Temple University - Of The Common-  
ADDRESSEE: wealth System of Higher Education  
STREET: 406 University Services Building

```
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: U.S.A.
; ZIP: 19122
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/05035
; FILING DATE: 19920615
; CLASSIFICATION: 514
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/718,302
; FILING DATE: June 18, 1991
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/869,911
; FILING DATE: April 14, 1991
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Monaco, Daniel A.
; REGISTRATION NUMBER: 30,480
; REFERENCE/DOCKET NUMBER: 6056-120 (CIP) 1
;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-8383
; TELEFAX: (215) 568-5549
;
; TELEX: None
;
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 266 Nucleotides
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single stranded
; TOPOLOGY: linear
;
PCT-US92-05035-4
;
Query Match 100.0%; Score 27; DB 5; Length 266;
Best Local Similarity 100.0%; Pred. No. 1.2e-06;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCTGACTTTGAGCCTCAGGCTCTGAGT 27
Db 64 TCTGACTTTGAGCCTCAGGCTCTGAGT 90

RESULT 8
US-09-310-842-1
; Sequence 1, Application US/09310842A
; Patent No. 6451593
; GENERAL INFORMATION:
; APPLICANT: Wittig, Prof. Burghardt
; APPLICANT: Jurgens, Claas
; TITLE OF INVENTION: Design Principle for Constructing Expression Constructs for Gene
; FILE REFERENCE: XI 597/99
; CURRENT APPLICATION NUMBER: US/09/310,842A
; CURRENT FILING DATE: 1999-05-12
; EARLIER APPLICATION NUMBER: DE 196 48 625.4
; EARLIER FILING DATE: 1996-11-13
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1078
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: gene
; LOCATION: (1)..(1078)
; OTHER INFORMATION: bcr3=abl2; Oligo DNA Dumbbell
;
; FEATURE:
; NAME/KEY: misc binding
; LOCATION: (1)..(2)
; OTHER INFORMATION: Intramolecular binding site; the T-nucleotides at position 1 to
; OTHER INFORMATION: 2 can be modified with amino or caroxy features
```

```
; FEATURE:
; NAME/KEY: misc binding
; LOCATION: (1077)..(1078)
; OTHER INFORMATION: Intramolecular binding site; the T-nucleotides at position 1077
; OTHER INFORMATION: to 1078 can be modified with amino or caroxy features
;
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Strandness: both; nucleic
; OTHER INFORMATION: acid (linear), hypothetical: No. 6451593 anti-sense: No
US-09-310-842-1
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Query Match 100.0%; Score 27; DB 4; Length 1078;
Best Local Similarity 100.0%; Pred. No. 1.2e-06;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 1 TCTGACTTTGAGCCTCAGGCTCTGAGT 27
Db 798 TCTGACTTTGAGCCTCAGGCTCTGAGT 824
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## RESULT 9

```
US-08-306-691B-35
; Sequence 35, Application US/08306691B
; Patent No. 5734039
; GENERAL INFORMATION:
; APPLICANT: Calabretta, Bruno
; APPLICANT: Skorski, Tomasz
; TITLE OF INVENTION: ANTISENSE
; TITLE OF INVENTION: OLIGONUCLEOTIDES TARGETING COOPERATING ONCOGENES
; NUMBER OF SEQUENCES: 55
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seidel, Gonda, Lavorgna & Monaco, P.C.
; STREET: Two Penn Center, Suite 1800
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: U.S.A.
; ZIP: 19102
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/306,691B
; FILING DATE: September 15, 1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Monaco, Daniel A.
; REGISTRATION NUMBER: 30,480
; REFERENCE/DOCKET NUMBER: 8321-8
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-8383
; TELEFAX: (215) 568-5549
; TELEX: No. 5734039e
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3623 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
;
US-08-306-691B-35
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```
Query Match 100.0%; Score 27; DB 1; Length 3623;
Best Local Similarity 100.0%; Pred. No. 1.3e-06;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 1 TCTGACTTTGAGCCTCAGGCTCTGAGT 27
Db 250 TCTGACTTTGAGCCTCAGGCTCTGAGT 276
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RESULT 10  
US-08-152-621-7  
; Sequence 7, Application US/08152621  
; Patent No. 5652222  
; GENERAL INFORMATION:  
; APPLICANT: Calabretta, Bruno  
; APPLICANT: Gewirtz, Alan M.  
; TITLE OF INVENTION: Selective Inhibition of  
; TITLE OF INVENTION: Leukemic Cell Proliferation by bcr-abl  
; TITLE OF INVENTION: Antisense Oligonucleotides  
; NUMBER OF SEQUENCES: 34  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SEIDEL, GONDA, LAVORNA  
; ADDRESSEE: & MONACO, P.C.  
; STREET: 1800 Two Penn Center  
; CITY: Philadelphia  
; STATE: Pennsylvania  
; COUNTRY: U.S.A.  
; ZIP: 19102  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb  
; COMPUTER: IBM PS/2  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: WordPerfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/152,621  
; FILING DATE: NO. 5652222ember 15, 1993  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/718,302  
; FILING DATE: June 18, 1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Monaco, Daniel A.  
; REGISTRATION NUMBER: 30,480  
; REFERENCE/DOCKET NUMBER: 6056-120 (CT.) 1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (215) 568-8383  
; TELEFAX: (215) 568-5549  
; TELEX: No. 5652222e  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 80 Nucleotides  
; TYPE: nucleic acid  
; STRANDEDNESS: single stranded  
; TOPOLOGY: linear  
US-08-152-621-7

Query Match 96.3%; Score 26; DB 1; Length 80;  
Best Local Similarity 100.0%; Pred. No. 4.3e-06;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCTGACTTTGAGCCTCAGGCTCTGAG 26  
|||||  
Db 55 TCTGACTTTGAGCCTCAGGCTCTGAG 80

RESULT 11  
US-08-306-691B-38  
; Sequence 38, Application US/08306691B  
; Patent No. 5734039  
; GENERAL INFORMATION:  
; APPLICANT: Calabretta, Bruno  
; APPLICANT: Skorski, Tomasz  
; TITLE OF INVENTION: ANTISENSE  
; TITLE OF INVENTION: OLIGONUCLEOTIDES TARGETING COOPERATING ONCOGENES  
; NUMBER OF SEQUENCES: 55  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Seidel, Gonda, Lavorna & Monaco, P.C.  
; STREET: Two Penn Center, Suite 1800  
; CITY: Philadelphia  
; STATE: Pennsylvania  
; COUNTRY: U.S.A.  
; ZIP: 19102

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb  
COMPUTER: IBM PS/2  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: WordPerfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/306,691B  
FILING DATE: September 15, 1994  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Monaco, Daniel A.  
REGISTRATION NUMBER: 30,480  
REFERENCE/DOCKET NUMBER: 8321-8  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (215) 568-8383  
TELEFAX: (215) 568-5549  
TELEX: No. 5734039e  
INFORMATION FOR SEQ ID NO: 38:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 80 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-306-691B-38

Query Match 96.3%; Score 26; DB 1; Length 80;  
Best Local Similarity 100.0%; Pred. No. 4.3e-06;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCTGACTTTGAGCCTCAGGCTCTGAG 26  
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Db 55 TCTGACTTTGAGCCTCAGGCTCTGAG 80

RESULT 12  
PCT-US92-05035-7  
; Sequence 7, Application PC/TUS9205035  
; GENERAL INFORMATION:  
; APPLICANT: Calabretta, Bruno  
; APPLICANT: Gewirtz, Alan M.  
; TITLE OF INVENTION: Selective Inhibition of  
; TITLE OF INVENTION: Leukemic Cell Proliferation by bcr-abl  
; TITLE OF INVENTION: Antisense Oligonucleotides  
; NUMBER OF SEQUENCES: 34  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Temple University - Of The Common-  
; ADDRESSEE: wealth System of Higher Education  
; STREET: 406 University Services Building  
; CITY: Philadelphia  
; STATE: Pennsylvania  
; COUNTRY: U.S.A.  
; ZIP: 19122  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb  
; COMPUTER: IBM PS/2  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: WordPerfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US92/05035  
; FILING DATE: 19920615  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/718,302  
; FILING DATE: June 18, 1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/869,911  
; FILING DATE: April 14, 1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Monaco, Daniel A.  
; REGISTRATION NUMBER: 30,480

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/ REFERENCE/DOCKET NUMBER: 6056-120 (CIP) 1
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (215) 568-8383
/ TELEFAX: (215) 568-5549
/ TELEX: None
/ INFORMATION FOR SEQ ID NO: 7:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 80 Nucleotides
/ TYPE: NUCLEIC ACID
/ STRANDEDNESS: single stranded
/ TOPOLOGY: linear
/ PCT-US92-05035-7

Query Match          96.3%; Score 26; DB 5; Length 80;
Best Local Similarity 100.0%; Pred. No. 4.3e-06;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCTGACTTTGAGCCTCAGGTCCTGAG 26
   |||||
Db 55 TCTGACTTTGAGCCTCAGGTCCTGAG 80

RESULT 13
US-09-168-947-45/c
/ Sequence 45, Application US/09168947
/ Patent No. 6589734
/ GENERAL INFORMATION:
/ APPLICANT: KACIAN, DANIEL L.
/ APPLICANT: FULTZ, TIMOTHY J.
/ APPLICANT: MCDONOUGH, SHEROL H.
/ TITLE OF INVENTION: DETECTION OF HIV
/ FILE REFERENCE: 218/130
/ CURRENT APPLICATION NUMBER: US/09/168,947
/ EARLIER FILING DATE: 1998-10-08
/ EARLIER APPLICATION NUMBER: 08/469,067
/ EARLIER FILING DATE: 1995-06-06
/ EARLIER APPLICATION NUMBER: 07/550,837
/ EARLIER FILING DATE: 1990-07-10
/ NUMBER OF SEQ ID NOS: 45
/ SOFTWARE: FASTSEQ for Windows Version 3.0
/ SEQ ID NO 45
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Synthesized nucleic acid molecule
/ US-09-168-947-45

Query Match          88.9%; Score 24; DB 4; Length 50;
Best Local Similarity 100.0%; Pred. No. 5.7e-05;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GACTTTGAGCCTCAGGTCCTGAGT 27
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Db 50 GACTTTGAGCCTCAGGTCCTGAGT 27

RESULT 14
US-08-013-419-1/c
/ Sequence 1, Application US/08013419
/ Patent No. 5300635
/ GENERAL INFORMATION:
/ APPLICANT: Macfarlane, Donald E.
/ TITLE OF INVENTION: Product and Process for Isolating RNA
/ NUMBER OF SEQUENCES: 2
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Howson and Howson
/ STREET: Spring House Corporate Center, P.O. Box 457
/ CITY: Spring House
/ STATE: Pennsylvania
/ COUNTRY: USA
/ ZIP: 19477
/ COMPUTER READABLE FORM:

Query Match          81.5%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.00077;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GACTTTGAGCCTCAGGTCCTGAG 25
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Db 22 GACTTTGAGCCTCAGGTCCTGAG 1

RESULT 15
US-08-122-795B-10/c
/ Sequence 10, Application US/08122795B
/ Patent No. 5635385
/ GENERAL INFORMATION:
/ APPLICANT: Lance H. Leopold
/ APPLICANT: Scott K. Shore
/ APPLICANT: Moolle V. R. Reddy
/ APPLICANT: E. Premkumar Reddy
/ TITLE OF INVENTION: MULTI-UNIT RIBOZYME
/ TITLE OF INVENTION: INHIBITION OF ONCOGENE EXPRESSION
/ NUMBER OF SEQUENCES: 11
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Seidel, Gonda, Lavorgna
/ ADDRESSEE: & Monaco, P.C.
/ STREET: Two Penn Center Plaza, Suite 1800
/ CITY: Philadelphia
/ STATE: Pennsylvania
/ COUNTRY: U.S.A.
/ ZIP: 19102
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb
/ COMPUTER: IBM PS/2
/ OPERATING SYSTEM: MS-DOS
/ SOFTWARE: WordPerfect 5.1
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/122,795B
/ FILING DATE:
/ CLASSIFICATION: 514
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 122,795
/ FILING DATE: 15 September 1993
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Monaco, Daniel A.
/ REGISTRATION NUMBER: 30,480
/ REFERENCE/DOCKET NUMBER: 6056-192
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (215) 568-8383
/ TELEFAX: (215) 568-5549
/ TELEX: No. 5635385e

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/013,419
FILING DATE: 19930201
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: URIF1USA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9206
TELEFAX: 215-540-5818
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
US-08-013-419-1
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; INFORMATION FOR SEQ ID NO: 10:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 22 Nucleotides

; TYPE: nucleic acid

; STRANDEDNESS: single stranded

; TOPOLOGY: linear

US-08-122-795B-10

Query Match

Best Local Similarity 81.5%; Score 22; DB 1; Length 22;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GACTTGAGCCTCAGGCTCTGA 25

Db 22 GACTTGAGCCTCAGGCTCTGA 1

Search completed: May 27, 2004, 12:08:03

Job time : 34.425 secs

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: May 27, 2004, 14:58:36 ; Search time 156.938 Seconds  
(without alignments)  
782.607 Million cell updates/sec

Title: US-09-121-239-22

Perfect score: 27  
Sequence: 1 TCTGACTTGACCTCAGGCTGTGAGT 27

Scoring table: OLIGO\_NUC  
Gapop\_60.0 , Gapext 60.0

Searched: 2960401 seqs, 2274450654 residues

Word size : 0  
Total number of hits satisfying chosen parameters: 5920802

Minimum DB seq length: 0  
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Post-processing: Listing first 45 summaries

Database : Published Applications\_NA.\*  
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15: /cgn2\_6/prodata/2/pubpna/US10C\_PUBCOMB.seq:\*  
16: /cgn2\_6/prodata/2/pubpna/US10D\_PUBCOMB.seq:\*  
17: /cgn2\_6/prodata/2/pubpna/US10\_NEW\_PUB.seq:\*  
18: /cgn2\_6/prodata/2/pubpna/US60\_NEW\_PUB.seq:\*  
19: /cgn2\_6/prodata/2/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	27	100.0	1078	15	US-10-228-811-1 Sequence 1, Appli
2	27	100.0	3393	15	US-10-263-480-1 Sequence 1, Appli
3	27	100.0	3450	16	US-10-457-954-5 Sequence 5, Appli
4	27	100.0	3840	15	US-10-204-041-3 Sequence 3, Appli
5	27	100.0	5434	13	US-10-170-385-182 Sequence 182, App
6	27	100.0	5527	9	US-09-880-107-3710 Sequence 3710, Ap
7	27	100.0	5744	16	US-10-439-703-5 Sequence 5, Appli
8	27	100.0	84539	9	US-09-962-436-36 Sequence 36, Appl
C 9	24	88.9	50	15	US-10-244-490-45 Sequence 45, Appl
C 10	22	81.5	22	9	US-09-995-912-4 Sequence 4, Appli
C 11	22	81.5	22	9	US-09-747-165-3 Sequence 3, Appli
C 12	21	77.8	21	13	US-10-382-634-20 Sequence 20, Appl
C 13	21	77.8	21	15	US-10-349-320-19 Sequence 19, Appl
14	16	59.3	468	10	US-09-918-995-19841 Sequence 19841, A

C 15	59.3	639	13	US-10-027-632-163921	Sequence 163921,
C 16	59.3	639	13	US-10-027-632-163922	Sequence 163922,
C 17	59.3	639	16	US-10-027-632-163921	Sequence 163921,
C 18	59.3	639	16	US-10-027-632-163922	Sequence 163922,
C 19	59.3	118502	13	US-10-087-192-397	Sequence 397, App
C 20	55.6	21	15	US-10-236-880-2	Sequence 2, Appli
C 21	55.6	403	10	US-09-918-995-24908	Sequence 24908, A
C 22	55.6	442	10	US-09-918-995-8048	Sequence 8048, Ap
C 23	55.6	487	13	US-10-027-632-67648	Sequence 67648, A
C 24	55.6	487	16	US-10-027-632-67648	Sequence 67648, A
C 25	55.6	554	9	US-09-864-761-9446	Sequence 9446, Ap
C 26	55.6	562	10	US-09-918-995-27376	Sequence 27376, A
C 27	55.6	566	15	US-10-029-386-5976	Sequence 5976, Ap
C 28	55.6	598	13	US-10-027-632-15713	Sequence 15713, A
C 29	55.6	598	16	US-10-027-632-15713	Sequence 15713, A
C 30	55.6	610	15	US-10-101-464A-186	Sequence 186, App
C 31	55.6	637	13	US-10-027-632-210218	Sequence 210218,
C 32	55.6	637	16	US-10-027-632-210218	Sequence 210218,
C 33	55.6	649	13	US-10-027-632-37896	Sequence 37896, A
C 34	55.6	649	16	US-10-027-632-37896	Sequence 37896, A
C 35	55.6	681	13	US-10-027-632-152558	Sequence 152558,
C 36	55.6	681	13	US-10-027-632-152558	Sequence 152558,
C 37	55.6	681	16	US-10-027-632-152558	Sequence 152558,
C 38	55.6	681	16	US-10-027-632-152558	Sequence 152558,
C 39	55.6	818	13	US-10-315-664-37	Sequence 37, Appl
C 40	55.6	825	13	US-10-181-611-1	Sequence 1, Appli
C 41	55.6	825	13	US-10-424-599-93197	Sequence 93197, A
C 42	55.6	950	9	US-09-978-295A-220	Sequence 220, App
C 43	55.6	950	9	US-09-978-697-220	Sequence 220, App
C 44	55.6	950	9	US-09-978-192A-220	Sequence 220, App
C 45	55.6	950	9	US-09-999-832A-220	Sequence 220, App

ALIGNMENTS

RESULT 1  
US-10-228-811-1  
; Sequence 1, Application US/10228811  
; Publication No. US20030054392A1  
; GENERAL INFORMATION:  
; APPLICANT: Wittig, Prof. Burghardt  
; APPLICANT: Jungmans, Claas  
; TITLE OF INVENTION: Design Principle for Constructing Expression Constructs for Gene  
; TITLE OF INVENTION: Therapy  
; FILE REFERENCE: XI 597/99  
; CURRENT APPLICATION NUMBER: US/10/238,811  
; PRIOR FILING DATE: 2002-08-27  
; PRIOR APPLICATION NUMBER: DE 196 48 625.4  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 1078  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; NAME/KEY: gene  
; LOCATION: (1)..(1078)  
; OTHER INFORMATION: bcr3=abl2; Oligo DNA Dumbbell  
; FEATURE:  
; NAME/KEY: misc.binding  
; LOCATION: (1)..(2)  
; OTHER INFORMATION: intramolecular binding site; the T-nucleotides at position 1 to  
; OTHER INFORMATION: 2 can be modified with amino or caroxy features  
; FEATURE:  
; NAME/KEY: misc.binding  
; LOCATION: (1077)..(1078)  
; OTHER INFORMATION: intramolecular binding site; the T-nucleotides at position 1077  
; OTHER INFORMATION: to 1078 can be modified with amino or caroxy features  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Strandness: both; nucleic  
; OTHER INFORMATION: acid (linear), hypothetical: No. US20030054392A1 anti-sense: No

US-10-228-811-1

Query Match 100.0%; Score 27; DB 15; Length 1078;  
Best Local Similarity 100.0%; Pred. No. 5.7e-06;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCTGACTTTGAGCCTCAGGCTCTGAGT 27  
|||||  
Db 798 TCTGACTTTGAGCCTCAGGCTCTGAGT 824  
|||||

RESULT 2

US-10-263-480-1  
; Sequence 1, Application US/10263480  
; Publication No. US20030170851A1  
; GENERAL INFORMATION:  
; APPLICANT: No. US20030170851A1artis AG  
; TITLE OF INVENTION: Organic Compounds  
; FILE REFERENCE: Case 4-32175PI/PROV  
; CURRENT APPLICATION NUMBER: US/10/263,480  
; CURRENT FILING DATE: 2002-10-03  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 1  
; LENGTH: 3393  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(3393)  
US-10-263-480-1

Query Match 100.0%; Score 27; DB 15; Length 3393;  
Best Local Similarity 100.0%; Pred. No. 5e-06;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCTGACTTTGAGCCTCAGGCTCTGAGT 27  
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Db 103 TCTGACTTTGAGCCTCAGGCTCTGAGT 129  
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RESULT 3

US-10-457-954-5  
; Sequence 5, Application US/10457954  
; Publication No. US20040005623A1  
; GENERAL INFORMATION:  
; APPLICANT: Longley, B. Jack  
; TITLE OF INVENTION: Method of determining tumor sensitivities to therapeutic drugs  
; FILE REFERENCE: 960296.98890  
; CURRENT APPLICATION NUMBER: US/10/457,954  
; CURRENT FILING DATE: 2003-06-10  
; PRIOR APPLICATION NUMBER: 60/387,370  
; PRIOR FILING DATE: 2002-06-10  
; PRIOR APPLICATION NUMBER: 60/387,406  
; PRIOR FILING DATE: 2002-06-10  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 5  
; LENGTH: 3450  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(3447)  
; FEATURE:  
; NAME/KEY: misc\_structure  
; LOCATION: (730)..(765)  
; OTHER INFORMATION: encode amino acids 244-255 for forming the sides of the enzymatic  
; OTHER INFORMATION: pocket  
; FEATURE:  
; NAME/KEY: misc\_structure  
; LOCATION: (931)..(1077)  
; OTHER INFORMATION: encode amino acids 311-359 for forming the sides of the enzymatic

OTHER INFORMATION: pocket

FEATURE:  
NAME/KEY: misc\_structure  
LOCATION: (1141)..(1206)  
OTHER INFORMATION: encode amino acids 381-402 for forming the enzymatic pocket's  
OTHER INFORMATION: activation loop  
US-10-457-954-5

Query Match 100.0%; Score 27; DB 16; Length 3450;  
Best Local Similarity 100.0%; Pred. No. 5e-06;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCTGACTTTGAGCCTCAGGCTCTGAGT 27  
|||||  
Db 160 TCTGACTTTGAGCCTCAGGCTCTGAGT 186  
|||||

RESULT 4

US-10-204-041-3  
; Sequence 3, Application US/10204041  
; Publication No. US20030176443A1  
; GENERAL INFORMATION:  
; APPLICANT: STEIN-GERLACH, MATTHIAS  
; APPLICANT: SALASSIDIS, KONSTADINOS  
; APPLICANT: BACHER, GERALD  
; APPLICANT: MULLER, STEFAN  
; TITLE OF INVENTION: Pyridylpyrimidine Derivatives as Effective Compounds Against Prion  
; TITLE OF INVENTION: Infections and Prion diseases  
; FILE REFERENCE: AXM-007.1P US  
; CURRENT APPLICATION NUMBER: US/10/204,041  
; CURRENT FILING DATE: 2002-08-16  
; PRIOR APPLICATION NUMBER: EP 01111858.5  
; PRIOR FILING DATE: 2001-05-16  
; PRIOR APPLICATION NUMBER: PCT/EP02/05420  
; PRIOR FILING DATE: 2002-05-16  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 3  
; LENGTH: 3840  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-204-041-3

Query Match 100.0%; Score 27; DB 15; Length 3840;  
Best Local Similarity 100.0%; Pred. No. 4.9e-06;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCTGACTTTGAGCCTCAGGCTCTGAGT 27  
|||||  
Db 467 TCTGACTTTGAGCCTCAGGCTCTGAGT 493  
|||||

RESULT 5

US-10-170-385-182  
; Sequence 182, Application US/10170385  
; Publication No. US20030203372A1  
; GENERAL INFORMATION:  
; APPLICANT: Ward, Neil Raymond  
; APPLICANT: Mundy, Christopher Robert  
; APPLICANT: Kan, On  
; APPLICANT: Harris, Robert Alan  
; APPLICANT: White, Jonathan  
; APPLICANT: Binley, Katie Mary  
; APPLICANT: Rayner, William Nigel  
; APPLICANT: Raylor, Stuart  
; APPLICANT: Kingsman, Susan Mary  
; APPLICANT: Krige, David  
; TITLE OF INVENTION: ANALYSIS METHOD  
; FILE REFERENCE: 532682000100  
; CURRENT APPLICATION NUMBER: US/10/170,385  
; CURRENT FILING DATE: 2002-06-12  
; PRIOR APPLICATION NUMBER: PCT/GB02/01662  
; PRIOR FILING DATE: 2002-04-08

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; PRIOR APPLICATION NUMBER: PCT/GB01/05458
; PRIOR FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 549
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 182
; LENGTH: 5434
; TYPE: DNA
; ORGANISM: Homo Sapiens
; US-10-170-385-182

Query Match      100.0%; Score 27; DB 13; Length 5434;
Best Local Similarity 100.0%; Pred. No. 4.7e-06;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCTGACTTTTGAGCCTCAGGGTCTGAGT 27
   |||||
Db 157 TCTGACTTTTGAGCCTCAGGGTCTGAGT 183

RESULT 6
US-09-880-107-3710
; Sequence 3710, Application US/09880107
; Patent No. US20020142981A1
; GENERAL INFORMATION:
; APPLICANT: Horne, Darci T.
; APPLICANT: Vockley, Joseph G.
; APPLICANT: Scherf, Uwe
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
; FILE REFERENCE: 44921-5028-WO
; CURRENT APPLICATION NUMBER: US/09/880,107
; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: US 60/211,379
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: US 60/237,054
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 3950
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3710
; LENGTH: 5527
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20020142981A1 X16416
US-09-880-107-3710

Query Match      100.0%; Score 27; DB 9; Length 5527;
Best Local Similarity 100.0%; Pred. No. 4.7e-06;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 250 TCTGACTTTTGAGCCTCAGGGTCTGAGT 276

RESULT 7
US-10-439-703-5
; Sequence 5, Application US/10439703
; Publication No. US20040018527A1
; GENERAL INFORMATION:
; APPLICANT: Chang, Jenny
; APPLICANT: O'Connell, Peter
; TITLE OF INVENTION: Differential Patterns of Gene Expression that Predict for Docetax
; FILE REFERENCE: Chemosenstivity and Chemoresistance
; FILE REFERENCE: HO-P2482US1/10205813
; CURRENT APPLICATION NUMBER: US/10/439,703
; CURRENT FILING DATE: 2003-05-16
; PRIOR APPLICATION NUMBER: US 60/381,141
; PRIOR FILING DATE: 2002-05-17
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 5744
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; TYPE: DNA
; ORGANISM: Human
; US-10-439-703-5

Query Match      100.0%; Score 27; DB 16; Length 5744;
Best Local Similarity 100.0%; Pred. No. 4.7e-06;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCTGACTTTTGAGCCTCAGGGTCTGAGT 27
   |||||
Db 467 TCTGACTTTTGAGCCTCAGGGTCTGAGT 493

RESULT 8
US-09-962-436-36
; Sequence 36, Application US/09962436
; Patent No. US20020081301A1
; GENERAL INFORMATION:
; APPLICANT: Soppet, Daniel
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatur
; FILE REFERENCE: 689290-75
; CURRENT APPLICATION NUMBER: US/09/962,436
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/60/235,082
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/234,924
; PRIOR FILING DATE: 2000-09-25
; NUMBER OF SEQ ID NOS: 568
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 36
; LENGTH: 84539
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-962-436-36

Query Match      100.0%; Score 27; DB 9; Length 84539;
Best Local Similarity 100.0%; Pred. No. 3.4e-06;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCTGACTTTTGAGCCTCAGGGTCTGAGT 27
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Db 49912 TCTGACTTTTGAGCCTCAGGGTCTGAGT 49938

RESULT 9
US-10-244-490-45/c
; Sequence 45, Application US/10244490
; Publication No. US20030152916A1
; GENERAL INFORMATION:
; APPLICANT: KACIAN, DANIEL L.
; APPLICANT: MCDONOUGH, SHERROL H.
; APPLICANT: FULTZ, TIMOTHY J.
; TITLE OF INVENTION: DETECTION OF HIV
; FILE REFERENCE: 218/130
; CURRENT APPLICATION NUMBER: US/10/244,490
; CURRENT FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: US/09/168,947
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 08/469,067
; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: 07/550,837
; PRIOR FILING DATE: 1990-07-10
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 45
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthesized nucleic acid molecule
US-10-244-490-45
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Query Match 88.9%; Score 24; DB 15; Length 50;  
Best Local Similarity 100.0%; Pred. No. 0.00042;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GACTTTGAGCCTCAGGCTCTGAGT 27  
Db 50 GACTTTGAGCCTCAGGCTCTGAGT 27

## RESULT 10

US-09-995-912-4/c  
; Sequence 4, Application US/09995912  
; Patent No. US2002013706A1  
; GENERAL INFORMATION:  
; APPLICANT: Shultz, John W.  
; APPLICANT: Lewis, Martin K.  
; APPLICANT: Andrews, Christine  
; TITLE OF INVENTION: RNA Polymers and Uses Thereof  
; FILE REFERENCE: PRMG-06684  
; CURRENT APPLICATION NUMBER: US/09/995,912  
; CURRENT FILING DATE: 2001-11-28  
; PRIOR APPLICATION NUMBER: 60/253,451  
; PRIOR FILING DATE: 2000-11-28  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 4  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic  
US-09-995-912-4

Query Match 81.5%; Score 22; DB 9; Length 22;  
Best Local Similarity 100.0%; Pred. No. 0.0065;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GACTTTGAGCCTCAGGCTCTGA 25  
Db 22 GACTTTGAGCCTCAGGCTCTGA 1

## RESULT 11

US-09-747-165-3/c  
; Sequence 3, Application US/09747165  
; Publication No. US20020192645A1  
; GENERAL INFORMATION:  
; APPLICANT: TSENG, RICHARD W.  
; APPLICANT: SAMOSZUK, MICHAEL K.  
; TITLE OF INVENTION: BCR-ABL GENE REARRANGMENT ASSAY METHOD  
; FILE REFERENCE: 034827/0302  
; CURRENT APPLICATION NUMBER: US/09/747,165  
; CURRENT FILING DATE: 2001-09-24  
; PRIOR APPLICATION NUMBER: 60/173,050  
; PRIOR FILING DATE: 1999-12-24  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 3  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Primer  
US-09-747-165-3

Query Match 81.5%; Score 22; DB 9; Length 22;  
Best Local Similarity 100.0%; Pred. No. 0.0065;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GACTTTGAGCCTCAGGCTCTGA 25  
Db 22 GACTTTGAGCCTCAGGCTCTGA 1

## RESULT 12

US-10-382-634-20/c  
; Sequence 20, Application US/10382634  
; Publication No. US20040038921A1  
; GENERAL INFORMATION:  
; APPLICANT: Kreutzer, Roalnd  
; TITLE OF INVENTION: Composition and Method for Inhibiting Expression of a Target Gene  
; FILE REFERENCE: 20200/2062  
; CURRENT APPLICATION NUMBER: US/10/382,634  
; CURRENT FILING DATE: 2003-03-07  
; PRIOR APPLICATION NUMBER: DE 101 55 280.7  
; PRIOR FILING DATE: 2001-10-26  
; PRIOR APPLICATION NUMBER: DE 101 58 411.3  
; PRIOR FILING DATE: 2001-11-29  
; PRIOR APPLICATION NUMBER: DE 101 60 151.4  
; PRIOR FILING DATE: 2001-12-07  
; PRIOR APPLICATION NUMBER: DE 102 30 996.5  
; PRIOR FILING DATE: 2002-07-09  
; PRIOR APPLICATION NUMBER: PCT/EP02/00152  
; PRIOR FILING DATE: 2002-01-09  
; PRIOR APPLICATION NUMBER: PCT/EP02/00151  
; PRIOR FILING DATE: 2002-01-09  
; PRIOR APPLICATION NUMBER: PCT/EP02/11971  
; PRIOR FILING DATE: 2002-10-25  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 20  
; LENGTH: 21  
; TYPE: DNA  
; ORGANISM: artificial sequence  
; FEATURE:  
; OTHER INFORMATION: PRIMER  
US-10-382-634-20

Query Match 77.8%; Score 21; DB 13; Length 21;  
Best Local Similarity 100.0%; Pred. No. 0.024;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 ACTTTGAGCCTCAGGCTCTGA 25  
Db 21 ACTTTGAGCCTCAGGCTCTGA 1

## RESULT 13

US-10-349-320-19/c  
; Sequence 19, Application US/10349320  
; Publication No. US20030190654A1  
; GENERAL INFORMATION:  
; APPLICANT: Heidenreich, Olaf  
; TITLE OF INVENTION: DOUBLE-STRANDED RNA (dsRNA) AND METHOD OF USE  
; FILE REFERENCE: 20200/2112  
; CURRENT APPLICATION NUMBER: US/10/349,320  
; CURRENT FILING DATE: 2003-01-22  
; PRIOR APPLICATION NUMBER: DE 102 02 419.7  
; PRIOR FILING DATE: 2002-01-22  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 19  
; LENGTH: 21  
; TYPE: DNA  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: primer  
US-10-349-320-19

Query Match 77.8%; Score 21; DB 15; Length 21;  
Best Local Similarity 100.0%; Pred. No. 0.024;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 ACTTTGAGCCTCAGGCTCTGA 25  
Db 21 ACTTTGAGCCTCAGGCTCTGA 1



RESULT 14  
 US-09-918-19841  
 ; Sequence 19841, Application US/09918995  
 ; Publication No. US20030073623A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Hyseq, Inc.  
 ; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED  
 ; FILE REFERENCE: 20411-756  
 ; CURRENT APPLICATION NUMBER: US/09/918,995  
 ; CURRENT FILING DATE: 2001-07-30  
 ; PRIOR APPLICATION NUMBER: US/09/235,076  
 ; PRIOR FILING DATE: 1999-01-20  
 ; NUMBER OF SEQ ID NOS: 38054  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 19841  
 ; LENGTH: 468  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: misc feature  
 ; LOCATION: (1)...(468)  
 ; OTHER INFORMATION: n = A,T,C or G  
 US-09-918-995-19841

Query Match 59.3%; Score 16; DB 10; Length 468;  
 Best Local Similarity 100.0%; Pred. No. 12;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TCACCTTGAGCCTCAG 18  
 |||||  
 DB 316 TCACCTTGAGCCTCAG 331

RESULT 15  
 US-10-027-632-163921/c  
 ; Sequence 163921, Application US/10027632  
 ; Publication No. US20020198371A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Wang, David G.  
 ; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
 ; FILE REFERENCE: 108827.129  
 ; CURRENT APPLICATION NUMBER: US/10/027,632  
 ; CURRENT FILING DATE: 2002-04-30  
 ; PRIOR APPLICATION NUMBER: US 60/218,006  
 ; PRIOR FILING DATE: 2000-07-12  
 ; PRIOR APPLICATION NUMBER: US 60/198,676  
 ; PRIOR FILING DATE: 2000-04-20  
 ; PRIOR APPLICATION NUMBER: US 60/193,483  
 ; PRIOR FILING DATE: 2000-03-29  
 ; PRIOR APPLICATION NUMBER: US 60/185,218  
 ; PRIOR FILING DATE: 2000-02-24  
 ; PRIOR APPLICATION NUMBER: US 60/167,363  
 ; PRIOR FILING DATE: 1999-11-23  
 ; PRIOR APPLICATION NUMBER: US 60/156,358  
 ; PRIOR FILING DATE: 1999-09-28  
 ; PRIOR APPLICATION NUMBER: US 60/146,002  
 ; PRIOR FILING DATE: 1999-08-09  
 ; NUMBER OF SEQ ID NOS: 325720  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 163921  
 ; LENGTH: 639  
 ; TYPE: DNA  
 ; ORGANISM: Human  
 US-10-027-632-163921

Query Match 59.3%; Score 16; DB 13; Length 639;  
 Best Local Similarity 100.0%; Pred. No. 12;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 TCAGCCTCAGGTCCTG 24  
 |||||  
 DB 537 TCAGCCTCAGGTCCTG 522  
 Search completed: May 27, 2004, 18:33:23  
 Job time : 157.938 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 26, 2004, 22:44:40 ; Search time 1400.96 Seconds  
(without alignments)  
575.518 Million cell updates/sec

Title: US-09-121-239-22

Perfect score: 27

Sequence: 1 TTGACTTGACCTCAGGCTGAGT 27

Scoring table: OLIGO\_NUC

Gapop\_60.0 , Gapext 60.0

Searched: 27513289 seqs, 14931090276 residues

Word size : 0

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

EST:\*

1: em\_estba:\*

2: em\_esthum:\*

3: em\_estin:\*

4: em\_estnu:\*

5: em\_estov:\*

6: em\_estpl:\*

7: em\_estro:\*

8: em\_htc:\*

9: gb\_est1:\*

10: gb\_est2:\*

11: gb\_est3:\*

12: gb\_est4:\*

13: gb\_est5:\*

14: gb\_est6:\*

15: em\_estfun:\*

16: em\_estom:\*

17: em\_gss\_hum:\*

18: em\_gss\_inv:\*

19: em\_gss\_pin:\*

20: em\_gss\_vrt:\*

21: em\_gss\_fun:\*

22: em\_gss\_man:\*

23: em\_gss\_mus:\*

24: em\_gss\_pro:\*

25: em\_gss\_rod:\*

26: em\_gss\_phg:\*

27: em\_gss\_vrl:\*

28: gb\_gss1:\*

29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	27	100.0	157	10 AW386252	AW386252 CM4-PT001
2	27	100.0	404	14 H81820	H81820 y668e09.rl
3	27	100.0	421	12 BM832613	BM832613 K-EST0107
4	27	100.0	781	13 BX097261	BX097261 BX097261

C	5	19	70.4	181	10	BE927145
	6	19	70.4	875	10	BF973844
	7	18	66.7	686	12	BI332596
	8	17	66.7	851	10	BF531871
	9	17	63.0	539	29	CE192426
	10	17	63.0	542	29	CE536813
	11	17	63.0	714	29	CE270642
C	12	17	63.0	778	29	CNS072JP
	13	17	63.0	780	28	BG206281
	14	17	63.0	788	28	BZ65134
	15	17	63.0	824	12	BI246488
C	16	17	63.0	874	29	AG160977
	17	16	59.3	129	14	CF250190
C	18	16	59.3	174	10	BE782656
	19	16	59.3	192	10	BE522588
	20	16	59.3	206	12	BI740150
	21	16	59.3	210	9	AV222166
	22	16	59.3	238	10	BE525308
	23	16	59.3	240	10	BE525590
	24	16	59.3	241	10	BE525578
	25	16	59.3	241	10	BE530312
	26	16	59.3	243	10	BB439432
	27	16	59.3	244	10	BE525566
	28	16	59.3	247	10	BE525452
	29	16	59.3	250	10	BE529949
	30	16	59.3	259	10	BE528577
	31	16	59.3	265	9	AV140149
	32	16	59.3	284	9	AV364585
	33	16	59.3	290	10	BB411430
	34	16	59.3	297	10	BE522587
	35	16	59.3	300	10	BE248616
	36	16	59.3	305	10	BB731714
	37	16	59.3	306	10	BE524258
	38	16	59.3	312	13	BY415640
	39	16	59.3	321	10	BB043130
	40	16	59.3	321	10	BE523402
C	41	16	59.3	324	9	AI482323
	42	16	59.3	330	10	BE525407
	43	16	59.3	331	10	BE525064
C	44	16	59.3	341	9	AJ444339
	45	16	59.3	341	10	BE525372

#### ALIGNMENTS

RESULT 1  
AW386252  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

AW386252 157 bp mRNA linear EST 04-FEB-2000  
CM4-PT0015-071299-057-d10 PT0015 Homo sapiens cDNA, mRNA sequence.  
AW386252  
AW386252.1 GI:6890976  
EST.  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
HCGP <http://www.ludwig.org.br/ORESTES>.  
1 (bases 1 to 157)  
The FAPESP/LICR Human Cancer Genome Project  
Unpublished (1999)  
Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: [asimpson@ludwig.org.br](mailto:asimpson@ludwig.org.br)  
This sequence was derived from the FAPESP/LICR Human Cancer Genome  
Project. This entry can be seen in the following URL  
(<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CM4&t2=CM4-PT0015-071299-057-d10&t3=1999-12-07&t4=1>)



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Matches 27;	Conservative	0;	Mismatches 0;	Indels 0;
				Gaps 0;

QY 1 CTTGACCTTGAGCCCTCCGGGCTCTGAGT 27  
Db 81 TCTGACTTTGAGCCCTCAGGCTCTGAGT 55

RESULT 5  
BE927145/c  
LOCUS BE927145 181 bp

LOCUS	BE927145.1	181 bp	EST 02-OCT-2000
DEFINITION	BE927145	181 bp	linear
ACCESSION	BE927145		
VERSION	BE927145.1		
KEYWORDS	EST.		
SOURCE	Human		
ORGANISM	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		

REFERENCE  
AUTHORS

1 (bases 1 to 181)

Dias Neto, E., Garcia Correia, R., Verjovsky-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., de Oliveira, P.S., Bucher, P., Jorgensen, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and

TITLE	U.S. A. 97 (7), 3491-3496 (2000)
Simpson, A.J. Shotgun sequencing of the human transcriptome with ORF expressed sequence tags	Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000) 20202663

JOURNAL  
MEDLINE  
PUBMED  
10737800  
PUBMED  
10737800  
PROC. NATL. ACAD. SCI. U.S.A. 97 (7), 3491-3496 (2000)  
20202663

2015000  
COMMENT  
Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research

Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
Brazil

Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: [asimpson@ludwig.org.br](mailto:asimpson@ludwig.org.br)

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL

Seq primer: puc 18 forward  
900-015-e08&t3=2000-09-01&t4=1  
(<http://www.ludwig.org.br/scripts/gethtml2.pl?ti=&t2=RC4-CN0007-010>)

High quality sequence start: 57  
High quality sequence stop: 130.

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FEATURES
Location/Qualifiers
1. .181
/organization="Home nation"
source

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/organism="Homo sapiens"
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/clone lib="CN0007"
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/note=Organ: colon normal; Vector: puc18; Site\_1: SmaI;  
Site\_2: SmaI; A mini-library was made by cloning products

derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research)

tissue mRNA and cDNA amplification were performed under profiles into the pUC 18 vector. Reverse transcription of

ORIGIN  
low stringency conditions."

Query Match 70.4%; Score 19; DB 10; Length 181;  
Best Local Similarity 100.0%; Pred. No. 2.2;

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Score: 200.00 (100.00%)
Matches: 19; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

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Qy 9 TGAGCCTCAGGGTCTGAGT 27

Db 109 TGAGCCTCAGGGTCTGAGT 91



Site\_2: Salt; Cloned unidirectionally. Primer: Oligo dt.  
Average insert size 1.9 Kb. Constructed by Life  
Technologies. Note: this is a NCI\_CGAP Library."

## ORIGIN

Query Match 66.7%; Score 18; DB 10; Length 851;  
Best Local Similarity 100.0%; Pred. No. 12;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 CTTTGAGCCTCAGGGTCT 23  
|||||  
Db 570 CTTTGAGCCTCAGGGTCT 587

## RESULT 9

CE192426 539 bp DNA linear GSS 25-SEP-2003  
LOCUS tigr-gss-dog-17000371470877 Dog Library Canis familiaris genomic,  
DEFINITION genomic survey sequence.

ACCESSION CE192426  
VERSION CE192426.1 GI:35348079  
KEYWORDS GSS.  
SOURCE Canis familiaris (dog)  
ORGANISM Canis familiaris

REFERENCE Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Kirkness,E.F., Bafna,V., Halpern,A.L., Levy,S., Remington,K.,  
Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and  
Venter,J.C.

The dog genome: survey sequencing and comparative analysis  
Science 301 (5641), 1898-1903 (2003)

TITLE The dog genome: survey sequencing and comparative analysis  
JOURNAL Science 301 (5641), 1898-1903 (2003)  
MEDLINE 22875432  
PUBMED 14512627

COMMENT Contact: Kirkness EF  
The Institute for Genomic Research  
Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,  
Rockville, MD 20850, USA  
Tel: 301-838-0200  
Fax: 301-838-0208  
Email: ekirknes@tigr.org  
Class: shotgun.

## FEATURES

source  
1. .539  
/organism="Canis familiaris"  
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peripheral blood"

## ORIGIN

Query Match 63.0%; Score 17; DB 29; Length 539;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 AGCCTCAGGCTCTGACT 27  
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Db 346 AGCCTCAGGCTCTGACT 362

## RESULT 10

CE536813 542 bp DNA linear GSS 28-SEP-2003  
LOCUS tigr-gss-dog-17000365931015 Dog Library Canis familiaris genomic,  
DEFINITION genomic survey sequence.

ACCESSION CE536813  
VERSION CE536813.1 GI:36853594  
KEYWORDS GSS.  
SOURCE Canis familiaris (dog)  
ORGANISM Canis familiaris

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE  
AUTHORS

Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
1 (bases 1 to 542)  
Kirkness,E.F., Bafna,V., Halpern,A.L., Levy,S., Remington,K.,  
Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and  
Venter,J.C.

The dog genome: survey sequencing and comparative analysis  
Science 301 (5641), 1898-1903 (2003)

TITLE The dog genome: survey sequencing and comparative analysis  
JOURNAL Science 301 (5641), 1898-1903 (2003)  
MEDLINE 22875432  
PUBMED 14512627

COMMENT Contact: Kirkness EF  
The Institute for Genomic Research  
Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,  
Rockville, MD 20850, USA  
Tel: 301-838-0200  
Fax: 301-838-0208  
Email: ekirknes@tigr.org  
Class: shotgun.

## FEATURES

source  
Location/Qualifiers  
1. .542  
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/mol\_type="genomic DNA"  
/strain="Standard Poodle"  
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/clone\_lib="Dog Library"  
/note="Site\_1: BstXI; Libraries were prepared from  
peripheral blood"

## ORIGIN

Query Match 63.0%; Score 17; DB 29; Length 542;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 TGAGCCTCAGGCTCTGA 25  
|||||  
Db 49 TGAGCCTCAGGCTCTGA 65

## RESULT 11

CE270642/c 714 bp DNA linear GSS 26-SEP-2003  
LOCUS tigr-gss-dog-1700033537646 Dog Library Canis familiaris genomic,  
DEFINITION genomic survey sequence.

ACCESSION CE270642  
VERSION CE270642.1 GI:36002203  
KEYWORDS GSS.  
SOURCE Canis familiaris (dog)  
ORGANISM Canis familiaris

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

REFERENCE 1 (bases 1 to 714)  
AUTHORS Kirkness,E.F., Bafna,V., Halpern,A.L., Levy,S., Remington,K.,  
Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and  
Venter,J.C.

The dog genome: survey sequencing and comparative analysis  
Science 301 (5641), 1898-1903 (2003)

TITLE The dog genome: survey sequencing and comparative analysis  
JOURNAL Science 301 (5641), 1898-1903 (2003)  
MEDLINE 22875432  
PUBMED 14512627

COMMENT Contact: Kirkness EF  
The Institute for Genomic Research  
Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,  
Rockville, MD 20850, USA  
Tel: 301-838-0200  
Fax: 301-838-0208  
Email: ekirknes@tigr.org  
Class: shotgun.

FEATURES  
source

Location/Qualifiers  
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/mol\_type="genomic DNA"  
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peripheral blood"

/evidence=not\_experimental

## ORIGIN

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QY 9 TGAGCCTCAGGGTCTGA 25  
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 Db 485 TGAGCCTCAGGGTCTGA 469

## RESULT 12

CNS072JP

LOCUS

DEFINITION 778 bp DNA linear GSS 07-JUL-2001  
 clone BAOAB012A05 of library BAOAB from strain CLIB 210 of

Kluyveromyces lactis, genomic survey sequence.

ACCESSION AL426299

VERSION AL426299.1 GI:12209493

KEYWORDS GSS.

SOURCE Kluyveromyces lactis

ORGANISM Kluyveromyces lactis

REFERENCE 1 (bases 1 to 778)

AUTHORS Souciet J.L., Aigle M., Artiguenave F., Blandin G.,

Bolotin-Fukuhara M., Bon E., Brottier P., Casaregola S.,

de-Montigny J., Dujon B., Durrens P., Lepingle A., Liorente B.,

Maupertuy A., Neuveglise C., Ozier-Kalogeropoulos O., Potier S.,

Saurin W., Tekala P., Toffano-Nioche C., Wesolowski-Louvel M.,

Wincker P. and Weissenbach J.

Genomic exploration of the hemiascomycetous yeasts: 1. A set of

yeast species for molecular evolution studies

FEBS Lett. 487 (1), 3-12 (2000)

PUBMED 20584711

11152876

REFERENCE 2 (bases 1 to 778)

AUTHORS Bolotin-Fukuhara M., Toffano-Nioche C., Artiguenave F.,

Duchateau-Nguyen G., Lemaire M., Marmeisse R., Montrocher R.,

Robert C., Terrier M., Wincker P. and Wesolowski-Louvel M.

Genomic exploration of the hemiascomycetous yeasts: 11.

Kluyveromyces lactis

FEBS Lett. 487 (1), 66-70 (2000)

PUBMED 11152886

11152886

REFERENCE 3 (bases 1 to 778)

AUTHORS Direct Submission

TITLE Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage,

2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail :

seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

This GSS is part of a random genomic sequencing program of thirteen

yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces

exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii,

Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces

lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia

angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila,

Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to

5 kb were prepared and both extremities were sequenced. See

keywords for description of this sequence and for the sequence of

the other extremity of this insert.

FEATURES

source

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/variety="lactis"

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/clone\_lib="BAOAB"

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SEC35 ; required for ER to golgi vesicle docking ]"

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SEC35 ; required for ER to golgi vesicle docking ]"

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 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCTGACTTTGAGCCTCA 17  
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 Db 518 TCTGACTTTGAGCCTCA 534

## RESULT 13

BG206281

LOCUS

DEFINITION 780 bp mRNA linear EST 21-APR-2001  
 RST5726 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.

ACCESSION BG206281

VERSION BG206281.1 GI:13727968

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 780)

AUTHORS Harrington J.J., Sherif B., Rundlett S., Jackson P.D., Perry R.,

Cain S., Leventhal C., Thornton M., Ramachandran R.,

Whittington J., Lerner L., Costanzo D., McElligott K., Booser S.,

Mays R., Smith E., Veloso N., Klika A., Hess J., Cothren K., Lo K.,

Offenbacher J., Danzig J. and Ducar M.

Creation of genome-wide protein expression libraries using random

activation of gene expression

Nat. Biotechnol. 19 (5), 440-445 (2001)

PUBMED 21227151

11329013

COMMENT Contact: Scott J. Cain

Athersys, Inc.

3201 Carnegie Ave, Cleveland, OH 44115, USA

Tel: 216 431 9900

Fax: 216 361 9596

Email: scain@atersys.com

High quality sequence stop: 425.

Location/Qualifiers

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/mol\_type="mRNA"

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/cell\_line="Ht1080"

/clone\_lib="Athersys RAGE Library"

/note="See 'Creation of Genome-wide Protein Expression

Libraries using Random Activation of Gene Expression',

Nature Biotechnology, in press. Note that even though the

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method was used, these sequence tags are not necessarily

expressed in Ht1080 under normal circumstances."

## ORIGIN

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QY 9 TGAGCCTCAGGGTCTGA 25  
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 Db 60 TGAGCCTCAGGGTCTGA 76

## RESULT 14

BZ865134

LOCUS

DEFINITION 788 bp DNA linear GSS 18-MAR-2003  
 CH240\_235MB TJ CHORI-240 Bos taurus genomic clone CH240\_235MB,

genomic survey sequence.

ACCESSION BZ865134

VERSION BZ865134.1 GI:29092539

KEYWORDS GSS.



SOURCE Bos taurus (cow)  
ORGANISM Bos taurus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;  
Bovidae; Bovinae; Bos.  
REFERENCE 1 (bases 1 to 788)  
AUTHORS Zhao, S., Shetty, J., Shatman, S., Teagave, G., Geer, K.,  
Shvartsbeyn, A., Georgegeorgis, E., Chen, D., Riggs, F., de Jong, P.,  
Crawford, A. M. and McSwan, J. C.  
TITLE Bovine BAC End Sequences from Library CHORI-240  
JOURNAL Unpublished (2003)  
COMMENT Contact: Shaying Zhao  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Dr., Rockville, MD 20850, USA  
Tel: 301 838 0200  
Fax: 301 838 0208  
Email: szhao@tigr.org  
Clones are derived from the bovine BAC library CHORI-240  
(<http://www.chori.org/bacpac/bovine240.htm>). For BAC library  
availability, please contact Pieter de Jong ([pdejong@mail.cho.org](mailto:pdejong@mail.cho.org)).  
Clones may be purchased from BACPAC Resources  
(<http://www.chori.org/bacpac/ordering/information.htm>). This work  
was undertaken as part of the International Bovine BAC Mapping  
Consortium (IBBMC) by AgResearch Ltd., New Zealand and The  
Institute of Genomic Research (TIGR), USA.  
Plate: 235 row: M column: 8  
Seq primer: SP6  
Class: BAC ends.

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/notes="Vector: pTARBAC1.3; Site 1: MboI; Site 2: MboI;  
Hereford bull L1 Domino 99375; CHORI-240 Bovine BAC  
library (Male) produced by Pieter de Jong"

ORIGIN  
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Best Local Similarity 100.0%; Pred. No. 44;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 7 TTTGAGCCTCAGGGTCT 23  
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DB 277 TTTGAGCCTCAGGGTCT 293  
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RESULT 15  
BI246488  
LOCUS 602958537F1 NCI\_CGAP\_Li9 Mus musculus cDNA clone IMAGE:5124201 5',  
DEFINITION mRNA sequence.  
ACCESSION BI246488  
VERSION BI246488.1 GI:114790501  
KEYWORDS EST.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 824)  
AUTHORS NIH-MGC <http://mgi.nci.nih.gov/>.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)  
Tissue Procurement: Jeffrey E. Green, M.D.  
CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: LLAM11303 row: j column: 10  
High quality sequence stop: 714.  
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/clone\_lib="NCI CGAP Li9"  
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Technologies. Note: this is a NCI\_CGAP Library."

ORIGIN  
Query Match 63.0%; Score 17; DB 12; Length 824;  
Best Local Similarity 100.0%; Pred. No. 45;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 6 CTTTGAGCCTCAGGGTCT 22  
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DB 551 CTTTGAGCCTCAGGGTCT 567  
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Search completed: May 27, 2004, 11:30:39  
Job time : 1400.96 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 27, 2004, 02:16:55 ; Search time 715.838 Seconds  
(without alignments)  
1634.815 Million cell updates/sec

Title: US-09-121-239-23

Perfect score: 27  
Sequence: 1 UCUGACUUUGAGCCUACGGGUCUGAGU 27

Scoring table: OLIGO\_NUC  
Gapop\_60.0 , Gapext 60.0

Searched: 3470272 seqs, 21671516995 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

GenEmbl.\*

1: gb\_ba.\*

2: gb\_htg.\*

3: gb\_in.\*

4: gb\_om.\*

5: gb\_ov.\*

6: gb\_pat.\*

7: gb\_ph.\*

8: gb\_pl.\*

9: gb\_pr.\*

10: gb\_ro.\*

11: gb\_sts.\*

12: gb\_sy.\*

13: gb\_un.\*

14: gb\_vi.\*

15: em\_ba.\*

16: em\_fun.\*

17: em\_hum.\*

18: em\_in.\*

19: em\_mu.\*

20: em\_om.\*

21: em\_or.\*

22: em\_ov.\*

23: em\_pat.\*

24: em\_ph.\*

25: em\_pl.\*

26: em\_ro.\*

27: em\_sts.\*

28: em\_un.\*

29: em\_vi.\*

30: em\_htg\_hum.\*

31: em\_htg\_inv.\*

32: em\_htg\_other.\*

33: em\_htg\_mus.\*

34: em\_htg\_pln.\*

35: em\_htg\_rnd.\*

36: em\_htg\_mam.\*

37: em\_htg\_vrt.\*

38: em\_sy.\*

39: em\_htgo\_hum.\*

40: em\_htgo\_mus.\*

41: em\_htgo\_other.\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

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C 1	27	100.0	27	6	BD222542	BD222542 Methods f
C 2	27	100.0	27	6	BD222543	BD222543 Methods f
C 3	27	100.0	27	6	BD222544	BD222544 Methods f
C 4	27	100.0	27	6	BD222545	BD222545 Methods f
C 5	27	100.0	54	6	BD222523	BD222523 Methods f
C 6	27	100.0	54	6	BD222524	BD222524 Methods f
C 7	27	100.0	54	6	BD222525	BD222525 Methods f
C 8	27	100.0	54	6	BD222526	BD222526 Methods f
C 9	27	100.0	102	9	HST922FU	X07537 Human ALL t
C 10	27	100.0	153	9	HUMABLB	M14754 Human abl m
C 11	27	100.0	204	9	HUMBCRA2	M25948 Human chron
C 12	27	100.0	205	6	I02402	I02402 Sequence 1
C 13	27	100.0	234	9	HUMCABLA1	M13098 Homo sapien
C 14	27	100.0	257	6	I58633	I58633 Sequence 1
C 15	27	100.0	257	6	I96199	I96199 Sequence 36
C 16	27	100.0	266	6	I58636	I58636 Sequence 4
C 17	27	100.0	266	6	I96200	I96200 Sequence 37
C 18	27	100.0	299	6	BD222547	BD222547 Methods f
C 19	27	100.0	350	6	BD222546	BD222546 Methods f
C 20	27	100.0	423	9	AB069693	AB069693 Homo sapi
C 21	27	100.0	468	9	HUMCMCABL	M25946 Human chron
C 22	27	100.0	468	9	HUMKS62A	M13096 Human chime
C 23	27	100.0	491	9	HUMALLBCR	M19730 Human acute
C 24	27	100.0	494	9	HUMALBLC	M30833 Human abl p
C 25	27	100.0	532	9	HUMABLEA	M14753 Human abl m
C 26	27	100.0	549	9	HSBREAAP3	Z35761 Homo sapien
C 27	27	100.0	679	9	HUMABLB	M30832 Human bcr/a
C 28	27	100.0	854	9	HUMABLD	M30829 Human bcr/a
C 29	27	100.0	922	9	HSAL31467	AJ131467 Homo sapi
C 30	27	100.0	997	9	HSAL31466	AJ131466 Homo sapi
C 31	27	100.0	1078	6	A92081	A92081 Sequence 5
C 32	27	100.0	1078	6	AR230688	AR230688 Sequence 5
C 33	27	100.0	1079	9	AF113911	AF113911 Homo sapi
C 34	27	100.0	3393	6	AX743957	AX743957 Sequence 35
C 35	27	100.0	3623	6	I96198	I96198 Sequence 35
C 36	27	100.0	3840	6	AX601393	AX601393 Sequence
C 37	27	100.0	3840	9	HUMABLA	M14752 Human c-abl
C 38	27	100.0	5527	6	AX411066	AX411066 Sequence
C 39	27	100.0	5527	9	HSABL	X16416 Human c-abl
C 40	27	100.0	5744	6	AX779943	AX779943 Sequence
C 41	27	100.0	84539	6	AX331386	AX331386 Sequence
C 42	27	100.0	84539	9	HSABLGR3	U07563 Human proto
C 43	27	100.0	176466	9	AL161733	AL161733 Human DNA
C 44	26	96.3	80	6	I58639	I58639 Sequence 7
C 45	26	96.3	80	6	I96201	I96201 Sequence 38

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DEFINITION	BD222542				
ACCESSION	BD222542				
VERSION	BD222542.1	GI:33032312			
KEYWORDS	JP 2002521037-A/20.				
SOURCE	synthetic construct				
ORGANISM	artificial sequences.				
REFERENCE	1 (bases 1 to 27)				
AUTHORS	Harvey, R.C. and Eastman, P.S.				
TITLE	Methods for detecting and measuring spliced nucleic acids				
JOURNAL	Patent: JP 2002521037-A 20 16-JUL-2002;				
	GEN PROBE INC				

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COMMENT OS Artificial Sequence
PN JP 2002521037-A/20
PD 16-JUL-2002
PF 23-JUL-1999 JP 2000561364
PR 23-JUL-1998 US 09/121239
PI RICHARD C HARVEY, PAUL S EASTMAN
PC C12Q1/68, C12N15/09, C12N15/00
CC Description of Artificial Sequence: Primer sequence as in SEQ
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CC without T7 promoter sequence
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Matches 18; Conservative 9; Mismatches 0; Indels 0; Gaps 0;
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Db 27 TCTGACTTTGAGCCTCAGGGTCTGAGT 1
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LOCUS 27 bp RNA linear PAT 17-JUL-2003
DEFINITION Methods for detecting and measuring spliced nucleic acids.
ACCESSION BD222543
VERSION 1 GI:33032313
KEYWORDS JP 2002521037-A/21.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 27)
AUTHORS Harvey, R.C. and Eastman, P.S.
TITLE Methods for detecting and measuring spliced nucleic acids
JOURNAL Patent: JP 2002521037-A 21 16-JUL-2002;
GEN PROBE INC
COMMENT OS Artificial Sequence
PN JP 2002521037-A/21
PD 16-JUL-2002
PF 23-JUL-1999 JP 2000561364
PR 23-JUL-1998 US 09/121239
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PC C12Q1/68, C12N15/09, C12N15/00
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DEFINITION Methods for detecting and measuring spliced nucleic acids.
ACCESSION BD222543
VERSION 1 GI:33032313
KEYWORDS JP 2002521037-A/21.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 27)
AUTHORS Harvey, R.C. and Eastman, P.S.
TITLE Methods for detecting and measuring spliced nucleic acids
JOURNAL Patent: JP 2002521037-A 21 16-JUL-2002;
GEN PROBE INC
COMMENT OS Artificial Sequence
PN JP 2002521037-A/21
PD 16-JUL-2002
PF 23-JUL-1999 JP 2000561364
PR 23-JUL-1998 US 09/121239
PI RICHARD C HARVEY, PAUL S EASTMAN
PC C12Q1/68, C12N15/09, C12N15/00
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DEFINITION Methods for detecting and measuring spliced nucleic acids.
ACCESSION BD222544
VERSION 1 GI:33032314
KEYWORDS JP 2002521037-A/22.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 27)
AUTHORS Harvey, R.C. and Eastman, P.S.
TITLE Methods for detecting and measuring spliced nucleic acids
JOURNAL Patent: JP 2002521037-A 22 16-JUL-2002;
GEN PROBE INC
COMMENT OS Artificial Sequence
PN JP 2002521037-A/22
PD 16-JUL-2002
PF 23-JUL-1999 JP 2000561364
PR 23-JUL-1998 US 09/121239
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LOCUS 27 bp RNA linear PAT 17-JUL-2003
DEFINITION Methods for detecting and measuring spliced nucleic acids.
ACCESSION BD222545
VERSION 1 GI:33032315
KEYWORDS JP 2002521037-A/23.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 27)
AUTHORS Harvey, R.C. and Eastman, P.S.
TITLE Methods for detecting and measuring spliced nucleic acids
JOURNAL Patent: JP 2002521037-A 23 16-JUL-2002;
GEN PROBE INC
COMMENT OS Artificial Sequence
PN JP 2002521037-A/23
PD 16-JUL-2002
PF 23-JUL-1999 JP 2000561364
PR 23-JUL-1998 US 09/121239
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LOCATION/QUALIFIERS

1..234

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db\_xref="taxon:9606"

chromosome="9"

map="9q34.1"

31..204

gene="ABL1"

note="G00-119-640; putative"

number=a1

205..>234

gene="ABL1"

note="C-abl"

number=A

ORIGIN

Query Match 100.0%; Score 27; DB 9; Length 234;

Best Local Similarity 66.7%; Pred. No. 6.3e-05;

Matches 18; Conservative 9; Mismatches 0; Indels 0; Gaps 0;

QY 1 UCUGACUUUGAGCCUCAGGUCUGAGU 27

54 TCTGACTTTTGAGCCTCAGGGTCTGAGT 80

RESULT 14

I58633

LOCUS

DEFINITION

Accession

Version

Keywords

Source

Organism

Unclassified.

1 (bases 1 to 257)

Calabretta,B. and Gewirtz,A.M.

Selective inhibition of leukemic cell proliferation by bcr-abl antisense oligonucleotides

Patent: US 5652222-A 1 29-JUL-1997;

Location/Qualifiers

1..257

organism="unknown"

mol\_type="unassigned DNA"

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Query Match 100.0%; Score 27; DB 6; Length 257;

Best Local Similarity 66.7%; Pred. No. 6.2e-05;

Matches 18; Conservative 9; Mismatches 0; Indels 0; Gaps 0;

QY 1 UCUGACUUUGAGCCUCAGGUCUGAGU 27

55 TCTGACTTTTGAGCCTCAGGGTCTGAGT 81

RESULT 15

I96199

LOCUS

DEFINITION

Accession

Version

Keywords

SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 257)  
AUTHORS Calabretta,B. and Skorski,T.  
TITLE Antisense oligonucleotides targeting cooperating oncogenes  
JOURNAL Patent: US 5734039-A 36 31-MAR-1998;  
FEATURES Location/Qualifiers  
          1..257  
          /organism="unknown"  
          /mol\_type="unassigned DNA"  
  
ORIGIN  
Query Match 100.0%; Score 27; DB 6; Length 257;  
Best Local Similarity 66.7%; Pred.No 6.2e-05;  
Matches 18; Conservative 9; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 UCUGACUUGAGCCUCAGGGUCUGAGU 27  
   :||||:||||:||||:||||:||||:  
Db 55 TCTGACTTTGAGGCTCAGGGTCTGAGT 81

Search completed: May 27, 2004, 12:06:11  
Job time : 716.838 secs





CC the analysis and detection of nucleic acids in biological samples. The  
 CC methods are useful in the human medical and veterinary fields, for  
 CC medical diagnoses and clinical monitoring of a patient's response to  
 CC therapy where a disease or medical condition is associated with a  
 CC particular type and/or level of mRNA present in the sample. The methods  
 CC are also useful for detecting or quantifying fusion or chimeric RNA  
 CC species, and for detecting a translocation as a marker for a given  
 CC condition or disease, e.g. translocations associate with cancers,  
 CC particularly forms of leukemia

XX Sequence 27 BP; 4 A; 6 C; 8 G; 9 T; 0 U; 0 Other;  
 SQ Query Match 100.0%; Score 27; DB 3; Length 27;  
 Best Local Similarity 66.7%; Pred. No. 3.9e-05;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 UCUGACUUUGAGCCUCAGGUCUGAGU 27  
 Db :|||||:|||||:|||||:|||||:  
 1 TCTGACTTTTGAGCCTCAGGCTCTGAGT 27

RESULT 2  
 AAZ60862  
 ID AAZ60862 standard; RNA; 27 BP.  
 XX  
 AC AAZ60862;  
 DT 16-MAY-2000 (first entry)  
 XX Oligonucleotide used to detect bcr b3-abl fusion transcripts.  
 XX Fusion transcript; translocation; bcr b3 region; abl gene;  
 KW amplification assay; detection assay; medical diagnosis;  
 KW clinical monitoring; chimeric RNA; fusion RNA; condition marker;  
 KW disease marker; cancer; leukemia; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200005418-A1.  
 XX  
 PD 03-FEB-2000.  
 XX  
 PF 23-JUL-1999; 99WO-US016832.  
 XX  
 PR 23-JUL-1998; 98US-00121239.  
 XX  
 PA (GENP-) GEN-PROBE INC.  
 XX  
 PI Harvey RC, Eastman PS;  
 XX  
 DR WPI; 2000-182730/16.  
 XX  
 PT Novel methods for preparing RNA from biological samples, used for the  
 PT detection and measurement of nucleic acids and fusion nucleic acids.  
 XX  
 PS Claim 19; Page 44; 49pp; English.  
 XX  
 CC Oligonucleotides AAZ60840-62 and AAZ60865-66 are used in the method of  
 CC the invention to detect fusion transcripts produced from a translocation  
 CC between the bcr b3 region and the abl gene. The specification describes a  
 CC method for detecting a fusion nucleic acid (particularly chimeric mRNA  
 CC species), in a biological sample. The method comprises contacting a  
 CC sample of fusion nucleic acid with primers, amplifying the hybridized  
 CC fusion nucleic acid, and detecting the target hybrid. The method is used  
 CC for the simple and rapid preparation of RNA from a biological sample,  
 CC particularly from the cytoplasm of eukaryotic cells, which is suitable  
 CC for use in an amplification and detection assay. The methods are used for  
 CC the analysis and detection of nucleic acids in biological samples. The  
 CC methods are useful in the human medical and veterinary fields, for  
 CC medical diagnoses and clinical monitoring of a patient's response to  
 CC therapy where a disease or medical condition is associated with a  
 CC particular type and/or level of mRNA present in the sample. The methods  
 CC are also useful for detecting or quantifying fusion or chimeric RNA  
 CC species, and for detecting a translocation as a marker for a given  
 CC condition or disease, e.g. translocations associate with cancers,  
 CC particularly forms of leukemia

CC species, and for detecting a translocation as a marker for a given  
 CC condition or disease, e.g. translocations associate with cancers,  
 CC particularly forms of leukemia

XX Sequence 27 BP; 4 A; 6 C; 8 G; 0 T; 9 U; 0 Other;  
 SQ Query Match 100.0%; Score 27; DB 3; Length 27;  
 Best Local Similarity 100.0%; Pred. No. 3.9e-05;  
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 UCUGACUUUGAGCCUCAGGUCUGAGU 27  
 Db |||||||:|||||:|||||:|||||:  
 1 UCUGACUUUGAGCCUCAGGUCUGAGU 27

RESULT 3  
 AAZ60860/c  
 ID AAZ60860 standard; RNA; 27 BP.  
 XX  
 AC AAZ60860;  
 DT 16-MAY-2000 (first entry)  
 XX Oligonucleotide used to detect bcr b3-abl fusion transcripts.  
 XX Fusion transcript; translocation; bcr b3 region; abl gene;  
 KW amplification assay; detection assay; medical diagnosis;  
 KW clinical monitoring; chimeric RNA; fusion RNA; condition marker;  
 KW disease marker; cancer; leukemia; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200005418-A1.  
 XX  
 PD 03-FEB-2000.  
 XX  
 PF 23-JUL-1999; 99WO-US016832.  
 XX  
 PR 23-JUL-1998; 98US-00121239.  
 XX  
 PA (GENP-) GEN-PROBE INC.  
 XX  
 PI Harvey RC, Eastman PS;  
 XX  
 DR WPI; 2000-182730/16.  
 XX  
 PT Novel methods for preparing RNA from biological samples, used for the  
 PT detection and measurement of nucleic acids and fusion nucleic acids.  
 XX  
 PS Claim 19; Page 43; 49pp; English.  
 XX  
 CC Oligonucleotides AAZ60840-62 and AAZ60865-66 are used in the method of  
 CC the invention to detect fusion transcripts produced from a translocation  
 CC between the bcr b3 region and the abl gene. The specification describes a  
 CC method for detecting a fusion nucleic acid (particularly chimeric mRNA  
 CC species), in a biological sample. The method comprises contacting a  
 CC sample of fusion nucleic acid with primers, amplifying the hybridized  
 CC fusion nucleic acid, and detecting the target hybrid. The method is used  
 CC for the simple and rapid preparation of RNA from a biological sample,  
 CC particularly from the cytoplasm of eukaryotic cells, which is suitable  
 CC for use in an amplification and detection assay. The methods are used for  
 CC the analysis and detection of nucleic acids in biological samples. The  
 CC methods are useful in the human medical and veterinary fields, for  
 CC medical diagnoses and clinical monitoring of a patient's response to  
 CC therapy where a disease or medical condition is associated with a  
 CC particular type and/or level of mRNA present in the sample. The methods  
 CC are also useful for detecting or quantifying fusion or chimeric RNA  
 CC species, and for detecting a translocation as a marker for a given  
 CC condition or disease, e.g. translocations associate with cancers,  
 CC particularly forms of leukemia

XX Sequence 27 BP; 9 A; 8 C; 6 G; 0 T; 4 U; 0 Other;

Query Match 100.0%; Score 27; DB 3; Length 27;  
Best Local Similarity 66.7%; Pred. No. 3.9e-05;  
Matches 18; Conservative 9; Mismatches 0; Indels 0; Gaps 0;

**Qy** 1 UCUGACUUUGAGGCCUCACGGGUCUGAGU 27  
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AAZ60859/c  
ID AAZ60859 standard; DNA; 27 BP.

AC	AAZ60859;
XX	
XX	
DT	16-MAY-2000 (first entry)
XX	
DE	Oligonucleotide used to detect bcr b3-abl fusion transcripts.
XX	
XX	
XX	Fusion transcript; translocation; bcr b3 region; abl gene;
KW	amplification assay; detection assay; medical diagnosis;
KW	clinical monitoring; chimeric RNA; fusion RNA; condition marker;
KW	disease marker; cancer; leukemia; ss.

OS Synthetic.

PN WO200005418-A1.

03-FEB-2000.

23-JUL-1999;

23-JUL-1998;

PA (GENP-) GEN-PROBE INC.

PI Harvey RC, Eastman PS;

WPI; 2000-182730/16.

Novel methods for preparing RNA from biological samples, used for the detection and measurement of nucleic acids and fusion nucleic acids.

PS Claim 19: Page 43: 49pp: English.

Oligonucleotides AA260840-62 and AA260855-66 are used in the method of the invention to detect fusion transcripts produced from a translocation between the bcr b3 region and the abl gene. The specification describes a method for detecting a fusion nucleic acid (particularly chimeric mRNA species), in a biological sample. The method comprises contacting a sample of fusion nucleic acid with primers, amplifying the hybridized fusion nucleic acid, and detecting the target hybrid. The method is used for the simple and rapid preparation of RNA from a biological sample, particularly from the cytoplasm of eukaryotic cells, which is suitable for use in an amplification and detection assay. The methods are used for the analysis and detection of nucleic acids in biological samples. The methods are useful in the human medical and veterinary fields, for medical diagnoses and clinical monitoring of a patient's response to therapy where a disease or medical condition is associated with a particular type and/or level of mRNA present in the sample. The methods are also useful for detecting or quantifying fusion or chimeric RNA species, and for detecting a translocation as a marker for a given condition or disease, e.g. translocations associate with cancers, particularly forms of leukemia

Sequence 27 BP; 9 A; 8 C; 6 G; 4 T; 0 U; 0 Other;

Query Match 100.0%; Score 27; DB 3; Length 27;  
Best Local Similarity 66.7%; Pred. No. 3.9e-05;  
Matches 18; Conservative 9; Mismatches 0; Indels

QY 1 UCUGACUUUGAGCCUCAGGGUCUGAGU 27  
: : : : : : : : : : : : : : : : : :

Db 27 TCTGACTTTGAGCCTCAGGGTCTGAGT 1

## RESULT 5

ID AAZ60843 standard; RNA; 54 BP.

AAZ60843;

DT 16-MAY-2000 (first entry)

DE Oligonucleotide used to detect bcr b3-abl fusion transcripts.

**KW** Fusion transcript; translocation; bcr b3 region; abl gene;  
**KW** amplification assay; detection assay; medical diagnosis;  
**KW** clinical monitoring; chimeric RNA; fusion RNA; condition marker;  
**KW** disease marker; cancer; leukemia; ss.

OS Synthetic.

PN WO200005418-A1.

03-FEB-2000:

23-JUL-1999; 99WO-US016832.

PR 23-JUL-1998; 98US-00121239.

PA (GENP-) GEN-PROBE INC.

PI Harvey RC, Eastman PS;

WPI; 2000-182730/16.

Novel methods for preparing RNA from biological samples, used for the detection and measurement of nucleic acids and fusion nucleic acids.

PS Claim 19: Page 40: 49pp: English.

Oligonucleotides AA260840-62 and AA260855-66 are used in the method of the invention to detect fusion transcripts produced from a translocation between the bcr b3 region and the abl gene. The specification describes a method for detecting a fusion nucleic acid (particularly chimeric mRNA species), in a biological sample. The method comprises contacting a sample of fusion nucleic acid with primers, amplifying the hybridized fusion nucleic acid, and detecting the target hybrid. The method is used for the simple and rapid preparation of RNA from a biological sample, particularly from the cytoplasm of eukaryotic cells, which is suitable for use in an amplification and detection assay. The methods are used for the analysis and detection of nucleic acids in biological samples. The methods are useful in the human medical and veterinary fields, for medical diagnoses and clinical monitoring of a patient's response to therapy where a disease or medical condition is associated with a particular type and/or level of mRNA present in the sample. The methods are also useful for detecting or quantifying fusion or chimeric RNA species, and for detecting a translocation as a marker for a given condition or disease, e.g. translocations associated with cancers, particularly forms of leukemia.

Sequence 54 BP; 11 A; 11 C; 12 G; 0 T; 20 U; 0 Other;

Query Match 100.0%; Score 27; DB 3; Length 54;  
Best Local Similarity 100.0%; Pred. No. 3.8e-05;  
Matches 27; Conservative 0; Mismatches 0; Indels

QY 1 UCUGACUUUGAGCCUCACGGGUCUGAGU 27

Db 1 UCUGACUUUGAGCCUCAGGGUCUGAGU 27

RESULT 6  
AAZ60841/c  
ID AAZ60841 standard; RNA; 54 BP.







[illegible]

XX 23-JUL-1999; 99WO-US016832.  
XX 23-JUL-1998; 98US-00121239.  
XX (GENP-) GEN-PROBE INC.  
XX Harvey RC, Eastman PS;  
XX WPI; 2000-182730/16.  
XX  
PT Novel methods for preparing RNA from biological samples, used for the  
PT detection and measurement of nucleic acids and fusion nucleic acids.  
XX  
PS Disclosure; Fig 2; 49pp; English.  
XX  
CC The present sequence represents a region surrounding a bcr-able splice  
CC junction. The specification describes oligonucleotides which are used to  
CC detect fusion transcripts produced from a translocation between the bcr  
CC b3 region and the abl gene. The specification also describes a method for  
CC detecting a fusion nucleic acid (particularly chimeric mRNA species), in  
CC a biological sample. The method comprises contacting a sample of fusion  
CC nucleic acid with primers, amplifying the hybridized fusion nucleic acid,  
CC and detecting the target hybrid. The method is used for the simple and  
CC rapid preparation of RNA from a biological sample, particularly from the  
CC cytoplasm of eukaryotic cells, which is suitable for use in an  
CC amplification and detection assay. The methods are used for the analysis  
CC and detection of nucleic acids in biological samples. The methods are  
CC useful in the human medical and veterinary fields, for medical diagnoses  
CC and clinical monitoring of a patient's response to therapy where a disease  
CC or medical condition is associated with a particular type and/or level of  
CC mRNA present in the sample. The methods are also useful for detecting or  
CC quantifying fusion or chimeric RNA species, and for detecting a  
CC translocation as a marker for a given condition or disease, e.g.  
CC translocations associate with cancers, particularly forms of leukemia  
XX  
SQ Sequence 350 BP; 85 A; 92 C; 89 G; 84 T; 0 U; 0 Other;

Query Match 100.0%; Score 27; DB 3; Length 350;  
Best Local Similarity 66.7%; Pred. No. 3.8e-05;  
Matches 18; Conservative 9; Mismatches 0; Indels 0; Gaps 0;  
QY 1 UCUGACUUGAGCCUCAGGUCUGAGU 27  
Db :||||:||||:||||:||||:||||:  
225 TCTGACTTTGAGCCTCAGGGCTGAGT 251

Search completed: May 27, 2004, 10:20:10  
Job time : 166.387 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 27, 2004, 02:25:18 ; Search time 34.425 Seconds  
(without alignments)  
435.256 Million cell updates/sec

Title: US-09-121-239-23

Perfect score: 27  
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Scoring table: OLIGO NUC  
Gapop 60.0 , Gapext 60.0

Searched: 682709 seqs, 277475446 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

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Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	27	100.0	204	PCT-US93-06251-5	Sequence 5, Appli
2	27	100.0	257	US-08-152-621-1	Sequence 1, Appli
3	27	100.0	257	US-08-306-691B-36	Sequence 36, Appli
4	27	100.0	257	PCT-US92-05035-1	Sequence 1, Appli
5	27	100.0	266	US-08-152-621-4	Sequence 4, Appli
6	27	100.0	266	US-08-306-691B-37	Sequence 37, Appli
7	27	100.0	266	PCT-US92-05035-4	Sequence 4, Appli
8	27	100.0	1078	US-09-310-842-1	Sequence 1, Appli
9	27	100.0	3823	US-08-306-691B-35	Sequence 35, Appli
10	26	96.3	80	US-08-152-621-7	Sequence 7, Appli
11	26	96.3	80	US-08-306-691B-38	Sequence 38, Appli
12	26	96.3	80	PCT-US92-05035-7	Sequence 38, Appli
13	24	88.9	50	US-09-168-947-45	Sequence 45, Appli
14	22	81.5	22	US-08-013-419-1	Sequence 1, Appli
15	22	81.5	22	US-08-122-798B-10	Sequence 10, Appli
16	22	81.5	22	US-08-525-818-1	Sequence 1, Appli
17	22	81.5	22	US-09-028-184-1	Sequence 1, Appli
18	22	81.5	22	PCT-US94-00680-1	Sequence 1, Appli
19	22	81.5	22	PCT-US94-09963A-10	Sequence 10, Appli
20	17	63.0	56	US-07-940-652-19	Sequence 19, Appli
21	17	63.0	56	US-08-255-553-19	Sequence 19, Appli
22	16	59.3	2992	US-08-841-349-10	Sequence 10, Appli
23	16	59.3	2992	US-09-431-184A-10	Sequence 10, Appli
24	15	55.6	20	US-08-761-131-7	Sequence 7, Appli
25	15	55.6	21	US-07-784-222-2	Sequence 2, Appli
26	15	55.6	21	US-09-502-954-2	Sequence 2, Appli
27	15	55.6	40	US-08-761-131-1	Sequence 1, Appli

28	15	55.6	40	1	US-08-761-131-2	Sequence 2, Appli
29	15	55.6	818	4	US-09-599-360B-37	Sequence 37, Appli
30	15	55.6	822	4	US-09-621-976-1361	Sequence 1361, Ap
31	15	55.6	2214	4	US-09-489-847-113	Sequence 113, App
32	15	55.6	2227	4	US-09-489-847-130	Sequence 30, Appl
33	15	55.6	7052	4	US-09-526-193A-22	Sequence 22, Appl
34	14	51.9	426	4	US-09-621-976-18309	Sequence 18309, A
35	14	51.9	474	4	US-09-615-192A-264	Sequence 264, App
36	14	51.9	888	4	US-09-171-209-7	Sequence 7, Appli
37	14	51.9	973	4	US-09-599-360B-71	Sequence 71, Appl
38	14	51.9	1910	2	US-08-808-931-17	Sequence 17, Appl
39	14	51.9	1910	3	US-08-808-323-17	Sequence 17, Appl
40	14	51.9	1910	3	US-09-050-603A-17	Sequence 17, Appl
41	14	51.9	1910	3	US-09-102-420B-17	Sequence 17, Appl
42	14	51.9	1910	4	US-09-497-698-17	Sequence 17, Appl
43	14	51.9	2050	4	US-09-620-312D-761	Sequence 761, App
44	14	51.9	2150	2	US-08-318-837-1	Sequence 1, Appli
45	14	51.9	2606	2	US-08-808-931-26	Sequence 26, Appl

## ALIGNMENTS

RESULT 1  
PCT-US93-06251-5  
; Sequence 5, Application PC/TUS9306251  
; GENERAL INFORMATION:  
; APPLICANT: Wickstrom, Eric and Rife, Jason P.  
; TITLE OF INVENTION: Trivalent Synthesis of Oligonucleotides Containing  
; NUMBER OF SEQUENCES: 93  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER  
; STREET: 400 Garden City Plaza  
; CITY: Garden City  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 11530  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US93/06251  
; FILING DATE: 19930630  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Digiglio, Frank S.  
; REGISTRATION NUMBER: 31,346  
; REFERENCE/DOCKET NUMBER: 8586  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 516-742-4343  
; TELEFAX: 516-742-4366  
; TELEX: 230 901 SANS UR  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 204 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
PCT-US93-06251-5

Query Match 100.0%; Score 27; DB 5; Length 204;

Best Local Similarity 66.7%; Pred No. 1.2e-06;

Matches 18; Conservative 9; Mismatches 0; Indels 0; Gaps 0;

QY 1 UCUGACUUUGAGCCUCAGGUCUGAGU 27

Db 39 TCTGACTTTGAGCCTCAGGGTCTGAGT 65

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RESULT 2
US-08-152-621-1
; Sequence 1, Application US/08152621
; Patent No. 5652222
; GENERAL INFORMATION:
; APPLICANT: Calabretta, Bruno
; APPLICANT: Gewirtz, Alan M.
; TITLE OF INVENTION: Selective Inhibition of
; TITLE OF INVENTION: Leukemic Cell Proliferation by bcr-abl
; TITLE OF INVENTION: Antisense Oligonucleotides
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEIDEL, GONDA, LAVORGNA
; ADDRESSEE: & MONACO, P.C.
; STREET: 1800 Two Penn Center
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: U.S.A.
; ZIP: 19102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/152,621
; FILING DATE: No. 5652222ember 15, 1993
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/718,302
; FILING DATE: June 18, 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Monaco, Daniel A.
; REGISTRATION NUMBER: 30,480
; REFERENCE/DOCKET NUMBER: 6056-120 (CT.) 1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-8383
; TELEFAX: (215) 568-5549
; TELEX: No. 5652222e
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 Nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single stranded
; TOPOLOGY: linear
US-08-152-621-1
Query Match 100.0%; Score 27; DB 1; Length 257;
Best Local Similarity 66.7%; Pred. No. 1.2e-06;
Matches 18; Conservative 9; Mismatches 0; Indels 0; Gaps 0;

QY 1 UCUGACUUUGAGCCUCAGGUCUGAGU 27
Db 55 TCTGACTTTGAGCCTCAGGGTCTGAGT 81

RESULT 3
US-08-306-691B-36
; Sequence 36, Application US/08306691B
; Patent No. 5734039
; GENERAL INFORMATION:
; APPLICANT: Calabretta, Bruno
; APPLICANT: Skorski, Tomasz
; TITLE OF INVENTION: ANTISENSE
; TITLE OF INVENTION: OLIGONUCLEOTIDES TARGETING COOPERATING ONCOGENES
; NUMBER OF SEQUENCES: 55
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seidel, Gonda, Lavorigna & Monaco, P.C.
; STREET: Two Penn Center, Suite 1800
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: U.S.A.
; ZIP: 19102
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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/306,691B
; FILING DATE: September 15, 1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Monaco, Daniel A.
; REGISTRATION NUMBER: 30,480
; REFERENCE/DOCKET NUMBER: 8321-8
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-8383
; TELEFAX: (215) 568-5549
; TELEX: No. 5734039e
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-306-691B-36
Query Match 100.0%; Score 27; DB 1; Length 257;
Best Local Similarity 66.7%; Pred. No. 1.2e-06;
Matches 18; Conservative 9; Mismatches 0; Indels 0; Gaps 0;

QY 1 UCUGACUUUGAGCCUCAGGUCUGAGU 27
Db 55 TCTGACTTTGAGCCTCAGGGTCTGAGT 81

RESULT 4
PCT-US92-05035-1
; Sequence 1, Application PC/TUS9205035
; GENERAL INFORMATION:
; APPLICANT: Calabretta, Bruno
; APPLICANT: Gewirtz, Alan M.
; TITLE OF INVENTION: Selective Inhibition of
; TITLE OF INVENTION: Leukemic Cell Proliferation by bcr-abl
; TITLE OF INVENTION: Antisense Oligonucleotides
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Temple University - Of The Common-
; ADDRESSEE: wealth System of Higher Education
; STREET: 406 University Services Building
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: U.S.A.
; ZIP: 19122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/05035
; FILING DATE: 19920615
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/718,302
; FILING DATE: June 18, 1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/869,911
; FILING DATE: April 14, 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Monaco, Daniel A.
; REGISTRATION NUMBER: 30,480
```

; REFERENCE/DOCKET NUMBER: 6056-120 (CIP) 1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (215) 568-8383  
; TELEFAX: (215) 568-5549  
; TELEX: None  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 257 Nucleotides  
; TYPE: NUCLEIC ACID  
; STRANDEDNESS: single stranded  
; TOPOLOGY: linear  
PCT-US92-05035-1

Query Match 100.0%; Score 27; DB 5; Length 257;  
Best Local Similarity 66.7%; Pred. No. 1.2e-06;  
Matches 18; Conservative 9; Mismatches 0; Indels 0; Gaps 0;

QY 1 UCUGACUUUGAGCCUCACGGGUCUGAGU 27  
Db 55 TCTGACTTTGAGCCTCAGGGTCTGAGT 81

## RESULT 5

US-08-152-621-4  
; Sequence 4, Application US/08152621  
; Patent No. 5652222  
; GENERAL INFORMATION:  
; APPLICANT: Calabretta, Bruno  
; APPLICANT: Gewirtz, Alan M.  
; TITLE OF INVENTION: Selective Inhibition of  
; TITLE OF INVENTION: Leukemic Cell Proliferation by bcr-abl  
; TITLE OF INVENTION: Antisense Oligonucleotides  
; NUMBER OF SEQUENCES: 34  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SEIDEL, GONDA, LAVORGNA  
; ADDRESSEE: & MONACO, P.C.  
; STREET: 1800 Two Penn Center  
; CITY: Philadelphia  
; STATE: Pennsylvania  
; COUNTRY: U.S.A.  
; ZIP: 19102  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb  
; COMPUTER: IBM PS/2  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: WordPerfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/152,621  
; FILING DATE: No. 5652222ember 15, 1993  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/718,302  
; FILING DATE: June 18, 1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Monaco, Daniel A.  
; REGISTRATION NUMBER: 30,480  
; REFERENCE/DOCKET NUMBER: 6056-120 (CT.) 1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (215) 568-8383  
; TELEFAX: (215) 568-5549  
; TELEX: No. 5652222e  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 266 Nucleotides  
; TYPE: nucleic acid  
; STRANDEDNESS: single stranded  
; TOPOLOGY: linear  
US-08-152-621-4

Query Match 100.0%; Score 27; DB 1; Length 266;  
Best Local Similarity 66.7%; Pred. No. 1.2e-06;  
Matches 18; Conservative 9; Mismatches 0; Indels 0; Gaps 0;

QY 1 UCUGACUUUGAGCCUCACGGGUCUGAGU 27  
Db 64 TCTGACTTTGAGCCTCAGGGTCTGAGT 90

## RESULT 6

US-08-306-691B-37  
; Sequence 37, Application US/08306691B  
; Patent No. 5734039  
; GENERAL INFORMATION:  
; APPLICANT: Calabretta, Bruno  
; APPLICANT: Skorski, Tomasz  
; TITLE OF INVENTION: ANTISENSE  
; TITLE OF INVENTION: OLIGONUCLEOTIDES TARGETING COOPERATING ONCOGENES  
; NUMBER OF SEQUENCES: 55  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Seidel, Gonda, Lavorgna & Monaco, P.C.  
; STREET: Two Penn Center, Suite 1800  
; CITY: Philadelphia  
; STATE: Pennsylvania  
; COUNTRY: U.S.A.  
; ZIP: 19102  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb  
; COMPUTER: IBM PS/2  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: WordPerfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/306,691B  
; FILING DATE: September 15, 1994  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Monaco, Daniel A.  
; REGISTRATION NUMBER: 30,480  
; REFERENCE/DOCKET NUMBER: 8321-8  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (215) 568-8383  
; TELEFAX: (215) 568-5549  
; TELEX: No. 5734039e  
; INFORMATION FOR SEQ ID NO: 37:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 266 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-306-691B-37

Query Match 100.0%; Score 27; DB 1; Length 266;  
Best Local Similarity 66.7%; Pred. No. 1.2e-06;  
Matches 18; Conservative 9; Mismatches 0; Indels 0; Gaps 0;

QY 1 UCUGACUUUGAGCCUCACGGGUCUGAGU 27  
Db 64 TCTGACTTTGAGCCTCAGGGTCTGAGT 90

## RESULT 7

PCT-US92-05035-4  
; Sequence 4, Application PC/TUS9205035  
; GENERAL INFORMATION:  
; APPLICANT: Calabretta, Bruno  
; APPLICANT: Gewirtz, Alan M.  
; TITLE OF INVENTION: Selective Inhibition of  
; TITLE OF INVENTION: Leukemic Cell Proliferation by bcr-abl  
; TITLE OF INVENTION: Antisense Oligonucleotides  
; NUMBER OF SEQUENCES: 34  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Temple University - Of The Common-  
; ADDRESSEE: wealth System of Higher Education  
; STREET: 406 University Services Building

```
/ CITY: Philadelphia
/ STATE: Pennsylvania
/ COUNTRY: U.S.A.
/ ZIP: 19122
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb
/ OPERATING SYSTEM: MS-DOS
/ SOFTWARE: WordPerfect 5.1
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: PCT/US92/05035
/ FILING DATE: 19920615
/ CLASSIFICATION: 514
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 07/718,302
/ FILING DATE: June 18, 1991
/ APPLICATION NUMBER: 07/869,911
/ FILING DATE: April 14, 1991
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Monaco, Daniel A.
/ REGISTRATION NUMBER: 30,480
/ REFERENCE/DOCKET NUMBER: 6056-120 (CIP) 1
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (215) 568-8383
/ TELEFAX: (215) 568-5549
/ TELEX: None
/ INFORMATION FOR SEQ ID NO: 4:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 266 Nucleotides
/ TYPE: NUCLEIC ACID
/ STRANDEDNESS: single stranded
/ TOPOLOGY: linear
/ PCT-US92-05035-4

Query Match 100.0%; Score 27; DB 5; Length 266;
Best Local Similarity 66.7%; Pred. No. 1.2e-06;
Matches 18; Conservative 9; Mismatches 0; Indels 0; Gaps 0;

QY 1 UCUGACUUGAGCCUCAGGUCUGAGU 27
Db 64 TCTGACTTTTGAGCCTCAGGCTCTGAGT 90

RESULT 8
US-09-310-842-1
/ Sequence 1, Application US/09310842A
/ Patent No. 6451593
/ GENERAL INFORMATION:
/ APPLICANT: Wittig, Prof. Burghardt
/ APPLICANT: Junghans, Claas
/ TITLE OF INVENTION: Design Principle for Constructing Expression Constructs for Gene
/ FILE REFERENCE: XI 597/99
/ CURRENT APPLICATION NUMBER: US/09/310,842A
/ CURRENT FILING DATE: 1999-05-12
/ EARLIER APPLICATION NUMBER: DE 196 48 625.4
/ EARLIER FILING DATE: 1996-11-13
/ NUMBER OF SEQ ID NOS: 13
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 1
/ LENGTH: 1078
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ NAME/KEY: gene
/ LOCATION: (1)..(1078)
/ OTHER INFORMATION: bcr3=abl2; Oligo DNA Dumbbell
/ FEATURE:
/ NAME/KEY: misc.binding
/ LOCATION: (1)..(2)
/ OTHER INFORMATION: intramolecular binding site; the T-nucleotides at position 1 to
/ OTHER INFORMATION: 2 can be modified with amino or caroxy features
```

```
/ FEATURE:
/ NAME/KEY: misc.binding
/ LOCATION: (1077)..(1078)
/ OTHER INFORMATION: intramolecular binding site; the T-nucleotides at position 1077
/ OTHER INFORMATION: to 1078 can be modified with amino or caroxy features
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Strandness: both; nucleic
/ OTHER INFORMATION: acid (linear), hypothetical: No. 6451593 anti-sense: No
/ US-09-310-842-1

Query Match 100.0%; Score 27; DB 4; Length 1078;
Best Local Similarity 66.7%; Pred. No. 1.2e-06;
Matches 18; Conservative 9; Mismatches 0; Indels 0; Gaps 0;

QY 1 UCUGACUUGAGCCUCAGGUCUGAGU 27
Db 798 TCTGACTTTTGAGCCTCAGGCTCTGAGT 824

RESULT 9
US-08-306-691B-35
/ Sequence 35, Application US/08306691B
/ Patent No. 5734039
/ GENERAL INFORMATION:
/ APPLICANT: Calabretta, Bruno
/ APPLICANT: Skorski, Tomasz
/ TITLE OF INVENTION: ANTISENSE
/ TITLE OF INVENTION: OLIGONUCLEOTIDES TARGETING COOPERATING ONCOGENES
/ NUMBER OF SEQUENCES: 55
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Seidel, Gonda, Lavorgna & Monaco, P.C.
/ STREET: Two Penn Center, Suite 1800
/ CITY: Philadelphia
/ STATE: Pennsylvania
/ COUNTRY: U.S.A.
/ ZIP: 19102
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb
/ COMPUTER: IBM PS/2
/ OPERATING SYSTEM: MS-DOS
/ SOFTWARE: WordPerfect 5.1
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/306,691B
/ FILING DATE: September 15, 1994
/ CLASSIFICATION: 514
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER:
/ FILING DATE:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Monaco, Daniel A.
/ REGISTRATION NUMBER: 30,480
/ REFERENCE/DOCKET NUMBER: 8321-8
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (215) 568-8383
/ TELEFAX: (215) 568-5549
/ TELEX: No. 5734039e
/ INFORMATION FOR SEQ ID NO: 35:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 3623 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: double
/ TOPOLOGY: linear
/ US-08-306-691B-35

Query Match 100.0%; Score 27; DB 1; Length 3623;
Best Local Similarity 66.7%; Pred. No. 1.3e-06;
Matches 18; Conservative 9; Mismatches 0; Indels 0; Gaps 0;

QY 1 UCUGACUUGAGCCUCAGGUCUGAGU 27
Db 250 TCTGACTTTTGAGCCTCAGGCTCTGAGT 276
```

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RESULT 10
US-08-152-621-7
; Sequence 7, Application US/08152621
; Patent No. 5652222
; GENERAL INFORMATION:
; APPLICANT: Calabretta, Bruno
; APPLICANT: Gewirtz, Alan M.
; TITLE OF INVENTION: Selective Inhibition of
; TITLE OF INVENTION: Leukemic Cell Proliferation by bcr-abl
; TITLE OF INVENTION: Antisense Oligonucleotides
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEIDEL, GONDA, LAVORGNA
; ADDRESSEE: & MONACO, P.C.
; STREET: 1800 Two Penn Center
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: U.S.A.
; ZIP: 19102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/152,621
; FILING DATE: No. 5652222ember 15, 1993
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/718,302
; FILING DATE: June 18, 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Monaco, Daniel A.
; REGISTRATION NUMBER: 30,480
; REFERENCE/DOCKET NUMBER: 6056-120 (CT.) 1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-8383
; TELEFAX: (215) 568-5549
; TELEX: No. 5652222e
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 80 Nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single stranded
; TOPOLOGY: linear
US-08-152-621-7
; Query Match 96.3%; Score 26; DB 1; Length 80;
; Best Local Similarity 69.2%; Pred. No. 4.3e-06;
; Matches 18; Conservative 8; Mismatches 0; Indels 0; Gaps 0;

QY 1 UCUGACUUUGAGCCUCACGGGUCUGAG 26
; :||:||||:||||:||||:||||:||||:
Db 55 TCTGACTTTGAGCCTCAGGGTCTGAG 80

RESULT 11
US-08-306-691B-38
; Sequence 38, Application US/08306691B
; Patent No. 5734039
; GENERAL INFORMATION:
; APPLICANT: Calabretta, Bruno
; APPLICANT: Skorski, Tomasz
; TITLE OF INVENTION: ANTISENSE
; TITLE OF INVENTION: OLIGONUCLEOTIDES TARGETING COOPERATING ONCOGENES
; NUMBER OF SEQUENCES: 55
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seidel, Gonda, Lavorgna & Monaco, P.C.
; STREET: Two Penn Center, Suite 1800
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: U.S.A.
; ZIP: 19102
```

```
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/306,691B
; FILING DATE: September 15, 1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Monaco, Daniel A.
; REGISTRATION NUMBER: 30,480
; REFERENCE/DOCKET NUMBER: 8321-8
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-8383
; TELEFAX: (215) 568-5549
; TELEX: No. 5734039e
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 80 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-306-691B-38
; Query Match 96.3%; Score 26; DB 1; Length 80;
; Best Local Similarity 69.2%; Pred. No. 4.3e-06;
; Matches 18; Conservative 8; Mismatches 0; Indels 0; Gaps 0;

QY 1 UCUGACUUUGAGCCUCACGGGUCUGAG 26
; :||:||||:||||:||||:||||:||||:
Db 55 TCTGACTTTGAGCCTCAGGGTCTGAG 80

RESULT 12
PCT-US92-05035-7
; Sequence 7, Application PC/TUS9205035
; GENERAL INFORMATION:
; APPLICANT: Calabretta, Bruno
; APPLICANT: Gewirtz, Alan M.
; TITLE OF INVENTION: Selective Inhibition of
; TITLE OF INVENTION: Leukemic Cell Proliferation by bcr-abl
; TITLE OF INVENTION: Antisense Oligonucleotides
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Temple University - Of The Common-
; ADDRESSEE: wealth System of Higher Education
; STREET: 406 University Services Building
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: U.S.A.
; ZIP: 19122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/05035
; FILING DATE: 19920615
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/718,302
; FILING DATE: June 18, 1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/869,911
; FILING DATE: April 14, 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Monaco, Daniel A.
; REGISTRATION NUMBER: 30,480
```

```

; REFERENCE/DOCKET NUMBER: 6056-120 (CIP) 1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-8383
; TELEFAX: (215) 568-5549
; TELEX: None
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 80 Nucleotides
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single stranded
; TOPOLOGY: linear
PCT-US92-05035-7

Query Match          96.3%; Score 26; DB 5; Length 80;
Best Local Similarity 69.2%; Pred. No. 4.3e-06;
Matches 18; Conservative 8; Mismatches 0; Indels 0; Gaps 0;

QY 1 UCAGCUUUGAGCCUCAGGUCUGAG 26
   :|||||:|||||:|||||:|||||:
Db 55 TCTGACTTTGAGCCTCAGGCTCTGAG 80

RESULT 13
US-09-168-947-45/c
; Sequence 45, Application US/09168947
; Patent No. 6589734
; GENERAL INFORMATION:
; APPLICANT: KACIAN, DANIEL L.
; APPLICANT: FULTZ, TIMOTHY J.
; APPLICANT: MCDONOUGH, SHERROL H.
; TITLE OF INVENTION: DETECTION OF HIV
; FILE REFERENCE: 218/130
; CURRENT APPLICATION NUMBER: US/09/168,947
; EARLIER FILING DATE: 1998-10-08
; EARLIER FILING DATE: 1995-06-06
; EARLIER FILING DATE: 1995-06-06
; EARLIER FILING DATE: 07/550,837
; EARLIER FILING DATE: 1990-07-10
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 45
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthesized nucleic acid molecule
US-09-168-947-45

Query Match          88.9%; Score 24; DB 4; Length 50;
Best Local Similarity 70.8%; Pred. No. 5.7e-05;
Matches 17; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 4 GACUUUGAGCCUCAGGUCUGAGU 27
   |||||:|||||:|||||:|||||:
Db 50 GACTTTGAGCCTCAGGCTCTGAGT 27

RESULT 14
US-08-013-419-1/c
; Sequence 1, Application US/08013419
; Patent No. 5300635
; GENERAL INFORMATION:
; APPLICANT: Macfarlane, Donald E.
; TITLE OF INVENTION: Product and Process for Isolating RNA
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESS: Howson and Howson
; STREET: Spring House Corporate Center, P.O. Box 457
; CITY: Spring House
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19477
; COMPUTER READABLE FORM:

```

```

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/013,419
; FILING DATE: 19930201
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Bak, Mary E.
; REGISTRATION NUMBER: 31,215
; REFERENCE/DOCKET NUMBER: URIF1USA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-540-9206
; TELEFAX: 215-540-5818
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
US-08-013-419-1

Query Match          81.5%; Score 22; DB 1; Length 22;
Best Local Similarity 72.7%; Pred. No. 0.00077;
Matches 16; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 4 GACUUUGAGCCUCAGGUCUGA 25
   |||||:|||||:|||||:|||||:
Db 22 GACTTTGAGCCTCAGGCTCTGA 1

RESULT 15
US-08-122-795B-10/c
; Sequence 10, Application US/08122795B
; Patent No. 5635385
; GENERAL INFORMATION:
; APPLICANT: Lance H. Leopold
; APPLICANT: Scott K. Shore
; APPLICANT: Moolle V. R. Reddy
; APPLICANT: E. Premkumar Reddy
; TITLE OF INVENTION: MULTI-UNIT RIBOZYME
; TITLE OF INVENTION: INHIBITION OF ONCOGENE EXPRESSION
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seidel, Gonda, Lavorgna
; ADDRESS: & Monaco, P.C.
; STREET: Two Penn Center Plaza, Suite 1800
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: U.S.A.
; ZIP: 19102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/122,795B
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 122,795
; FILING DATE: 15 September 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Monaco, Daniel A.
; REGISTRATION NUMBER: 30,480
; REFERENCE/DOCKET NUMBER: 6056-192
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-8383
; TELEFAX: (215) 568-5549
; TELEX: No. 5635385e

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; INFORMATION FOR SEQ ID NO: 10:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 22 Nucleotides

; TYPE: nucleic acid

; STRANDEDNESS: single stranded

; TOPOLOGY: linear

; US-08-122-795B-10

Query Match 81.5%; Score 22; DB 1; Length 22;

Best Local Similarity 72.7%; Pred. NO. 0.00077;

Matches 16; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 4 GACUUGAGCCUCACGGUCUGA 25

Db 22 GACTTGTAGCCCTCAGGGTCTGA 1

Search completed: May 27, 2004, 12:08:03

Job time : 34.425 secs

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OM nucleic - nucleic search, using sw model

Run on: May 27, 2004, 14:58:36 ; Search time 156.938 Seconds  
(without alignments)  
782.607 Million cell updates/sec

Title: US-09-121-239-23

Perfect score: 27  
Sequence: 1 UCUGACUUUGAGCCUCAGGUCUGAGU 27

Scoring table: OLIGO\_NUC  
Gapop\_60.0 , Gapext 60.0

Searched: 2960401 seqs, 2274450654 residues

Word size : 0  
Total number of hits satisfying chosen parameters: 5920802

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published Applications\_NA.\*  
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2: /cgn2\_6/prodata/2/pubpna/PCT\_NEW\_PUB.seq:\*  
3: /cgn2\_6/prodata/2/pubpna/US06\_NEW\_PUB.seq:\*  
4: /cgn2\_6/prodata/2/pubpna/US06\_PUBCOMB.seq:\*  
5: /cgn2\_6/prodata/2/pubpna/US07\_NEW\_PUB.seq:\*  
6: /cgn2\_6/prodata/2/pubpna/PCTUS\_PUBCOMB.seq:\*  
7: /cgn2\_6/prodata/2/pubpna/US08\_NEW\_PUB.seq:\*  
8: /cgn2\_6/prodata/2/pubpna/US08\_PUBCOMB.seq:\*  
9: /cgn2\_6/prodata/2/pubpna/US09A\_PUBCOMB.seq:\*  
10: /cgn2\_6/prodata/2/pubpna/US09B\_PUBCOMB.seq:\*  
11: /cgn2\_6/prodata/2/pubpna/US09C\_PUBCOMB.seq:\*  
12: /cgn2\_6/prodata/2/pubpna/US09\_NEW\_PUB.seq:\*  
13: /cgn2\_6/prodata/2/pubpna/US10A\_PUBCOMB.seq:\*  
14: /cgn2\_6/prodata/2/pubpna/US10B\_PUBCOMB.seq:\*  
15: /cgn2\_6/prodata/2/pubpna/US10C\_PUBCOMB.seq:\*  
16: /cgn2\_6/prodata/2/pubpna/US10D\_PUBCOMB.seq:\*  
17: /cgn2\_6/prodata/2/pubpna/US10\_NEW\_PUB.seq:\*  
18: /cgn2\_6/prodata/2/pubpna/US60\_NEW\_PUB.seq:\*  
19: /cgn2\_6/prodata/2/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	27	100.0	1078	15	US-10-228-811-1
2	27	100.0	3393	15	US-10-263-480-1
3	27	100.0	3450	16	US-10-457-954-5
4	27	100.0	3840	15	US-10-204-041-3
5	27	100.0	5434	13	US-10-170-385-182
6	27	100.0	5527	9	US-09-880-107-3710
7	27	100.0	5744	16	US-10-439-703-5
8	27	100.0	84539	9	US-09-962-436-36
9	24	88.9	50	15	US-10-244-490-45
10	22	81.5	22	9	US-09-995-912-4
11	22	81.5	22	9	US-09-747-165-3
12	21	77.8	21	13	US-10-382-634-20
13	21	77.8	21	15	US-10-349-320-19
14	16	59.3	468	10	US-09-918-995-19841

C	15	16	59.3	639	13	US-10-027-632-163921	Sequence 163921,
	16	59.3	639	13	US-10-027-632-163922	Sequence 163922,	
C	17	16	59.3	639	16	US-10-027-632-163921	Sequence 163921,
C	18	16	59.3	639	16	US-10-027-632-163922	Sequence 163922,
C	19	16	59.3	118502	13	US-10-087-192-397	Sequence 397, App
C	20	15	55.6	21	15	US-10-236-880-2	Sequence 2, Appli
	21	15	55.6	403	10	US-09-918-995-24908	Sequence 24908, A
C	22	15	55.6	442	10	US-09-918-995-8048	Sequence 8048, Ap
	23	15	55.6	487	13	US-10-027-632-67648	Sequence 67648, A
	24	15	55.6	487	16	US-10-027-632-67648	Sequence 67648, A
	25	15	55.6	554	9	US-09-864-761-9446	Sequence 9446, Ap
	26	15	55.6	562	10	US-09-918-995-27376	Sequence 27376, A
C	27	15	55.6	566	15	US-10-029-386-5976	Sequence 5976, Ap
	28	15	55.6	598	13	US-10-027-632-15713	Sequence 15713, A
C	29	15	55.6	598	16	US-10-027-632-15713	Sequence 15713, A
	30	15	55.6	610	15	US-10-101-464A-186	Sequence 186, App
	31	15	55.6	637	13	US-10-027-632-210218	Sequence 210218,
	32	15	55.6	637	16	US-10-027-632-210218	Sequence 210218,
	33	15	55.6	649	13	US-10-027-632-37896	Sequence 37896, A
	34	15	55.6	649	16	US-10-027-632-37896	Sequence 37896, A
	35	15	55.6	681	13	US-10-027-632-152558	Sequence 152558,
	36	15	55.6	681	13	US-10-027-632-152559	Sequence 152559,
	37	15	55.6	681	16	US-10-027-632-152558	Sequence 152558,
	38	15	55.6	681	16	US-10-027-632-152559	Sequence 152559,
	39	15	55.6	818	13	US-10-315-664-37	Sequence 37, Appl
	40	15	55.6	820	15	US-10-181-611-1	Sequence 1, Appli
	41	15	55.6	825	13	US-10-424-599-93197	Sequence 93197, A
	42	15	55.6	950	9	US-09-978-295A-220	Sequence 220, App
	43	15	55.6	950	9	US-09-978-697-220	Sequence 220, App
	44	15	55.6	950	9	US-09-978-192A-220	Sequence 220, App
	45	15	55.6	950	9	US-09-999-832A-220	Sequence 220, App

ALIGNMENTS

RESULT 1  
US-10-228-811-1  
; Sequence 1, Application US/10228811  
; Publication No. US20030054392A1  
; GENERAL INFORMATION:  
; APPLICANT: Wittig, Prof. Burghardt  
; APPLICANT: Jungmans, Claas  
; TITLE OF INVENTION: Design Principle for Constructing Expression Constructs for Gene  
; TITLE OF INVENTION: Therapy  
; FILE REFERENCE: XI 597/99  
; CURRENT APPLICATION NUMBER: US/10/228,811  
; PRIOR FILING DATE: 2002-08-27  
; PRIOR APPLICATION NUMBER: DE 196 48 625.4  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 1078  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; NAME/KEY: gene  
; LOCATION: (1)..(1078)  
; OTHER INFORMATION: bcr3=abl2; Oligo DNA Dumbbell  
; FEATURE:  
; NAME/KEY: misc binding  
; LOCATION: (1)..(2)  
; OTHER INFORMATION: intramolecular binding site; the T-nucleotides at position 1 to  
; OTHER INFORMATION: 2 can be modified with amino or caroxy features  
; FEATURE:  
; NAME/KEY: misc binding  
; LOCATION: (1077)..(1078)  
; OTHER INFORMATION: intramolecular binding site; the T-nucleotides at position 1077  
; OTHER INFORMATION: to 1078 can be modified with amino or caroxy features  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Strandness: both; nucleic  
; OTHER INFORMATION: acid (linear), hypothetical: No. US20030054392A1 anti-sense: No

US-10-228-811-1

Query Match 100.0%; Score 27; DB 15; Length 1078;  
Best Local Similarity 66.7%; Pred. No. 5.7e-06;  
Matches 18; Conservative 9; Mismatches 0; Indels 0; Gaps 0;

QY 1 UCUGACUUUGAGCCUCAGGUCUGAGU 27  
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Db 798 TCTGACTTTGAGCCTCAGGCTCTGAGT 824

RESULT 2

US-10-263-480-1  
; Sequence 1, Application US/10263480  
; Publication No. US20030170851A1  
; GENERAL INFORMATION:  
; APPLICANT: No. US20030170851A1artis AG  
; TITLE OF INVENTION: Organic Compounds  
; FILE REFERENCE: Case 4-32175PI/PROV  
; CURRENT APPLICATION NUMBER: US/10/263,480  
; CURRENT FILING DATE: 2002-10-03  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 1  
; LENGTH: 3393  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(3393)  
US-10-263-480-1

Query Match 100.0%; Score 27; DB 15; Length 3393;  
Best Local Similarity 66.7%; Pred. No. 5e-06;  
Matches 18; Conservative 9; Mismatches 0; Indels 0; Gaps 0;

QY 1 UCUGACUUUGAGCCUCAGGUCUGAGU 27  
:|||||:|||||:|||||:|||||:|||||:  
Db 103 TCTGACTTTGAGCCTCAGGCTCTGAGT 129

RESULT 3

US-10-457-954-5  
; Sequence 5, Application US/10457954  
; Publication No. US20040005623A1  
; GENERAL INFORMATION:  
; APPLICANT: Longley, B. Jack  
; TITLE OF INVENTION: Method of determining tumor sensitivities to therapeutic drugs  
; FILE REFERENCE: 960296.98890  
; CURRENT APPLICATION NUMBER: US/10/457,954  
; CURRENT FILING DATE: 2003-06-10  
; PRIOR APPLICATION NUMBER: 60/387,370  
; PRIOR FILING DATE: 2002-06-10  
; PRIOR APPLICATION NUMBER: 60/387,406  
; PRIOR FILING DATE: 2002-06-10  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 5  
; LENGTH: 3450  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(3447)  
; FEATURE:  
; NAME/KEY: misc\_structure  
; LOCATION: (730)..(765)  
; OTHER INFORMATION: encode amino acids 244-255 for forming the sides of the enzymatic  
; OTHER INFORMATION: pocket  
; FEATURE:  
; NAME/KEY: misc\_structure  
; LOCATION: (931)..(1077)  
; OTHER INFORMATION: encode amino acids 311-359 for forming the sides of the enzymatic

OTHER INFORMATION: pocket

FEATURE:  
NAME/KEY: misc\_structure  
LOCATION: (1141)..(1206)  
OTHER INFORMATION: encode amino acids 381-402 for forming the enzymatic pocket's  
OTHER INFORMATION: activation loop  
US-10-457-954-5

Query Match 100.0%; Score 27; DB 16; Length 3450;  
Best Local Similarity 66.7%; Pred. No. 5e-06;  
Matches 18; Conservative 9; Mismatches 0; Indels 0; Gaps 0;

QY 1 UCUGACUUUGAGCCUCAGGUCUGAGU 27  
:|||||:|||||:|||||:|||||:|||||:  
Db 160 TCTGACTTTGAGCCTCAGGCTCTGAGT 186

RESULT 4

US-10-204-041-3  
; Sequence 3, Application US/10204041  
; Publication No. US20030176443A1  
; GENERAL INFORMATION:  
; APPLICANT: STEIN-GERLACH, MATTHIAS  
; APPLICANT: SALASSIDIS, KONSTADINOS  
; APPLICANT: BACHER, GERALD  
; APPLICANT: MULLER, STEFAN  
; TITLE OF INVENTION: Pyridylpyrimidine Derivatives as Effective Compounds Against Prior  
; FILE REFERENCE: AXM-007.1P US  
; CURRENT APPLICATION NUMBER: US/10/204,041  
; CURRENT FILING DATE: 2002-08-16  
; PRIOR APPLICATION NUMBER: EP 01111858.5  
; PRIOR FILING DATE: 2001-05-16  
; PRIOR APPLICATION NUMBER: PCT/EP02/05420  
; PRIOR FILING DATE: 2002-05-16  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 3  
; LENGTH: 3840  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-204-041-3

Query Match 100.0%; Score 27; DB 15; Length 3840;  
Best Local Similarity 66.7%; Pred. No. 4.9e-06;  
Matches 18; Conservative 9; Mismatches 0; Indels 0; Gaps 0;

QY 1 UCUGACUUUGAGCCUCAGGUCUGAGU 27  
:|||||:|||||:|||||:|||||:|||||:  
Db 467 TCTGACTTTGAGCCTCAGGCTCTGAGT 493

RESULT 5

US-10-170-385-182  
; Sequence 182, Application US/10170385  
; Publication No. US20030203372A1  
; GENERAL INFORMATION:  
; APPLICANT: Ward, Neil Raymond  
; APPLICANT: Mundy, Christopher Robert  
; APPLICANT: Kan, On  
; APPLICANT: Harris, Robert Alan  
; APPLICANT: White, Jonathan  
; APPLICANT: Binley, Katie Mary  
; APPLICANT: Rayner, William Nigel  
; APPLICANT: Naylor, Stuart  
; APPLICANT: Kingeman, Susan Mary  
; APPLICANT: Krige, David  
; TITLE OF INVENTION: ANALYSIS METHOD  
; FILE REFERENCE: 532682000100  
; CURRENT APPLICATION NUMBER: US/10/170,385  
; CURRENT FILING DATE: 2002-06-12  
; PRIOR APPLICATION NUMBER: PCT/GB02/01662  
; PRIOR FILING DATE: 2002-04-08

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; PRIOR APPLICATION NUMBER: PCT/GB01/05458
; PRIOR FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 549
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 182
; LENGTH: 5434
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-170-385-182

Query Match
Best Local Similarity 100.0%; Score 27; DB 13; Length 5434;
Matches 18; Conservative 9; Mismatches 0; Indels 0; Gaps 0;

QY 1 UCUGACUUUGAGCCUCAGGUCUGAGU 27
Db 157 TCTGACTTTGAGCCTCAGGGTCTGAGT 183

RESULT 6
US-09-880-107-3710
; Sequence 3710, Application US/09880107
; Patent No. US20020142981A1
; GENERAL INFORMATION:
; APPLICANT: Horne, Darci T.
; APPLICANT: Vockley, Joseph G.
; APPLICANT: Scherf, Uwe
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
; FILE REFERENCE: 44921-5028-WO
; CURRENT APPLICATION NUMBER: US/09/880,107
; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: US 60/211,379
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: US 60/237,054
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 3950
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3710
; LENGTH: 5527
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20020142981A1 X16416
US-09-880-107-3710

Query Match
Best Local Similarity 100.0%; Score 27; DB 9; Length 5527;
Matches 18; Conservative 9; Mismatches 0; Indels 0; Gaps 0;

QY 1 UCUGACUUUGAGCCUCAGGUCUGAGU 27
Db 250 TCTGACTTTGAGCCTCAGGGTCTGAGT 276

RESULT 7
US-10-439-703-5
; Sequence 5, Application US/10439703
; Publication No. US20040018527A1
; GENERAL INFORMATION:
; APPLICANT: Chang, Jenny
; APPLICANT: O'Connell, Peter
; TITLE OF INVENTION: Differential Patterns of Gene Expression that Predict for Docetax
; FILE REFERENCE: Chemosensitivity and Chemoresistance
; FILE REFERENCE: HO-P2482US1/10205813
; CURRENT APPLICATION NUMBER: US/10/439,703
; CURRENT FILING DATE: 2003-05-16
; PRIOR APPLICATION NUMBER: US 60/381,141
; PRIOR FILING DATE: 2002-05-17
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 5744
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; TYPE: DNA
; ORGANISM: Human
US-10-439-703-5

Query Match
Best Local Similarity 100.0%; Score 27; DB 16; Length 5744;
Matches 18; Conservative 9; Mismatches 0; Indels 0; Gaps 0;

QY 1 UCUGACUUUGAGCCUCAGGUCUGAGU 27
Db 467 TCTGACTTTGAGCCTCAGGGTCTGAGT 493

RESULT 8
US-09-962-436-36
; Sequence 36, Application US/09962436
; Patent No. US20020081301A1
; GENERAL INFORMATION:
; APPLICANT: Soppet, Daniel
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatur
; FILE REFERENCE: 689290-75
; CURRENT APPLICATION NUMBER: US/09/962,436
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/60/235,082
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/234,924
; PRIOR FILING DATE: 2000-09-25
; NUMBER OF SEQ ID NOS: 568
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 36
; LENGTH: 84539
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-962-436-36

Query Match
Best Local Similarity 100.0%; Score 27; DB 9; Length 84539;
Matches 18; Conservative 9; Mismatches 0; Indels 0; Gaps 0;

QY 1 UCUGACUUUGAGCCUCAGGUCUGAGU 27
Db 49912 TCTGACTTTGAGCCTCAGGGTCTGAGT 49938

RESULT 9
US-10-244-490-45/c
; Sequence 45, Application US/10244490
; Publication No. US20030152916A1
; GENERAL INFORMATION:
; APPLICANT: KACIAN, DANIEL L.
; APPLICANT: FULTZ, TIMOTHY J.
; APPLICANT: MCDONOUGH, SHERROL H.
; TITLE OF INVENTION: DETECTION OF HIV
; FILE REFERENCE: 218/130
; CURRENT APPLICATION NUMBER: US/10/244,490
; CURRENT FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: US/09/168,947
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 08/469,067
; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: 07/550,837
; PRIOR FILING DATE: 1990-07-10
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 45
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthesized nucleic acid molecule
US-10-244-490-45
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Query Match 88.9%; Score 24; DB 15; Length 50;  
Best Local Similarity 70.8%; Pred. No. 0.00042;  
Matches 17; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 4 GACUUGAGCCUCAGGUCUGAGU 27  
Db 50 GACTTTGAGCCTCAGGCTCTGAGT 27  
||||:||||:||||:||||:||||:

## RESULT 10

US-09-995-912-4/c  
; Sequence 4, Application US/09995912  
; Patent No. US20020137076A1  
; GENERAL INFORMATION:  
; APPLICANT: Shultz, John W.  
; APPLICANT: Lewis, Martin K.  
; APPLICANT: Andrews, Christine  
; TITLE OF INVENTION: RNA Polymers and Uses Thereof  
; FILE REFERENCE: PRMG-06684  
; CURRENT APPLICATION NUMBER: US/09/995,912  
; CURRENT FILING DATE: 2001-11-28  
; PRIOR APPLICATION NUMBER: 60/253,451  
; PRIOR FILING DATE: 2000-11-28  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: Patentin version 3.1  
; SEQ ID NO 4  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic  
US-09-995-912-4

Query Match 81.5%; Score 22; DB 9; Length 22;  
Best Local Similarity 72.7%; Pred. No. 0.0065;  
Matches 16; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 4 GACUUGAGCCUCAGGUCUGA 25  
Db 22 GACTTTGAGCCTCAGGCTCTGA 1  
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## RESULT 11

US-09-747-165-3/c  
; Sequence 3, Application US/09747165  
; Publication No. US20020192645A1  
; GENERAL INFORMATION:  
; APPLICANT: TSENG, RICHARD W.  
; APPLICANT: SAMOSZUK, MICHAEL K.  
; TITLE OF INVENTION: BCR-ABL GENE REARRANGMENT ASSAY METHOD  
; FILE REFERENCE: 034827/0302  
; CURRENT APPLICATION NUMBER: US/09/747,165  
; CURRENT FILING DATE: 2001-09-24  
; PRIOR APPLICATION NUMBER: 60/173,050  
; PRIOR FILING DATE: 1999-12-24  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 3  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Primer  
US-09-747-165-3

Query Match 81.5%; Score 22; DB 9; Length 22;  
Best Local Similarity 72.7%; Pred. No. 0.0065;  
Matches 16; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 4 GACUUGAGCCUCAGGUCUGA 25  
Db 22 GACTTTGAGCCTCAGGCTCTGA 1  
||||:||||:||||:||||:||||:

## RESULT 12

US-10-382-634-20/c  
; Sequence 20, Application US/10382634  
; Publication No. US20040038921A1  
; GENERAL INFORMATION:  
; APPLICANT: Kreutzer, Roalnd  
; TITLE OF INVENTION: Composition and Method for Inhibiting Expression of a Target Gene  
; FILE REFERENCE: 20200/2062  
; CURRENT APPLICATION NUMBER: US/10/382,634  
; CURRENT FILING DATE: 2003-03-07  
; PRIOR APPLICATION NUMBER: DE 101 55 280.7  
; PRIOR FILING DATE: 2001-10-26  
; PRIOR APPLICATION NUMBER: DE 101 58 411.3  
; PRIOR FILING DATE: 2001-11-29  
; PRIOR APPLICATION NUMBER: DE 101 60 151.4  
; PRIOR FILING DATE: 2001-12-07  
; PRIOR APPLICATION NUMBER: DE 102 30 996.5  
; PRIOR FILING DATE: 2002-07-09  
; PRIOR APPLICATION NUMBER: PCT/EP02/00152  
; PRIOR FILING DATE: 2002-01-09  
; PRIOR APPLICATION NUMBER: PCT/EP02/00151  
; PRIOR FILING DATE: 2002-01-09  
; PRIOR APPLICATION NUMBER: PCT/EP02/11971  
; PRIOR FILING DATE: 2002-10-25  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: Patentin version 3.2  
; SEQ ID NO 20  
; LENGTH: 21  
; TYPE: DNA  
; ORGANISM: artificial sequence  
; FEATURE:  
; OTHER INFORMATION: PRIMER  
US-10-382-634-20

Query Match 77.8%; Score 21; DB 13; Length 21;  
Best Local Similarity 71.4%; Pred. No. 0.024;  
Matches 15; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 5 ACUUUGAGCCUCAGGUCUGA 25  
Db 21 ACTTTGAGCCTCAGGCTCTGA 1  
||||:||||:||||:||||:||||:

## RESULT 13

US-10-349-320-19/c  
; Sequence 19, Application US/10349320  
; Publication No. US20030190654A1  
; GENERAL INFORMATION:  
; APPLICANT: Heidenreich, Olaf  
; TITLE OF INVENTION: DOUBLE-STRANDED RNA (dsRNA) AND METHOD OF USE  
; FILE REFERENCE: 20200/2112  
; CURRENT APPLICATION NUMBER: US/10/349,320  
; CURRENT FILING DATE: 2003-01-22  
; PRIOR APPLICATION NUMBER: DE 102 02 419.7  
; PRIOR FILING DATE: 2002-01-22  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: Patentin version 3.1  
; SEQ ID NO 19  
; LENGTH: 21  
; TYPE: DNA  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: primer  
US-10-349-320-19

Query Match 77.8%; Score 21; DB 15; Length 21;  
Best Local Similarity 71.4%; Pred. No. 0.024;  
Matches 15; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 5 ACUUUGAGCCUCAGGUCUGA 25  
Db 21 ACTTTGAGCCTCAGGCTCTGA 1  
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RESULT 14  
 US-09-918-995-19841  
 ; Sequence 19841, Application US/0918995  
 ; Publication No. US20030073623A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Hyseq, Inc.  
 ; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED  
 ; FILE REFERENCE: 20411-756  
 ; CURRENT APPLICATION NUMBER: US/09/918,995  
 ; PRIOR FILING DATE: 2001-07-30  
 ; PRIOR APPLICATION NUMBER: US/09/235,076  
 ; PRIOR FILING DATE: 1999-01-20  
 ; NUMBER OF SEQ ID NOS: 38054  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 19841  
 ; LENGTH: 468  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: misc feature  
 ; LOCATION: (1)-(468)  
 ; OTHER INFORMATION: n = A,T,C or G  
 US-09-918-995-19841

Query Match 59.3%; Score 16; DB 10; Length 468;  
 Best Local Similarity 68.8%; Pred. No. 12;  
 Matches 11; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 3 UCACUUGAGCCUCAG 18  
 Db 316 TGACTTGAGCCTCAG 331

RESULT 15  
 US-10-027-632-163921/c  
 ; Sequence 163921, Application US/10027632  
 ; Publication No. US20020198371A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Wang, David G.  
 ; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
 ; FILE REFERENCE: 108827.129  
 ; CURRENT APPLICATION NUMBER: US/10/027,632  
 ; PRIOR FILING DATE: 2002-04-30  
 ; PRIOR APPLICATION NUMBER: US 60/218,006  
 ; PRIOR FILING DATE: 2000-07-12  
 ; PRIOR APPLICATION NUMBER: US 60/198,676  
 ; PRIOR FILING DATE: 2000-04-20  
 ; PRIOR APPLICATION NUMBER: US 60/193,483  
 ; PRIOR FILING DATE: 2000-03-29  
 ; PRIOR APPLICATION NUMBER: US 60/185,218  
 ; PRIOR FILING DATE: 2000-02-24  
 ; PRIOR APPLICATION NUMBER: US 60/167,363  
 ; PRIOR FILING DATE: 1999-11-23  
 ; PRIOR APPLICATION NUMBER: US 60/156,358  
 ; PRIOR FILING DATE: 1999-09-28  
 ; PRIOR APPLICATION NUMBER: US 60/146,002  
 ; PRIOR FILING DATE: 1999-08-09  
 ; NUMBER OF SEQ ID NOS: 325720  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 163921  
 ; LENGTH: 639  
 ; TYPE: DNA  
 ; ORGANISM: Human  
 US-10-027-632-163921

Query Match 59.3%; Score 16; DB 13; Length 639;  
 Best Local Similarity 75.0%; Pred. No. 12;  
 Matches 12; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 9 UCAGCCUCAGGUCUG 24  
 Db 537 TGAGCCTCAGGCTCG 522  
 Search completed: May 27, 2004, 18:33:23  
 Job time : 156.938 secs

**THIS PAGE BLANK (USPTO)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 26, 2004, 22:44:40 ; Search time 1400.96 Seconds  
(without alignments)  
575.518 Million cell updates/sec

Title: US-09-121-239-23

Perfect score: 27  
Sequence: 1 UCUGACUUAGCCUCAGGUCUGAGU 27

Scoring table: OLIGO\_NUC  
Gapop\_60.0 , Gapext 60.0

Searched: 27513289 seqs, 14931090276 residues

Word size : 0

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

EST:\*

1: em\_estba:\*

2: em\_esthum:\*

3: em\_estin:\*

4: em\_estnu:\*

5: em\_estov:\*

6: em\_estpl:\*

7: em\_estro:\*

8: em\_htc:\*

9: gb\_est1:\*

10: gb\_est2:\*

11: gb\_htc:\*

12: gb\_est3:\*

13: gb\_est4:\*

14: gb\_est5:\*

15: em\_estfun:\*

16: em\_estom:\*

17: em\_gss\_hum:\*

18: em\_gss\_inv:\*

19: em\_gss\_pin:\*

20: em\_gss\_vit:\*

21: em\_gss\_fun:\*

22: em\_gss\_mam:\*

23: em\_gss\_mus:\*

24: em\_gss\_pro:\*

25: em\_gss\_rod:\*

26: em\_gss\_phg:\*

27: em\_gss\_vrl:\*

28: gb\_gss1:\*

29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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1	27	100.0	157	10	AW386252	CM4-PT001
2	27	100.0	404	14	H81820	Y688e09.r1
3	27	100.0	421	12	BM832613	K-EST0107
4	27	100.0	781	13	BM832613	BM832613 K-EST0107

C	5	19	70.4	181	10	BB927145	BB927145 RC4-CN000
	6	19	70.4	875	10	BF973844	BF973844 602411947
	7	18	66.7	686	12	BF332596	BF332596 602980736
	8	18	66.7	851	10	BF531871	BF531871 602072805
	9	17	63.0	539	29	CE192426	CE192426 tigr-g88-
	10	17	63.0	542	29	CE536813	CE536813 tigr-g88-
	11	17	63.0	714	29	CE270642	CE270642 tigr-g88-
C	11	17	63.0	778	29	CNS072JP	AL426299 clone BA0
	12	17	63.0	780	12	BG206281	BG206281 RST35726
	13	17	63.0	788	28	BZ865134	BZ865134 CH240_235
	14	17	63.0	824	12	BI246488	BI246488 602958537
	15	17	63.0	874	29	AG160977	AG160977 Pan trogl
C	16	17	59.3	129	14	CF250190	CF250190 e8a009.F0
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	18	16	59.3	192	10	BB522588	BB522588 M26H12STM
	19	16	59.3	206	12	BI740150	BI740150 EST0195 C
	20	16	59.3	210	9	AV222166	AV222166 AV222166
	21	16	59.3	238	10	BE525308	BE525308 M61C9STM
	22	16	59.3	240	10	BE525590	BE525590 M62821STM
	23	16	59.3	241	10	BE525578	BE525578 M62G17STM
	24	16	59.3	241	10	BE530312	BE530312 M77021STM
	25	16	59.3	243	10	BB439432	BB439432 BB439432
	26	16	59.3	244	10	BE525566	BE525566 M62G13STM
	27	16	59.3	247	10	BE525452	BE525452 M62C03STM
	28	16	59.3	250	10	BE523949	BE523949 M76E15STM
	29	16	59.3	259	10	BE528577	BE528577 M72103STM
	30	16	59.3	265	9	AV140149	AV140149 AV140149
	31	16	59.3	284	9	AV364585	AV364585 AV364585
	32	16	59.3	290	10	BB441430	BB441430 BB441430
	33	16	59.3	297	10	BE522587	BE522587 M26H11STM
	34	16	59.3	300	10	BB248616	BB248616 BB248616
	35	16	59.3	305	10	BB731714	BB731714 BB731714
	36	16	59.3	306	10	BE524258	BE524258 M47G9STM
	37	16	59.3	312	13	BY415640	BY415640 BY415640
	38	16	59.3	321	10	BB043130	BB043130 BB043130
	39	16	59.3	321	10	BE523402	BE523402 M36E5STM
	40	16	59.3	324	9	AI482323	AI482323 V955F02.X
C	41	16	59.3	330	10	BE525407	BE525407 M9C15STM A
	42	16	59.3	331	10	BE525064	BE525064 M5B2STM
	43	16	59.3	341	9	AJ444339	AJ444339 AJ444339
C	44	16	59.3	341	10	BE525372	BE525372 M8G5STM A
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#### ALIGNMENTS

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AW386252  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

AW386252 157 bp mRNA linear EST 04-FEB-2000  
CM4-PT0015-071299-057-d10 PT0015 Homo sapiens cDNA, mRNA sequence.  
AW386252  
AW386252.1 GI:6890976  
EST.  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 157)  
HCGP <http://www.ludwig.org.br/ORESTES>.  
The FAPESP/LICR Human Cancer Genome Project  
Unpublished (1999)  
Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: [asimpson@ludwig.org.br](mailto:asimpson@ludwig.org.br)  
This sequence was derived from the FAPESP/LICR Human Cancer Genome  
Project. This entry can be seen in the following URL.  
(<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CM4&t2=CM4-PT0015-071299-057-d10&t3=1999-12-07&t4=1>)

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High quality sequence stop: 157.

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ORIGIN
    Query Match      100.0%; Score 27; DB 10; Length 157;
    Best Local Similarity 66.7%; Pred. No. 6.8e-05;
    Matches 18; Conservative 9; Mismatches 0; Indels 0; Gaps 0;

QY 1 UCUGACUUUGAGCCUCACGGGUCUGAGU 27
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Db 91 TCTGACTTTGAGCCTCAGGGTCTGAGT 117

RESULT 2
H81820/c
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DEFINITION
    Ys68e09.r1 Soares retina N2b4HR Homo sapiens cDNA clone
    IMAGE:219976 5' similar to gb:M14752 PROTO-ONCOGENE
    TYROSINE-PROTEIN KINASE ABL (HUMAN); mRNA sequence.
H81820
H81820.1 GI:1059909
Homo sapiens
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 404)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevasakis,E., Waterston,R., Williamson,A., Wohlmann,P. and
Wilson,R.
The WashU-Merck EST Project
Unpublished (1995)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence stops: 382
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1427 Std Error: 0.00
Seq primer: M13RP1
High quality sequence stop: 382.
Location/Qualifiers
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        /db_xref="taxon:9606"
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        /sex="male"
        /tissue_type="retina"
        /dev_stage="55 year old"
        /lab_host="DH10B (ampicillin resistant)"

FEATURES
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            /mol_type="mRNA"
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/clone_lib="Soares retina N2b4HR"
/note="Organ: eye; Vector: p7T3D (Pharmacia) with a
modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5',
TGTTACCAATCTGAAGTGGAGCGCGCGCTTTTCTTTTCTTTT 3'],
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified p7T3 vector
(Pharmacia). The retinas were obtained from a 55 year old
Caucasian and total cellular poly(A)+ RNA was extracted 6
hrs after their removal. The retina RNA was kindly
provided by Roderick R. McInnes M.D. Ph.D. from the
University of Toronto. Library constructed by Bento
Soares and M.Fatima Bonaldo. "
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Query Match 100.0%; Score 27; DB 13; Length 781;  
Best Local Similarity 66.7%; Pred. No. 0.00011;  
Matches 18; Conservative 9; Mismatches 0; Indels 0; Caps 0;

Query Match	100.0%;	Score 27;
Best Local Similarity	66.7%;	Pred. No.

Query Match 100.0%; Score 27; DB 13; Length 781;  
Best Local Similarity 66.7%; Pred. No. 0.00011;  
Matches 18; Conservative 9; Mismatches 0; Indels 0; Caps 0;

Qy	1	UCUGACUUUGAGGCCUCAGGGUCUGAGU	27
		: : : : : : : : : : : : : : : :	
D <sub>b</sub>	81	TCTGACCTTTGAGCCCTCAGGGTCTGAGT	55

RESULT 5  
BE927145/c

RESULT 5	181 bp	mRNA	linear	EST 02-OCT-2000
BE927145/c				
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DEFINITION	BC4-CN00077-010900-015-e08 CN0007			
ACCESSION	BE927145			
VERSION	BE927145.1			
KEYWORDS	GI:10453130			
SOURCE	EST.			
ORGANISM	Homo sapiens (human)			
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	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			

DE92/143:1 01:10433313  
EST.  
Homo sapiens (human)  
KEYWORDS  
SOURCE

SEQUENCE KEYWORDS	SEQUENCE SOURCE	ORGANISM	REFERENCE AUTHORS	TITLE
00227145.1	00227145.1	Homo sapiens (human)	Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F. F., Goldman, G.H., Carvalho, A. F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.	Shotgun sequencing of the human transcriptome with ORF expressed
		Homo sapiens		
		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
		Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
		1 (bases 1 to 181)		

<b>TITLE</b>	Simpson, A.U. Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
<b>JOURNAL</b>	Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
<b>MEDLINE</b>	20202663
<b>PIRME</b>	10737800

MEDLINE

MEDLINE  
20202663  
PUBMED  
10737800  
COMMENT  
Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
Brazil

Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: [asimpson@ludwig.org.br](mailto:asimpson@ludwig.org.br)  
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL  
(<http://www.ludwig.org.br/scripts/gethtml2.p?tbl=at2=RC4-CN0007-010>)  
Seq primer: puc 18 forward  
900-015-e08at3=2000-09-01&t4=1  
High quality sequence start: 57  
High quality sequence stop: 130.

900-015-eu8x8c3=2000-09-01&ts=1)  
Seq primer: puc 18 forward  
High quality sequence start: 57  
High quality sequence stop: 130.

## FEATURES

FEATURES	source
Location/Qualifiers	
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/mol_type="mRNA"	
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/note="Organ: colon normal; Vector: puc18; Site\_1: Sma1; Site\_2: Sma1; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 1996,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

**Query:** Ma

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Db	109	TGAGCCTCAGGCTCTGAGT	91	



Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.  
Average insert size 1.9 kb. Constructed by Life  
Technologies. Note: This is a NCI\_CGAP Library."

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ORIGIN
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Best Local Similarity 66.7%; Pred. No. 12;
Matches 12; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 6 CUUUGAGCCUCAGGUCU 23
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Db 570 CTTTGAGCCTCAGGCT 587

RESULT 9
LOCUS CE192426          539 bp DNA linear GSS 25-SEP-2003
DEFINITION tigr-gss-dog-17000371470877 Dog Library Canis familiaris genomic,
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ACCESSION CE192426 GI:35348079
VERSION GSS.
KEYWORDS Canis familiaris (dog)
SOURCE Canis familiaris
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE 1 (bases 1 to 539)
AUTHORS Kirkness,E.F., Bafna,V., Halpern,A.L., Levy,S., Remington,K.,
        Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and
        Venter,J.C.
The dog genome: survey sequencing and comparative analysis
Science 301 (5641), 1898-1903 (2003)
MEDLINE 22875432
PUBMED 14512627
COMMENT Contact: Kirkness EF
The Institute for Genomic Research
Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
Rockville, MD 20850, USA
Tel: 301-838-0200
Fax: 301-838-0208
Email: ekirknes@tigr.org
Class: shotgun.
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Db 346 AGCCTCAGGCTCGACT 362

RESULT 10
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ACCESSION CE536813 GI:36853594
VERSION GSS.
KEYWORDS Canis familiaris (dog)
SOURCE Canis familiaris
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE 1 (bases 1 to 542)
AUTHORS Kirkness,E.F., Bafna,V., Halpern,A.L., Levy,S., Remington,K.,
        Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and
        Venter,J.C.
The dog genome: survey sequencing and comparative analysis
Science 301 (5641), 1898-1903 (2003)
MEDLINE 22875432
PUBMED 14512627
COMMENT Contact: Kirkness EF
The Institute for Genomic Research
Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
Rockville, MD 20850, USA
Tel: 301-838-0200
Fax: 301-838-0208
Email: ekirknes@tigr.org
Class: shotgun.
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    peripheral blood"

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Matches 13; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 9 UGAGCCUCAGGUCUGA 25
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Db 49 TGAGCCTCAGGCTCTGA 65

RESULT 11
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DEFINITION tigr-gss-dog-1700033537646 Dog Library Canis familiaris genomic,
            genomic survey sequence.
ACCESSION CE270642 GI:36002203
VERSION GSS.
KEYWORDS Canis familiaris (dog)
SOURCE Canis familiaris
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE 1 (bases 1 to 714)
AUTHORS Kirkness,E.F., Bafna,V., Halpern,A.L., Levy,S., Remington,K.,
        Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and
        Venter,J.C.
The dog genome: survey sequencing and comparative analysis
Science 301 (5641), 1898-1903 (2003)
MEDLINE 22875432
PUBMED 14512627
COMMENT Contact: Kirkness EF
The Institute for Genomic Research
Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
Rockville, MD 20850, USA
Tel: 301-838-0200
Fax: 301-838-0208
Email: ekirknes@tigr.org
Class: shotgun.
Location/Qualifiers
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    /strain="Standard Poodle"
    /db_xref="taxon:9615"
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    peripheral blood"

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## peripheral blood"

## /evidence=not\_experimental

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Best Local Similarity 76.5%; Pred. No. 43;
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QY 9 UGAGCCUCAGGGUCUGA 25
   :|||||:|||||:|||||
Db 485 TGAGCTCAGGGTCTGA 469

RESULT 12
CNS072JP
LOCUS          778 bp DNA linear GSS 07-JUL-2001
DEFINITION    clone BA0AB012A05 of library BA0AB from strain CLIB 210 of
ACCESSION     Kluveromyces lactis, genomic survey sequence.
VERSION       AL426299
KEYWORDS      GSS.
SOURCE        Kluveromyces lactis
ORGANISM      Kluveromyces lactis
REFERENCE     1 (bases 1 to 778)
AUTHORS       Souciet,J.L., Aigle,M., Artiguenave,F., Blandin,G.,
              Bolotin-Fukuhara,M., Bon,E., Brottier,P., Casaregola,S.,
              de-Montigny,J., Dujon,B., Durrens,P., Lepingle,A., Llorente,B.,
              Maupertuy,A., Neuveglise,C., Ozier-Kalogeropoulos,O., Potier,S.,
              Saurin,W., Tekala,F., Toffano-Nioche,C., Wesolowski-Louvel,M.,
              Wincker,P. and Weissenbach,J.
              Genomic exploration of the hemiascomycetous yeasts: 1. A set of
              yeast species for molecular evolution studies
              FEBS Lett. 487 (1), 3-12 (2000)
JOURNAL       20584711
MEDLINE       11152876
PUBMED        11152876
REFERENCE     2 (bases 1 to 778)
AUTHORS       Bolotin-Fukuhara,M., Toffano-Nioche,C., Artiguenave,F.,
              Duchateau-Nguyen,G., Lemaire,M., Marmeisse,R., Montrocher,R.,
              Robert,C., Ternier,M., Wincker,P. and Wesolowski-Louvel,M.
              Genomic exploration of the hemiascomycetous yeasts: 11.
              Kluveromyces lactis
              FEBS Lett. 487 (1), 66-70 (2000)
JOURNAL       20584721
MEDLINE       11152886
PUBMED        11152886
REFERENCE     3 (bases 1 to 778)
AUTHORS       Direct Submission
TITLE         Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage,
              2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail :
              seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
JOURNAL       This GSS is part of a random genomic sequencing program of thirteen
              yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces
              exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii,
              Saccharomyces kluyveri, Kluveromyces thermotolerans, Kluveromyces
              lactis var. lactis, Kluveromyces marxianus var. marxianus, Pichia
              angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila,
              Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to
              5 kb were prepared and both extremities were sequenced. See
              keywords for description of this sequence and for the sequence of
              the other extremity of this insert.
FEATURES      Location/Qualifiers
               1..778
                /organism="Kluveromyces lactis"
                /mol_type="genomic DNA"
                /strain="CLIB 210"
                /variety="lactis"
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                /clone="BA0AB012A05"
                /clone_lib="BA0AB"
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                /notes="similar to Saccharomyces cerevisiae ORF YGR120c [
                SEC35 ; required for ER to golgi vesicle docking ]"
              misc_feature

ORIGIN
Query Match          63.0%; Score 17; DB 29; Length 714;
Best Local Similarity 76.5%; Pred. No. 43;
Matches 13; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 9 UGAGCCUCAGGGUCUGA 25
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Db 485 TGAGCTCAGGGTCTGA 469

RESULT 12
CNS072JP
LOCUS          778 bp DNA linear GSS 07-JUL-2001
DEFINITION    clone BA0AB012A05 of library BA0AB from strain CLIB 210 of
ACCESSION     Kluveromyces lactis, genomic survey sequence.
VERSION       AL426299
KEYWORDS      GSS.
SOURCE        Kluveromyces lactis
ORGANISM      Kluveromyces lactis
REFERENCE     1 (bases 1 to 778)
AUTHORS       Souciet,J.L., Aigle,M., Artiguenave,F., Blandin,G.,
              Bolotin-Fukuhara,M., Bon,E., Brottier,P., Casaregola,S.,
              de-Montigny,J., Dujon,B., Durrens,P., Lepingle,A., Llorente,B.,
              Maupertuy,A., Neuveglise,C., Ozier-Kalogeropoulos,O., Potier,S.,
              Saurin,W., Tekala,F., Toffano-Nioche,C., Wesolowski-Louvel,M.,
              Wincker,P. and Weissenbach,J.
              Genomic exploration of the hemiascomycetous yeasts: 1. A set of
              yeast species for molecular evolution studies
              FEBS Lett. 487 (1), 3-12 (2000)
JOURNAL       20584711
MEDLINE       11152876
PUBMED        11152876
REFERENCE     2 (bases 1 to 778)
AUTHORS       Bolotin-Fukuhara,M., Toffano-Nioche,C., Artiguenave,F.,
              Duchateau-Nguyen,G., Lemaire,M., Marmeisse,R., Montrocher,R.,
              Robert,C., Ternier,M., Wincker,P. and Wesolowski-Louvel,M.
              Genomic exploration of the hemiascomycetous yeasts: 11.
              Kluveromyces lactis
              FEBS Lett. 487 (1), 66-70 (2000)
JOURNAL       20584721
MEDLINE       11152886
PUBMED        11152886
REFERENCE     3 (bases 1 to 778)
AUTHORS       Direct Submission
TITLE         Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage,
              2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail :
              seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
JOURNAL       This GSS is part of a random genomic sequencing program of thirteen
              yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces
              exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii,
              Saccharomyces kluyveri, Kluveromyces thermotolerans, Kluveromyces
              lactis var. lactis, Kluveromyces marxianus var. marxianus, Pichia
              angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila,
              Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to
              5 kb were prepared and both extremities were sequenced. See
              keywords for description of this sequence and for the sequence of
              the other extremity of this insert.
FEATURES      Location/Qualifiers
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                /notes="similar to Saccharomyces cerevisiae ORF YGR120c [
                SEC35 ; required for ER to golgi vesicle docking ]"
              misc_feature

ORIGIN
Query Match          63.0%; Score 17; DB 29; Length 778;
Best Local Similarity 64.7%; Pred. No. 44;
Matches 11; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 UCUGACUCUUGAGCCUCA 17
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Db 518 TGTGACTTTGAGCCTCA 534

RESULT 13
BG206281
LOCUS          780 bp mRNA linear EST 21-APR-2001
DEFINITION    RST25726 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
ACCESSION     BG206281
VERSION       BG206281.1 GI:13727968
KEYWORDS      EST.
SOURCE        Homo sapiens (human)
ORGANISM      Homo sapiens
REFERENCE     1 (bases 1 to 780)
AUTHORS       Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R.,
              Cain,S., Leventhal,C., Thornton,M., Ramachandran,R.,
              Whittington,J., Lerner,L., Costanzo,D., McElligott,K., Booser,S.,
              Mays,R., Smith,E., Veloso,N., Klika,A., Hess,J., Cothren,K., Lo,K.,
              Offenbacher,J., Danzig,J. and Ducar,M.
              Creation of genome-wide protein expression libraries using random
              activation of gene expression
              Nat. Biotechnol. 19 (5), 440-445 (2001)
JOURNAL       21227151
MEDLINE       11329013
PUBMED        11329013
COMMENT       Contact: Scott J. Cain
              Athersys, Inc.
              3201 Carnegie Ave, Cleveland, OH 44115, USA
              Tel: 216 431 9900
              Fax: 216 361 9596
              Email: scain@athersys.com
              High quality sequence stop: 425.
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                /clone_lib="Athersys RAGE Library"
                /note="See 'Creation of Genome-wide Protein Expression
                Libraries using Random Activation of Gene Expression',
                Nature Biotechnology, in press. Note that even though the
                cell type indicated is HT1080, since a random activation
                method was used, these sequence tags are not necessarily
                expressed in HT1080 under normal circumstances."

ORIGIN
Query Match          63.0%; Score 17; DB 12; Length 780;
Best Local Similarity 76.5%; Pred. No. 44;
Matches 13; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 9 UGAGCCUCAGGGUCUGA 25
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Db 60 TGAGCTCAGGGTCTGA 76

RESULT 14
BZ865134
LOCUS          788 bp DNA linear GSS 18-MAR-2003
DEFINITION    CH240_235M8.TJ CHORI-240 Bos taurus genomic clone CH240_235M8,
              genomic survey sequence.
ACCESSION     BZ865134
VERSION       BZ865134.1 GI:29092539
KEYWORDS      GSS.

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SOURCE      Bos taurus (cow)
ORGANISM    Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
            Bovidae; Bovinae; Bos.
REFERENCE   1 (bases 1 to 788)
AUTHORS    Zhao,S., Shetty,J., Shatsman,S., Tsengaye,G., Geer,K.,
            Shvartsbeyn,A., Gebregorgis,E., Chen,D., Riggs,F., de Jong,P.,
            Crawford,A.M. and McEwan,J.C.
TITLE      Bovine BAC End Sequences from Library CHORI-240
JOURNAL    Unpublished (2003)
COMMENT    Contact: Shaying Zhao
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850, USA
            Tel: 301 838 0200
            Fax: 301 838 0208
            Email: szhao@igr.org
            Clones are derived from the bovine BAC library CHORI-240
            (http://www.chori.org/bacpac/bovine240.htm). For BAC library
            availability, please contact Pieter de Jong (pdejong@mail.cho.org).
            Clones may be purchased from BACPAC Resources
            (http://www.chori.org/bacpac/ordering/information.htm). This work
            was undertaken as part of the International Bovine BAC-Mapping
            Consortium (IBBMC) by AgResearch Ltd., New Zealand and The
            Institute of Genomic Research (TIGR), USA.
            Plate: 235 row: M column: 8
            Seq primer: SP6
            Class: BAC ends.

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                     /sex="Male"
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                     /clone_lib="CHORI-240"
                     /note="Vector: pTARBAC1.3; Site 1: MboI; Site 2: MboI;
                     Hereford bull L1 Domino 99375; CHORI-240 Bovine BAC
                     library (Male) produced by Pieter de Jong"

ORIGIN
Query Match      63.0%; Score 17; DB 28; Length 788;
Best Local Similarity 64.7%; Pred. No. 44;
Matches 11; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY      7 UUUGAGCCUCUAGGGUCU 23
Db      ::::::::::::::::::::

RESULT 15
BI246488
LOCUS     602958537F1 NCI_CGAP_Li9 Mus musculus cDNA clone IMAGE:5124201 5',
DEFINITION mRNA sequence.
ACCESSION BI246488
VERSION   BI246488.1 GI:14790501
KEYWORDS  EST.
SOURCE    Mus musculus (house mouse)
ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 824)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgabbs-r@mail.nih.gov
            Tissue Procurement: Jeffrey E. Green, M.D.
            cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Inyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11303 row: j column: 10
High quality sequence stop: 714.
Location/Qualifiers
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                     /clone="IMAGE:5124201"
                     /lab_host="DH10B (T1 phage-resistant)"
                     /clone_lib="NCI CGAP Li9"
                     /note="Organ: liver; Vector: pCMV-SPORT6; Site 1: NotI;
                     Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
                     Average insert size 1.9 kb. Constructed by Life
                     Technologies. Note: this is a NCI_CGAP Library."

ORIGIN
Query Match      63.0%; Score 17; DB 12; Length 824;
Best Local Similarity 70.6%; Pred. No. 45;
Matches 12; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY      6 CUUUGAGCCUCUAGGGUC 22
Db      ::::::::::::::::::::

Search completed: May 27, 2004, 11:30:40
Job time : 1401.96 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 27, 2004, 02:16:55 ; Search time 689.325 Seconds  
(without alignments)  
1634.815 Million cell updates/sec

Title: US-09-121-239-27

Perfect score: 26

Sequence: 1 CACTCAGCCACTGGATTAAAGCAGAG 26

Scoring table: OLIGO\_NUC

Gapop\_60.0 , Gapext 60.0

Searched: 3470272 seqs, 21671516995 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

GenEmbl.\*

1: gb\_ba.\*

2: gb\_htg.\*

3: gb\_in.\*

4: gb\_om.\*

5: gb\_ov.\*

6: gb\_pat.\*

7: gb\_ph.\*

8: gb\_pl.\*

9: gb\_pr.\*

10: gb\_ro.\*

11: gb\_sy.\*

12: gb\_un.\*

13: gb\_vi.\*

14: gb\_vl.\*

15: em\_ba.\*

16: em\_fun.\*

17: em\_hum.\*

18: em\_in.\*

19: em\_mu.\*

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21: em\_or.\*

22: em\_ov.\*

23: em\_pat.\*

24: em\_ph.\*

25: em\_pl.\*

26: em\_ro.\*

27: em\_sts.\*

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29: em\_vi.\*

30: em\_htg\_hum.\*

31: em\_htg\_inv.\*

32: em\_htg\_other.\*

33: em\_htg\_mus.\*

34: em\_htg\_pln.\*

35: em\_htg\_rod.\*

36: em\_htg\_man.\*

37: em\_htg\_vrt.\*

38: em\_sy.\*

39: em\_htgo\_hum.\*

40: em\_htgo\_mus.\*

41: em\_htgo\_other.\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

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C 2	26	100.0	52	6	A93226	A93226 Sequence 49
C 3	26	100.0	53	6	A93224	A93224 Sequence 47
C 4	26	100.0	54	6	A93225	A93225 Sequence 48
C 5	26	100.0	55	6	A93227	A93227 Sequence 50
C 6	26	100.0	56	6	A93228	A93228 Sequence 51
C 7	26	100.0	56	6	I12446	I12446 Sequence 16
C 8	26	100.0	56	6	I14508	I14508 Sequence 16
C 9	26	100.0	57	6	A93229	A93229 Sequence 52
C 10	26	100.0	58	6	A93230	A93230 Sequence 53
C 11	26	100.0	59	6	A93231	A93231 Sequence 54
C 12	26	100.0	90	9	HUMBCRAL	M25947 Human chron
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C 15	26	100.0	205	6	I02402	I02402 Sequence 1
C 16	26	100.0	250	9	AF321981	AF321981 Homo sapi
C 17	26	100.0	266	6	I58636	I58636 Sequence 4
C 18	26	100.0	266	6	I96200	I96200 Sequence 37
C 19	26	100.0	305	9	AF192533	AF192533 Homo sapi
C 20	26	100.0	350	6	BD222546	BD222546 Methods f
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C 23	26	100.0	561	9	HUMMK562B	M13095 Human myelo
C 24	26	100.0	679	9	HUMABLB	M30832 Human bcr/a
C 25	26	100.0	854	9	HUMABLD	M30829 Human bcr/a
C 26	26	100.0	997	9	HS131466	AJ131466 Homo sapi
C 27	26	100.0	1078	6	A92081	A92081 Sequence 5
C 28	26	100.0	1078	6	AR230688	AR230688 Sequence
C 29	26	100.0	1157	6	BD177069	BD177069 Standard
C 30	26	100.0	2255	6	E00984	E00984 Probe detec
C 31	26	100.0	2255	6	I04527	I04527 Sequence 1
C 32	26	100.0	2811	6	AX780333	AX780333 Sequence
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C 35	26	100.0	4739	6	AX331144	AX331144 Sequence
C 36	26	100.0	4739	9	HSBCRR	X02596 Human mRNA
C 37	26	100.0	5000	9	HUMBCRE	L02935 Human major
C 38	26	100.0	90591	2	AC025139	AC025139 Homo sapi
C 39	26	100.0	111249	9	AP000343	AP000343 Homo sapi
C 40	26	100.0	152141	9	HSU07000	U07000 Human break
C 41	26	100.0	155461	9	AC114966	AC114966 Homo sapi
C 42	26	100.0	158231	2	AC093306	AC093306 Homo sapi
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LOCUS	BD222549					
DEFINITION	BD222549					
ACCESSION	BD222549					
VERSION	BD222549.1	GI:33032319				
KEYWORDS	JP 2002521037-A/27					
SOURCE		synthetic construct				
ORGANISM		artificial sequences.				
REFERENCE	1	(bases 1 to 26)				
AUTHORS		Harvey, R.C. and Eastman, P.S.				
TITLE		Methods for detecting and measuring spliced nucleic acids				
JOURNAL		Patent: JP 2002521037-A 27 16-JUL-2002;				
		GEN PROBE INC				

```

COMMENT
OS Artificial Sequence
PN JP 2002521037-A/27
PD 16-JUL-2002
PR 23-JUL-1999 JP 20005611364
PR 23-JUL-1998 US 09/121239
PI RICHARD C HARVEY, PAUL S EASTMAN
CC C12Q1/68, C12N15/09, C12N15/00
CC Description of Artificial Sequence: Probe for bcr b3 FH key
FT source 1..26
FT Location/Qualifiers
FT /organism='Artificial Sequence'.

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Db 1 CACTGAGCCACTGGATTAAAGCAGAG 26
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DEFINITION Sequence 49 from Patent WO9746672.
ACCESSION A93226
VERSION A93226.1 GI:6741611
KEYWORDS
SOURCE
ORGANISM
unidentified
unclassified.
REFERENCE 1 (bases 1 to 52)
AUTHORS
Szakiel, G. and Haas, R.
TITLE
ANTISENSE NUCLEIC ACIDS AND HAMMERHEAD RIBOZYMES
JOURNAL
Patent: WO 9746672-A 49 11-DEC-1997;
DEUTSCHES KREBSFORSCH (DE); SZAKIEL GEORG (DE)
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RESULT 3
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LOCUS
DEFINITION Sequence 47 from Patent WO9746672.
ACCESSION A93224
VERSION A93224.1 GI:6741609
KEYWORDS
SOURCE
ORGANISM
unidentified
unclassified.
REFERENCE 1 (bases 1 to 53)
AUTHORS
Szakiel, G. and Haas, R.
TITLE
ANTISENSE NUCLEIC ACIDS AND HAMMERHEAD RIBOZYMES
JOURNAL
Patent: WO 9746672-A 47 11-DEC-1997;
DEUTSCHES KREBSFORSCH (DE); SZAKIEL GEORG (DE)
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Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CACTGAGCCACTGGATTAAAGCAGAG 26
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Db 43 CACTGAGCCACTGGATTAAAGCAGAG 18
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RESULT 4
A93225/c
LOCUS
DEFINITION Sequence 48 from Patent WO9746672.
ACCESSION A93225
VERSION A93225.1 GI:6741610
KEYWORDS
SOURCE
ORGANISM
unidentified
unclassified.
REFERENCE 1 (bases 1 to 54)
AUTHORS
Szakiel, G. and Haas, R.
TITLE
ANTISENSE NUCLEIC ACIDS AND HAMMERHEAD RIBOZYMES
JOURNAL
Patent: WO 9746672-A 48 11-DEC-1997;
DEUTSCHES KREBSFORSCH (DE); SZAKIEL GEORG (DE)
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ORIGIN
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Best Local Similarity 100.0%; Pred. No. 3.1e-05;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CACTGAGCCACTGGATTAAAGCAGAG 26
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Db 43 CACTGAGCCACTGGATTAAAGCAGAG 18
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RESULT 5
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LOCUS
DEFINITION Sequence 50 from Patent WO9746672.
ACCESSION A93227
VERSION A93227.1 GI:6741612
KEYWORDS
SOURCE
ORGANISM
unidentified
unclassified.
REFERENCE 1 (bases 1 to 55)
AUTHORS
Szakiel, G. and Haas, R.
TITLE
ANTISENSE NUCLEIC ACIDS AND HAMMERHEAD RIBOZYMES
JOURNAL
Patent: WO 9746672-A 50 11-DEC-1997;
DEUTSCHES KREBSFORSCH (DE); SZAKIEL GEORG (DE)
FEATURES
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Best Local Similarity 100.0%; Pred. No. 3.1e-05;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CACTGAGCCACTGGATTAAAGCAGAG 26
|||||
Db 43 CACTGAGCCACTGGATTAAAGCAGAG 18
|||||

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QY 1 CACTCAGCCACTGGATTAAAGCAGAG 26
  |||
Db 43 CACTCAGCCACTGGATTAAAGCAGAG 18

RESULT 6
LOCUS A93228 56 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 51 from Patent WO9746672.
ACCESSION A93228
VERSION A93228.1 GI:6741613
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 56)
AUTHORS Sczakiel,G. and Haas,R.
TITLE ANTISENSE NUCLEIC ACIDS AND HAMMERHEAD RIBOZYMES
JOURNAL Patent: WO 9746672-A 51 11-DEC-1997;
DEUTSCHES KREBSFORSCH (DE); SCZAKIEL GEORG (DE)
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QY 1 CACTCAGCCACTGGATTAAAGCAGAG 26
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Db 43 CACTCAGCCACTGGATTAAAGCAGAG 18

RESULT 7
LOCUS I12446 56 bp DNA linear PAT 26-JUL-1995
DEFINITION Sequence 16 from patent US 5424413.
ACCESSION I12446
VERSION I12446.1 GI:909830
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 56)
AUTHORS Hogan,J.J., Arnold,L.J. Jr., Nelson,N.C. and Bezverkov,R.
TITLE Branched nucleic acid probes
JOURNAL Patent: US 5424413-A 16 13-JUN-1995;
DEUTSCHES KREBSFORSCH (DE); SCZAKIEL GEORG (DE)
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Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CACTCAGCCACTGGATTAAAGCAGAG 26
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Db 10 CACTCAGCCACTGGATTAAAGCAGAG 35

RESULT 8
LOCUS I14508 56 bp DNA linear PAT 26-SRP-1995
DEFINITION Sequence 16 from patent US 5451503.
ACCESSION I14508
VERSION I14508.1 GI:996991
KEYWORDS
SOURCE Unknown.

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ORGANISM Unknown.
REFERENCE 1 (bases 1 to 56)
AUTHORS Hogan,J.J., Arnold,L.J. Jr., Nelson,N.C. and Bezverkov,R.
TITLE Method for use of branched nucleic acid probes
JOURNAL Patent: US 5451503-A 16 19-SEP-1995;
DEUTSCHES KREBSFORSCH (DE); SCZAKIEL GEORG (DE)
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DEFINITION Sequence 52 from Patent WO9746672.
ACCESSION A93229
VERSION A93229.1 GI:6741614
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 57)
AUTHORS Sczakiel,G. and Haas,R.
TITLE ANTISENSE NUCLEIC ACIDS AND HAMMERHEAD RIBOZYMES
JOURNAL Patent: WO 9746672-A 52 11-DEC-1997;
DEUTSCHES KREBSFORSCH (DE); SCZAKIEL GEORG (DE)
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QY 1 CACTCAGCCACTGGATTAAAGCAGAG 26
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Db 43 CACTCAGCCACTGGATTAAAGCAGAG 18

RESULT 10
LOCUS A93230 58 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 53 from Patent WO9746672.
ACCESSION A93230
VERSION A93230.1 GI:6741615
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 58)
AUTHORS Sczakiel,G. and Haas,R.
TITLE ANTISENSE NUCLEIC ACIDS AND HAMMERHEAD RIBOZYMES
JOURNAL Patent: WO 9746672-A 53 11-DEC-1997;
DEUTSCHES KREBSFORSCH (DE); SCZAKIEL GEORG (DE)
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Db 43 CACTGAGCCACTGGATTAAAGCAGAG 18

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LOCUS A93231
DEFINITION Sequence 54 from Patent WO9746672.
ACCESSION A93231
VERSION A93231.1 GI:6741616
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 59)
AUTHORS Sczakiel,G. and Haas,R.
TITLE ANTISENSE NUCLEIC ACIDS AND HAMMERHEAD RIBOZYMES
JOURNAL Patent: WO 9746672-A 54 11-DEC-1997;
DEUTSCHES KREBSFORSCH (DE); SCZAKIEL GEORG (DE)
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Db 43 CACTGAGCCACTGGATTAAAGCAGAG 18

RESULT 12
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DEFINITION Human chronic myelocytic leukemia c-abl oncogene breakpoint cluster
ACCESSION M25947
VERSION M25947.1 GI:179381
KEYWORDS breakpoint cluster region; c-abl oncogene; chronic myelocytic leukemia.
SEGMENT 1 of 3
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 90)
AUTHORS De Klein,A., Hermans,A., Bootsma,D., Grosveld,G., Heisterkamp,N., Stam,K. and Groffen,J.
TITLE The role of the Philadelphia translocation in chronic myelocytic leukemia
JOURNAL Ann. Clin. Res. 18 (5-6), 278-283 (1986)
MEDLINE 87183193
PUBMED 3471171
COMMENT Original source text: Human fibroblast cell line K562, cDNA to mRNA, clone pV1-3.
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RESULT 14
LOCUS S72478
DEFINITION BCR...ABL {b3/a3 junction, translocation breakpoint} [human, Japanese CML patient 1 and ALL patient 2, peripheral blood, mononuclear cells, mRNA Mutant, 3 genes, 140 nt].
ACCESSION S72478
VERSION S72478.1 GI:786452
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 140)
AUTHORS Iwata,S., Mizutani,S., Nakazawa,S. and Yata,J.
TITLE Heterogeneity of the breakpoint in the ABL gene in cases with BCR/ABL transcript lacking ABL exon a2
JOURNAL Leukemia 8 (10), 1696-1702 (1994)
MEDLINE 95019811
PUBMED 7934165
ORIGIN

Query Match      100.0%; Score 26; DB 6; Length 102;
Best Local Similarity 100.0%; Pred. No. 3e-05;
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RESULT 15
LOCUS S72478
DEFINITION BCR...ABL {b3/a3 junction, translocation breakpoint} [human, Japanese CML patient 1 and ALL patient 2, peripheral blood, mononuclear cells, mRNA Mutant, 3 genes, 140 nt].
ACCESSION S72478
VERSION S72478.1 GI:786452
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 140)
AUTHORS Iwata,S., Mizutani,S., Nakazawa,S. and Yata,J.
TITLE Heterogeneity of the breakpoint in the ABL gene in cases with BCR/ABL transcript lacking ABL exon a2
JOURNAL Leukemia 8 (10), 1696-1702 (1994)
MEDLINE 95019811
PUBMED 7934165
ORIGIN

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REMARK GenBank staff at the National Library of Medicine created this entry [NCBI G152818] from the original journal article.

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RESULT 15

102402  
LOCUS 102402 205 bp ss-DNA linear PAT 21-MAY-1993  
DEFINITION Sequence 1 from Patent US 4874853.  
ACCESSION 102402  
VERSION 102402.1 GI:270541  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 205)  
AUTHORS Rossi, J.J.  
TITLE Synthetic oligonucleotides useful in diagnosis of chronic  
myelogenous leukemia  
JOURNAL Patent: US 4874853-A 1 17-OCT-1989;  
City of Hope; Duarte, CA  
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ORIGIN

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Db 76 CACTAGCCACTGGATTAAAGCAGAG 101

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Job time : 690.325 secs

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GenCore version 5.1.6  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	26	100.0	26	3	Aaz60866 Oligonucleotide used to detect bcr b3-abl fusion transcripts.
C 2	26	100.0	52	2	Aav01788 Antisense
C 3	26	100.0	53	2	Aav01789 Antisense
C 4	26	100.0	54	2	Aav01790 Antisense
C 5	26	100.0	55	2	Aav01791 Antisense
C 6	26	100.0	56	2	Aaq46950 Branched
C 7	26	100.0	56	2	Aav01792 Antisense
C 8	26	100.0	57	2	Aav01793 Antisense
C 9	26	100.0	58	2	Aav01794 Antisense
C 10	26	100.0	59	2	Aav01795 Antisense
C 11	26	100.0	102	3	Aaz55997 Structure
C 12	26	100.0	140	6	Abs73168 DNA encod
C 13	26	100.0	200	2	Aat88785 Leukaemic
C 14	26	100.0	205	1	Aan91666 Bcr-abl f
C 15	26	100.0	250	6	Abs73175 Human tra
C 16	26	100.0	266	2	Aaq34628 Human bcr
C 17	26	100.0	266	2	Aav20459 Human bcr
C 18	26	100.0	305	6	Abs73174 DNA encod
C 19	26	100.0	350	3	Aaz60863 Region eu
C 20	26	100.0	468	6	Abs73171 Human tra
C 21	26	100.0	504	5	Aas85023 DNA encod
C 22	26	100.0	504	8	Ach38242 Human end
C 23	26	100.0	561	6	Abs73169 Human tra

24	26	100.0	679	6	ABs73172	DNA encod
C 25	26	100.0	766	5	ABv29306	Human pro
C 26	26	100.0	766	5	ABv23449	Human pro
27	26	100.0	854	6	ABs73170	DNA encod
28	26	100.0	997	6	ABs73173	DNA encod
29	26	100.0	1097	2	Aat91764	Chimeric
30	26	100.0	1157	9	Aac64640	Hepatitis
31	26	100.0	1212	5	Aas85028	DNA encod
32	26	100.0	2255	1	AAN60228	Sequence
33	26	100.0	4725	5	AAS76375	DNA encod
34	26	100.0	4739	6	ABL63316	Breast ca
35	26	100.0	4739	7	ACC00031	Human Bcr
C 36	26	100.0	4756	5	AAS85030	DNA encod
37	26	100.0	4775	5	AAS76377	DNA encod
38	26	100.0	152141	7	ACA64961	Human BCR
C 39	25	96.2	40	3	AAA86914	Native bcr
C 40	25	96.2	41	3	AAA86915	bcr/abl t
41	25	96.2	59	1	AAN97243	BCR/ABL t
42	25	96.2	59	1	AAN97244	ABL target
43	25	96.2	59	2	AQ55681	N. gonorr
44	25	96.2	59	2	AQ55680	N. gonorr
45	25	96.2	59	2	AAZ09295	Chronic m

ALIGNMENTS

RESULT 1  
AAZ60866  
ID AAZ60866 standard; RNA; 26 BP.  
XX AC AAZ60866;  
XX DT 16-MAY-2000 (first entry).  
XX DE Oligonucleotide used to detect bcr b3-abl fusion transcripts.  
XX KW Fusion transcript; translocation; bcr b3 region; abl gene;  
KW amplification assay; detection assay; medical diagnosis;  
KW clinical monitoring; chimeric RNA; fusion RNA; condition marker;  
KW disease marker; cancer; leukemia; ss.  
XX OS Synthetic.  
XX PN WO200005418-A1.  
XX PD 03-FEB-2000.  
XX PF 23-JUL-1999; 99WO-US016832.  
XX PR 23-JUL-1999; 98US-00121239.  
XX PA (GENP-) GEN-PROBE INC.  
XX PI Harvey RC, Eastman PS;  
XX DR WPI; 2000-182730/16.  
XX PT Novel methods for preparing RNA from biological samples, used for the  
XX detection and measurement of nucleic acids and fusion nucleic acids.  
XX PS Claim 19; Page 44; 49pp; English.  
XX CC Oligonucleotides AAZ60840-62 and AAZ60865-66 are used in the method of  
CC the invention to detect fusion transcripts produced from a translocation  
CC between the bcr b3 region and the abl gene. The specification describes a  
CC method for detecting a fusion nucleic acid (particularly chimeric mRNA  
CC species), in a biological sample. The method comprises contacting a  
CC sample of fusion nucleic acid with primers, amplifying the hybridized  
CC fusion nucleic acid, and detecting the target hybrid. The method is used  
CC for the simple and rapid preparation of RNA from a biological sample,  
CC particularly from the cytoplasm of eukaryotic cells, which is suitable  
CC for use in an amplification and detection assay. The methods are used for

CC the analysis and detection of nucleic acids in biological samples. The  
 CC methods are useful in the human medical and veterinary fields, for  
 CC medical diagnoses and clinical monitoring of a patient's response to  
 CC therapy where a disease or medical condition is associated with a  
 CC particular type and/or level of mRNA present in the sample. The methods  
 CC are also useful for detecting or quantifying fusion or chimeric RNA  
 CC species, and for detecting a translocation as a marker for a given  
 CC condition or disease, e.g. translocations associate with cancers,  
 CC particularly forms of leukemia  
 XX  
 SQ Sequence 26 BP; 8 A; 7 C; 6 G; 5 T; 0 U; 0 Other;

Query Match 100.0%; Score 26; DB 3; Length 26;  
 Best Local Similarity 100.0%; Pred. No. 4.3e-05;  
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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## RESULT 2

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 ID AAV01788 standard; RNA; 52 BP.

XX  
 AC AAV01788;

DT 04-JUN-1998 (first entry)

DE Antisense RNA sequence of the specification.

XX Antisense; inhibitor; gene expression; chromosomal translocation;  
 KW translocation point; pharmaceutical composition;  
 KW chronic myelogenous leukaemia; acute lymphoblastic leukaemia;  
 KW acute myelogenous leukaemia; Non-Hodgkin lymphoma; treatment; ss.

XX Synthetic.

XX WO9746672-A2.

XX 11-DEC-1997.

XX 05-JUN-1997; 97WO-EP002923.

XX 05-JUN-1996; 96EP-00109034.

XX (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.

XX PI Sczakiel G, Haas R, Kronenwett R;

XX WPI; 1998-042181/04.

XX Nucleic acid molecule containing chromosomal translocation point - useful  
 FT to treat chromosomal translocation disorders, e.g. chronic myelogenous  
 PT leukaemia.

XX Claim 6; Page 37; 49pp; English.

XX AAV01779-804 represent antisense RNA sequences. For long chain antisense  
 CC RNA, the association rate with their target RNA in vitro correlates with  
 CC their effectiveness in vivo. Antisense molecules are potent inhibitors of  
 CC gene expression and viral functions. The antisense molecules AAV01779-804  
 CC exemplify novel nucleic acid molecules of the invention. These nucleic  
 CC acid molecules contain portions complementary to a first and second  
 CC chromosomal DNA sequence. The nucleic acid molecule forms at least part  
 CC of a chromosomal translocation resulting in a fusion gene containing the  
 CC translocation point. The DNA sequence, as well as vectors and host cells  
 CC containing it are useful in pharmaceutical compositions for treating  
 CC disorders based on chromosomal translocations, preferably for chronic  
 CC myelogenous leukaemia. The pharmaceutical composition may also be used to  
 CC treat acute lymphoblastic leukaemias, acute myelogenous leukaemias and  
 CC Non-Hodgkin lymphomas

SQ Sequence 52 BP; 12 A; 10 C; 16 G; 0 T; 14 U; 0 Other;  
 Query Match 100.0%; Score 26; DB 2; Length 52;  
 Best Local Similarity 100.0%; Pred. No. 4.4e-05;  
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CACTAGCCACTGGATTAAAGCAGAG 26  
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## RESULT 3

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 ID AAV01789 standard; RNA; 53 BP.

XX  
 AC AAV01789;

DT 04-JUN-1998 (first entry)

DE Antisense RNA sequence of the specification.

XX Antisense; inhibitor; gene expression; chromosomal translocation;  
 KW translocation point; pharmaceutical composition;  
 KW chronic myelogenous leukaemia; acute lymphoblastic leukaemia;  
 KW acute myelogenous leukaemia; Non-Hodgkin lymphoma; treatment; ss.

XX Synthetic.

XX WO9746672-A2.

XX 11-DEC-1997.

XX 05-JUN-1997; 97WO-EP002923.

XX 05-JUN-1996; 96EP-00109034.

XX (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.

XX PI Sczakiel G, Haas R, Kronenwett R;

XX WPI; 1998-042181/04.

XX Nucleic acid molecule containing chromosomal translocation point - useful  
 FT to treat chromosomal translocation disorders, e.g. chronic myelogenous  
 PT leukaemia.

XX Claim 6; Page 37; 49pp; English.

XX AAV01779-804 represent antisense RNA sequences. For long chain antisense  
 CC RNA, the association rate with their target RNA in vitro correlates with  
 CC their effectiveness in vivo. Antisense molecules are potent inhibitors of  
 CC gene expression and viral functions. The antisense molecules AAV01779-804  
 CC exemplify novel nucleic acid molecules of the invention. These nucleic  
 CC acid molecules contain portions complementary to a first and second  
 CC chromosomal DNA sequence. The nucleic acid molecule forms at least part  
 CC of a chromosomal translocation resulting in a fusion gene containing the  
 CC translocation point. The DNA sequence, as well as vectors and host cells  
 CC containing it are useful in pharmaceutical compositions for treating  
 CC disorders based on chromosomal translocations, preferably for chronic  
 CC myelogenous leukaemia. The pharmaceutical composition may also be used to  
 CC treat acute lymphoblastic leukaemias, acute myelogenous leukaemias and  
 CC Non-Hodgkin lymphomas

SQ Sequence 53 BP; 13 A; 10 C; 16 G; 0 T; 14 U; 0 Other;

Query Match 100.0%; Score 26; DB 2; Length 53;  
 Best Local Similarity 100.0%; Pred. No. 4.4e-05;  
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CACTAGCCACTGGATTAAAGCAGAG 26  
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 Db 43 CACTAGCCACTGGATTAAAGCAGAG 18

RESULT 4  
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ID AAV01790 standard; RNA; 54 BP.  
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AC AAV01790;  
XX  
DT 04-JUN-1998 (first entry)  
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DE Antisense RNA sequence of the specification.  
XX  
KW Antisense; inhibitor; gene expression; chromosomal translocation;  
KW translocation point; pharmaceutical composition;  
KW chronic myelogenous leukaemia; acute lymphoblastic leukaemia;  
KW acute myelogenous leukaemia; Non-Hodgkin lymphoma; treatment; ss.  
XX  
OS Synthetic.  
XX  
PN WO9746672-A2.  
XX  
PD 11-DEC-1997.  
XX  
PP 05-JUN-1997; 97WO-EP002923.  
XX  
PR 05-JUN-1996; 96EP-00109034.  
XX  
PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.  
XX  
PI Sczakiel G, Haas R, Kronenwett R;  
XX  
DR WPI; 1998-042181/04.  
XX  
PT Nucleic acid molecule containing chromosomal translocation point - useful  
PT to treat chromosomal translocation disorders, e.g. chronic myelogenous  
PT leukaemia.  
XX  
PS Claim 6; Page 37; 49pp; English.  
XX  
CC AAV01779-804 represent antisense RNA sequences. For long chain antisense  
CC RNA, the association rate with their target RNA in vitro correlates with  
CC their effectiveness in vivo. Antisense molecules are potent inhibitors of  
CC gene expression and viral functions. The antisense molecules AAV01779-804  
CC exemplify novel nucleic acid molecules of the invention. These nucleic  
CC acid molecules contain portions complementary to a first and second  
CC of a chromosomal DNA sequence. The nucleic acid molecule forms at least part  
CC of a chromosomal translocation resulting in a fusion gene containing the  
CC translocation point. The DNA sequence, as well as vectors and host cells  
CC containing it are useful in pharmaceutical compositions for treating  
CC disorders based on chromosomal translocations, preferably for chronic  
CC myelogenous leukaemia. The pharmaceutical composition may also be used to  
CC treat acute lymphoblastic leukaemias, acute myelogenous leukaemias and  
CC Non-Hodgkin lymphomas  
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Best Local Similarity 100.0%; Pred. No. 4.4e-05;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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DB 43 CACTCAGCCACTGGATTAAAGCAGAG 18  
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AC AAV01791;  
XX  
DT 04-JUN-1998 (first entry)  
XX  
DE Antisense RNA sequence of the specification.

XX Antisense; inhibitor; gene expression; chromosomal translocation;  
KW translocation point; pharmaceutical composition;  
KW chronic myelogenous leukaemia; acute lymphoblastic leukaemia;  
KW acute myelogenous leukaemia; Non-Hodgkin lymphoma; treatment; ss.  
XX  
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XX  
PN WO9746672-A2.  
XX  
PD 11-DEC-1997.  
XX  
PP 05-JUN-1997; 97WO-EP002923.  
XX  
PR 05-JUN-1996; 96EP-00109034.  
XX  
PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.  
XX  
PI Sczakiel G, Haas R, Kronenwett R;  
XX  
DR WPI; 1998-042181/04.  
XX  
PT Nucleic acid molecule containing chromosomal translocation point - useful  
PT to treat chromosomal translocation disorders, e.g. chronic myelogenous  
PT leukaemia.  
XX  
PS Claim 6; Page 37; 49pp; English.  
XX  
CC AAV01779-804 represent antisense RNA sequences. For long chain antisense  
CC RNA, the association rate with their target RNA in vitro correlates with  
CC their effectiveness in vivo. Antisense molecules are potent inhibitors of  
CC gene expression and viral functions. The antisense molecules AAV01779-804  
CC exemplify novel nucleic acid molecules of the invention. These nucleic  
CC acid molecules contain portions complementary to a first and second  
CC of a chromosomal DNA sequence. The nucleic acid molecule forms at least part  
CC of a chromosomal translocation resulting in a fusion gene containing the  
CC translocation point. The DNA sequence, as well as vectors and host cells  
CC containing it are useful in pharmaceutical compositions for treating  
CC disorders based on chromosomal translocations, preferably for chronic  
CC myelogenous leukaemia. The pharmaceutical composition may also be used to  
CC treat acute lymphoblastic leukaemias, acute myelogenous leukaemias and  
CC Non-Hodgkin lymphomas  
XX  
SQ Sequence 55 BP; 13 A; 10 C; 16 G; 0 T; 16 U; 0 Other;  
Query Match 100.0%; Score 26; DB 2; Length 55;  
Best Local Similarity 100.0%; Pred. No. 4.4e-05;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CACTCAGCCACTGGATTAAAGCAGAG 26  
DB 43 CACTCAGCCACTGGATTAAAGCAGAG 18  
RESULT 6  
AAQ46950  
ID AAQ46950 standard; DNA; 56 BP.  
XX  
AC AAQ46950;  
XX  
DT 25-MAR-2003 (revised)  
DT 21-JAN-1994 (first entry)  
XX  
DE Branched probe to CMLa translocation region of chromosome 22.  
XX  
KW Chronic myelogenous leukaemia; CMLa chimeric bcr/abl;  
KW acute lymphocytic leukaemia; ALL; Genetic translocation; chromosome 22;  
KW target sequence; universal detection oligomer; branched probe;  
KW chemiluminescent acridinium ester; ss.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers





DR WPI; 1998-042181/04.  
 XX Nucleic acid molecule containing chromosomal translocation point - useful  
 PT to treat chromosomal translocation disorders, e.g. chronic myelogenous  
 PT leukaemia.  
 XX  
 XX Claim 6; Page 37; 49pp; English.  
 XX  
 CC AAV01779-804 represent antisense RNA sequences. For long chain antisense  
 CC RNA, the association rate with their target RNA in vitro correlates with  
 CC their effectiveness in vivo. Antisense molecules are potent inhibitors of  
 CC gene expression and viral functions. The antisense molecules are potent inhibitors of  
 CC exemplify novel nucleic acid molecules of the invention. These nucleic  
 CC acid molecules contain portions complementary to a first and second  
 CC chromosomal DNA sequence. The nucleic acid molecule forms at least part  
 CC of a chromosomal translocation resulting in a fusion gene containing the  
 CC translocation point. The DNA sequence, as well as vectors and host cells  
 CC containing it are useful in pharmaceutical compositions for treating  
 CC disorders based on chromosomal translocations, preferably for chronic  
 CC myelogenous leukaemia. The pharmaceutical composition may also be used to  
 CC treat acute lymphoblastic leukaemias, acute myelogenous leukaemias and  
 CC Non-Hodgkin lymphomas  
 XX  
 SQ Sequence 57 BP; 14 A; 11 C; 16 G; 0 T; 16 U; 0 Other;  
 Query Match 100.0%; Score 26; DB 2; Length 57;  
 Best Local Similarity 100.0%; Pred. No. 4.4e-05;  
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CACTAGCCCACTGGATTAAAGCAGAG 26  
 DB 43 CACTAGCCCACTGGATTAAAGCAGAG 18  
 RESULT 9  
 AAV01794/C  
 ID AAV01794 standard; RNA; 58 BP.  
 XX  
 AC AAV01794;  
 DT 04-JUN-1998 (first entry)  
 XX  
 DE Antisense RNA sequence of the specification.  
 XX  
 KW Antisense; inhibitor; gene expression; chromosomal translocation;  
 KW translocation point; pharmaceutical composition;  
 KW chronic myelogenous leukaemia; acute lymphoblastic leukaemia;  
 KW acute myelogenous leukaemia; Non-Hodgkin lymphoma; treatment; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN WO9746672-A2.  
 XX  
 PD 11-DEC-1997.  
 XX  
 PF 05-JUN-1997; 97WO-EP002923.  
 XX  
 PR 05-JUN-1996; 96EP-00109034.  
 XX  
 PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.  
 XX  
 PI Sczakiel G, Haas R, Kronenwett R;  
 XX  
 DR WPI; 1998-042181/04.  
 XX  
 PT Nucleic acid molecule containing chromosomal translocation point - useful  
 PT to treat chromosomal translocation disorders, e.g. chronic myelogenous  
 PT leukaemia.  
 XX  
 XX Claim 6; Page 37; 49pp; English.  
 XX  
 CC AAV01779-804 represent antisense RNA sequences. For long chain antisense  
 CC RNA, the association rate with their target RNA in vitro correlates with  
 CC their effectiveness in vivo. Antisense molecules are potent inhibitors of  
 CC gene expression and viral functions. The antisense molecules are potent inhibitors of  
 CC exemplify novel nucleic acid molecules of the invention. These nucleic  
 CC acid molecules contain portions complementary to a first and second  
 CC chromosomal DNA sequence. The nucleic acid molecule forms at least part  
 CC of a chromosomal translocation resulting in a fusion gene containing the  
 CC translocation point. The DNA sequence, as well as vectors and host cells  
 CC containing it are useful in pharmaceutical compositions for treating  
 CC disorders based on chromosomal translocations, preferably for chronic  
 CC myelogenous leukaemia. The pharmaceutical composition may also be used to  
 CC treat acute lymphoblastic leukaemias, acute myelogenous leukaemias and  
 CC Non-Hodgkin lymphomas  
 XX  
 SQ Sequence 57 BP; 14 A; 11 C; 16 G; 0 T; 16 U; 0 Other;  
 Query Match 100.0%; Score 26; DB 2; Length 57;  
 Best Local Similarity 100.0%; Pred. No. 4.4e-05;  
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CACTAGCCCACTGGATTAAAGCAGAG 26  
 DB 43 CACTAGCCCACTGGATTAAAGCAGAG 18  
 RESULT 9  
 AAV01794/C  
 ID AAV01794 standard; RNA; 58 BP.  
 XX  
 AC AAV01794;  
 DT 04-JUN-1998 (first entry)  
 XX  
 DE Antisense RNA sequence of the specification.  
 XX  
 KW Antisense; inhibitor; gene expression; chromosomal translocation;  
 KW translocation point; pharmaceutical composition;  
 KW chronic myelogenous leukaemia; acute lymphoblastic leukaemia;  
 KW acute myelogenous leukaemia; Non-Hodgkin lymphoma; treatment; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN WO9746672-A2.  
 XX  
 PD 11-DEC-1997.  
 XX  
 PF 05-JUN-1997; 97WO-EP002923.  
 XX  
 PR 05-JUN-1996; 96EP-00109034.  
 XX  
 PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.  
 XX  
 PI Sczakiel G, Haas R, Kronenwett R;  
 XX  
 DR WPI; 1998-042181/04.  
 XX  
 PT Nucleic acid molecule containing chromosomal translocation point - useful  
 PT to treat chromosomal translocation disorders, e.g. chronic myelogenous  
 PT leukaemia.  
 XX  
 XX Claim 6; Page 37; 49pp; English.  
 XX  
 CC AAV01779-804 represent antisense RNA sequences. For long chain antisense  
 CC RNA, the association rate with their target RNA in vitro correlates with

CC their effectiveness in vivo. Antisense molecules are potent inhibitors of  
 CC gene expression and viral functions. The antisense molecules AAV01779-804  
 CC exemplify novel nucleic acid molecules of the invention. These nucleic  
 CC acid molecules contain portions complementary to a first and second  
 CC chromosomal DNA sequence. The nucleic acid molecule forms at least part  
 CC of a chromosomal translocation resulting in a fusion gene containing the  
 CC translocation point. The DNA sequence, as well as vectors and host cells  
 CC containing it are useful in pharmaceutical compositions for treating  
 CC disorders based on chromosomal translocations, preferably for chronic  
 CC myelogenous leukaemia. The pharmaceutical composition may also be used to  
 CC treat acute lymphoblastic leukaemias, acute myelogenous leukaemias and  
 CC Non-Hodgkin lymphomas  
 XX  
 SQ Sequence 58 BP; 14 A; 11 C; 17 G; 0 T; 16 U; 0 Other;  
 Query Match 100.0%; Score 26; DB 2; Length 58;  
 Best Local Similarity 100.0%; Pred. No. 4.4e-05;  
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CACTAGCCCACTGGATTAAAGCAGAG 26  
 DB 43 CACTAGCCCACTGGATTAAAGCAGAG 18  
 RESULT 10  
 AAV01795/C  
 ID AAV01795 standard; RNA; 59 BP.  
 XX  
 AC AAV01795;  
 DT 04-JUN-1998 (first entry)  
 XX  
 DE Antisense RNA sequence of the specification.  
 XX  
 KW Antisense; inhibitor; gene expression; chromosomal translocation;  
 KW translocation point; pharmaceutical composition;  
 KW chronic myelogenous leukaemia; acute lymphoblastic leukaemia;  
 KW acute myelogenous leukaemia; Non-Hodgkin lymphoma; treatment; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN WO9746672-A2.  
 XX  
 PD 11-DEC-1997.  
 XX  
 PF 05-JUN-1997; 97WO-EP002923.  
 XX  
 PR 05-JUN-1996; 96EP-00109034.  
 XX  
 PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.  
 XX  
 PI Sczakiel G, Haas R, Kronenwett R;  
 XX  
 DR WPI; 1998-042181/04.  
 XX  
 PT Nucleic acid molecule containing chromosomal translocation point - useful  
 PT to treat chromosomal translocation disorders, e.g. chronic myelogenous  
 PT leukaemia.  
 XX  
 XX Claim 6; Page 37; 49pp; English.  
 XX  
 CC AAV01779-804 represent antisense RNA sequences. For long chain antisense  
 CC RNA, the association rate with their target RNA in vitro correlates with  
 CC their effectiveness in vivo. Antisense molecules are potent inhibitors of  
 CC gene expression and viral functions. The antisense molecules AAV01779-804  
 CC exemplify novel nucleic acid molecules of the invention. These nucleic  
 CC acid molecules contain portions complementary to a first and second  
 CC chromosomal DNA sequence. The nucleic acid molecule forms at least part  
 CC of a chromosomal translocation resulting in a fusion gene containing the  
 CC translocation point. The DNA sequence, as well as vectors and host cells  
 CC containing it are useful in pharmaceutical compositions for treating  
 CC disorders based on chromosomal translocations, preferably for chronic  
 CC myelogenous leukaemia. The pharmaceutical composition may also be used to

CC treat acute lymphoblastic leukaemias, acute myelogenous leukaemias and  
CC Non-Hodgkin lymphomas  
XX  
SQ Sequence 59 BP; 15 A; 11 C; 17 G; 0 T; 16 U; 0 Other;  
Query Match 100.0%; Score 26; DB 2; Length 59;  
Best Local Similarity 100.0%; Pred. No. 4.4e-05;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CACTAGCCACTGGATTAAAGCAGAG 26  
Db 43 CACTAGCCACTGGATTAAAGCAGAG 18  
RESULT 11  
AAZ55997/C  
ID AAZ55997 standard; RNA; 102 BP.  
XX  
AC AAZ55997;  
XX  
DT 19-APR-2000 (first entry)  
XX  
DE Structured antisense RNA molecule, HAS210.  
XX  
KW Structured antisense molecule; two-stage binding; stem-loop;  
KW hybridisation; antisense therapy; gene therapy; HAS210; BCR-ABL p210;  
KW chronic myelogenous leukaemia; CML; acute lymphocytic leukaemia; ALL; ss.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
PN WO9967379-A2.  
XX  
PD 29-DEC-1999.  
XX  
PF 23-JUN-1999; 99WO-GB001956.  
XX  
PR 23-JUN-1998; 98GB-00013531.  
PR 26-JUN-1998; 98US-0090867P.  
XX  
PA (MEDI-) MEDICAL RES COUNCIL.  
XX  
PI Stocks M, Rabbitts T;  
XX  
DR WPI; 2000-126630/11.  
XX  
PT New antisense nucleic acid containing two regions complementary to a  
PT target, particularly for treating leukemia.  
XX  
PS Example 3; Page 27; 49pp; English.  
XX  
CC The invention relates to structured antisense nucleic acid molecules  
CC comprising two regions (R1 and R2) which are both complementary to a  
CC target nucleic acid molecule, wherein one region (R1) is available for  
CC hybridisation while the second region (R2) is temporarily masked, for  
CC example in a stem-loop structure. The structured antisense molecule  
CC initially binds, very specifically, to its target through a short R1,  
CC after which the longer R2 becomes unmasked and interacts with more of the  
CC target to provide increased stability of hybridisation. Binding of R1  
CC will be short lived if not followed by binding of R2. The stem-loop  
CC structure containing R2 may contain destabilising elements (e.g.,  
CC mismatches, G-U pairs or bulges), causing the masked R2 stem loop to be  
CC thermodynamically less stable than the R2/target hybrid. The structured  
CC antisense molecules may be used to modulate expression (in vivo or in  
CC vitro) of a gene product encoded by the target nucleotide, for example, a  
CC transcription factor. Vectors for the expression of the structured  
CC antisense ribonucleotides may be used in gene therapy. The structured  
CC antisense molecules combine the high specificity of binding associated  
CC with a short antisense molecule with the high stability of binding to  
CC target of long antisense molecules. The present sequence represents  
CC HAS210, an example of a structured antisense RNA molecule, used in an  
CC exemplification of the present invention. This structured antisense  
CC molecule is targetted to BCR-ABL p210 mRNA, which is a transcript of a

CC BCR-ABL fusion gene, where the ABL portion is located 3' of the BCR  
CC portion. BCR-ABL fusions result from the chromosomal translocation t(9;  
CC 22)(q34;q11), and are associated with chronic myelogenous leukaemia (CML)  
CC and acute lymphocytic leukaemia (ALL)  
XX  
SQ Sequence 102 BP; 21 A; 22 C; 27 G; 0 T; 32 U; 0 Other;  
Query Match 100.0%; Score 26; DB 3; Length 102;  
Best Local Similarity 100.0%; Pred. No. 4.4e-05;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CACTAGCCACTGGATTAAAGCAGAG 26  
Db 56 CACTAGCCACTGGATTAAAGCAGAG 31  
RESULT 12  
ABS73168  
ID ABS73168 standard; DNA; 140 BP.  
XX  
AC ABS73168;  
XX  
DT 04-DEC-2002 (first entry)  
XX  
DE DNA encoding human translocation (9; 22)(q34; q11) protein #1.  
XX  
KW Chromosome aberration; oncogenic fusion protein; cancer;  
KW proliferative disease; cellular protein isoform; heat shock protein 90;  
KW HSP-90; rheumatoid arthritis; cancer; haematopoietic disorder;  
KW T cell lymphoma; B cell lymphoma; chronic myeloid leukaemia; CML;  
KW acute myeloid leukaemia; AML; chronic myelomonocytic leukaemia; CMML;  
KW acute lymphoblastic leukaemia; ALL; APL; NHL; solid tumour;  
KW papillary thyroid carcinoma; Ewing's sarcoma; melanoma; liposarcoma;  
KW rhabdomyosarcoma; synovial sarcoma; viral infection; gene; ds.  
XX  
OS Homo sapiens.  
XX  
PN WO200269900-A2.  
XX  
PD 12-SEP-2002.  
XX  
PF 01-MAR-2002; 2002WO-US006518.  
XX  
PR 01-MAR-2001; 2001US-0272751P.  
XX  
PA (CONF-) CONFORMA THERAPEUTICS CORP.  
XX  
PI Fritz LC, Burrows FU;  
XX  
DR WPI; 2002-698710/75.  
DR P-PSDB; ABG95009.  
XX  
PT Treating genetically-defined disease associated with chromosomal  
PT aberrations yielding oncogenic fusion proteins, e.g. cell proliferative  
PT diseases, involves administering an inhibitor of heat shock protein 90.  
XX  
PS Disclosure; Page 91; 389pp; English.  
XX  
CC The invention describes a method of treating genetically-defined disease  
CC associated with chromosomal aberrations yielding oncogenic fusion  
CC proteins (I), treating cancerous cells containing (I) in a heterogeneous  
CC cell population, treating proliferative diseases associated with mutant  
CC protein or cellular protein isoforms (II) dependent on heat shock protein  
CC (HSP)-90, or selectively treating cells expressing (II) involving  
CC administering HSP90-inhibitor. The method is useful for treating  
CC genetically-defined disease with chromosomal aberration yielding  
CC oncogenic fusion protein, treating cancerous cells containing fusion  
CC protein in heterogeneous cell population, treating proliferative disease  
CC (e.g. rheumatoid arthritis or cancer) associated with mutant protein or  
CC cellular protein isoform dependent on heat shock protein (HSP)-90 (e.g.  
CC p53), or selectively treating cells expressing mutant protein or cellular  
CC protein isoform in a patient heterozygous for (II). The method is useful  
CC for treating a disease e.g. haematopoietic disorder such as T or B cell

CC lymphoma, chronic myeloid leukaemia (CML), APL, ALL, AML, NHL and CML, or a disease characterised by a solid tumour such as papillary thyroid carcinoma, Ewing's sarcoma, melanoma, liposarcoma, rhabdomyosarcoma and CC synovial sarcoma. The method is also useful for treating viral CC infections. This represents the DNA sequence of a chromosome aberration XX  
SQ Sequence 140 BP; 38 A; 30 C; 36 G; 36 T; 0 U; 0 Other;

Query Match 100.0%; Score 26; DB 6; Length 140;  
Best Local Similarity 100.0%; Pred. No. 4.5e-05;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CACTCAGCCACTGGATTAAAGCAGAG 26  
DB 70 CACTCAGCCACTGGATTAAAGCAGAG 95

## RESULT 13

NAT88785  
ID AAT88785 standard; DNA; 200 BP.

XX AC AAT88785;

XX DT 23-MAR-1998 (first entry)

XX DE Leukaemic cell BCR-ABL mRNA PCR product target sequence.

XX KW Leukaemia; BCR-ABL; cell line K562; target; immunoassay; probe;  
XX KW hybridisation; diagnostic; luciferase; genetic disease; ss.

XX OS Unidentified.

XX PN CA2186998-A.

XX PD 31-MAY-1997.

XX PF 02-OCT-1996; 96CA-02186998.

XX PR 30-NOV-1995; 95US-00565055.

XX PA (UYWI-) UNIV WINDSOR.

XX PI Christopoulos TK;

XX DR WPI; 1997-415964/39.

XX PT Immunoassays and nucleic acid hybridisation assays - using protein-  
XX PT encoding nucleic acid fragments as labels.

XX PS Disclosure; Page 26; 39pp; English.

XX CC A novel assay has been developed for determining an analyte. The assay  
XX CC comprises labelling the analyte with a nucleic acid fragment that encodes  
XX CC a protein, expressing the nucleic acid, and detecting the protein. The  
XX CC present sequence represents a target sequence from a leukaemic cell (cell  
XX CC line K562), used in an example of the present assay. The assay is used  
XX CC for the determination of antigens or nucleic acids for diagnostic or  
XX CC research purposes, e.g. detecting low levels of tumour markers, analysing  
XX CC nucleic acid mutations associated with genetic diseases, diagnosing and  
XX CC monitoring pathogen infections, or searching for new disease markers. The  
XX CC immunoassay when using a luciferase for detection is more sensitive than  
XX CC an enzyme-amplified, time-resolved fluorometric immunoassay and does not  
XX CC require preparation of a luciferase-antibody conjugate

XX SQ Sequence 200 BP; 49 A; 52 C; 51 G; 48 T; 0 U; 0 Other;

Query Match 100.0%; Score 26; DB 2; Length 200;  
Best Local Similarity 100.0%; Pred. No. 4.5e-05;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CACTCAGCCACTGGATTAAAGCAGAG 26  
DB 122 CACTCAGCCACTGGATTAAAGCAGAG 147

## RESULT 14

AAN91666  
ID AAN91666 standard; DNA; 205 BP.

XX AC AAN91666;

XX DT 14-MAR-1990 (first entry)

XX DE Bcr-abl fusion message for leukaemia.

XX KW Reciprocal translocation.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX FT exon 1..31

XX FT /tag= a

XX FT /note= "bcr exon 2"

XX FT exon 32..106

XX FT /tag= b

XX FT /note= "bcr exon 3"

XX FT exon 106..205

XX FT /tag= b

XX FT /note= "abl exon 2"

XX EP338713-A.

XX PD 25-OCT-1989.

XX PF 11-APR-1989; 89EP-00303538.

XX PR 18-APR-1988; 88US-00182434.

XX PA (CITY ) CITY OF HOPE.

XX PI Rossi JJ;

XX DR WPI; 1989-311152/43.

XX PT New synthetic oligo:nucleotide probes - used for detection of BCR-ABL RNA  
XX PT from blood or bone marrow of chronic myelogenous leukaemia patients.

XX PS Disclosure; Page 3; 4pp; English.

XX CC Part of 8 kb RNA transcript, showing the fusion of abl and bcr. The abl  
XX CC gene is from human chromosome 9, and this is spliced to a region on  
XX CC chromosome 22 called the breakpoint cluster region (bcr). CML has  
XX CC reciprocal translocation of human chromosomes 9 and 22

XX SQ Sequence 205 BP; 50 A; 55 C; 52 G; 48 T; 0 U; 0 Other;

Query Match 100.0%; Score 26; DB 1; Length 205;  
Best Local Similarity 100.0%; Pred. No. 4.5e-05;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CACTCAGCCACTGGATTAAAGCAGAG 26

DB 76 CACTCAGCCACTGGATTAAAGCAGAG 101

## RESULT 15

ABS73175  
ID ABS73175 standard; DNA; 250 BP.

XX AC ABS73175;

XX DT 04-DEC-2002 (first entry)

XX DE Human translocation (9: 22)(q34: q11) #3.

XX KW Chromosome aberration; oncogenic fusion protein; cancer;

KW proliferative disease; cellular protein isoform; heat shock protein 90;  
KW HSP-90; rheumatoid arthritis; cancer; haematopoietic disorder;  
KW T cell lymphoma; B cell lymphoma; chronic myeloid leukaemia; CML;  
KW acute myeloid leukaemia; AML; chronic myelomonocytic leukaemia; CMML;  
KW acute lymphoblastic leukaemia; ALL; APL; NHL; solid tumour;  
KW papillary thyroid carcinoma; Ewing's sarcoma; melanoma; liposarcoma;  
KW rhabdomyosarcoma; synovial sarcoma; viral infection; gene; ds.  
XX  
OS Homo sapiens.  
XX  
XX  
PN WO200269900-A2.  
XX  
XX  
PD 12-SEP-2002.  
XX  
XX  
PF 01-MAR-2002; 2002WO-US006518.  
XX  
XX  
PR 01-MAR-2001; 2001US-0272751P.  
XX  
XX  
PA (CONF-) CONFORMA THERAPEUTICS CORP.  
XX  
PI Fritz LC, Burrows FJ;  
XX  
XX  
DR WPI; 2002-698710/75.  
XX  
XX  
PT Treating genetically-defined disease associated with chromosomal  
PT aberrations yielding oncogenic fusion proteins, e.g. cell proliferative  
PT diseases, involves administering an inhibitor of heat shock protein 90.  
XX  
XX  
PS Disclosure; Page 97; 389pp; English.  
XX  
XX The invention describes a method of treating genetically-defined disease  
CC associated with chromosomal aberrations yielding oncogenic fusion  
CC proteins (I), treating cancerous cells containing (I) in a heterogeneous  
CC cell population, treating proliferative diseases associated with mutant  
CC protein or cellular protein isoforms (II) dependent on heat shock protein  
CC (HSP)-90, or selectively treating cells expressing (II) involving  
CC administering HSP90-inhibitor. The method is useful for treating  
CC genetically-defined disease with chromosomal aberration yielding  
CC oncogenic fusion protein, treating cancerous cells containing fusion  
CC protein in heterogeneous cell population, treating proliferative disease  
CC (e.g. rheumatoid arthritis or cancer) associated with mutant protein or  
CC cellular protein isoform dependent on heat shock protein (HSP)-90 (e.g.  
CC p53), or selectively treating cells expressing mutant protein or cellular  
CC protein isoform in a patient heterozygous for (II). The method is useful  
CC for treating a disease e.g. haematopoietic disorder such as T or B cell  
CC lymphoma, chronic myeloid leukaemia (CML), APL, ALL, NHL and CMML,  
CC or a disease characterised by a solid tumour such as papillary thyroid  
CC carcinoma, Ewing's sarcoma, melanoma, liposarcoma, rhabdomyosarcoma and  
CC synovial sarcoma. The method is also useful for treating viral  
CC infections. This represents the DNA sequence of a chromosome aberration  
XX  
SQ Sequence 250 BP; 65 A; 62 C; 63 G; 60 T; 0 U; 0 Other;

Query Match 100.0%; Score 26; DB 6; Length 250;  
Best Local Similarity 100.0%; Pred. No. 4.5e-05;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CACTGACCCACTGGATTAGCAGAG 26  
Db 113 CACTGACCCACTGGATTAGCAGAG 138

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Job time : 160.225 secs

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OM nucleic - nucleic search, using sw model

Run on: May 27, 2004, 02:25:18 ; Search time 33.15 Seconds  
(without alignments)  
435.256 Million cell updates/sec

Title: US-09-121-239-27

Perfect score: 26

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Scoring table: OLIGO\_NUC

Gapop\_60.0 , Gapext 60.0

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Word size : 0

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents NA.\*

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- 2: /cgn2\_6/prodata/2/ina/5B COMB.seq.\*
- 3: /cgn2\_6/prodata/2/ina/6A COMB.seq.\*
- 4: /cgn2\_6/prodata/2/ina/6B COMB.seq.\*
- 5: /cgn2\_6/prodata/2/ina/PCTUS COMB.seq.\*
- 6: /cgn2\_6/prodata/2/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	26	100.0	56	1	US-07-940-652-16
2	26	100.0	56	1	US-08-255-553-16
3	26	100.0	90	5	PCT-US93-06251-4
4	26	100.0	266	1	US-08-152-621-4
5	26	100.0	266	1	US-08-306-691B-37
6	26	100.0	266	5	PCT-US92-05035-4
7	26	100.0	1078	4	US-09-310-842-1
8	25	96.2	40	3	US-09-358-972-125
9	25	96.2	41	3	US-09-358-972-126
10	25	96.2	66	1	US-07-940-652-13
11	25	96.2	66	1	US-08-255-553-13
12	20	76.9	40	1	US-08-761-131-2
13	18	69.2	18	1	US-08-761-131-4
14	16	61.5	128779	4	US-09-497-855A-38
15	15	57.7	22	3	US-09-358-972-127
16	15	57.7	22	3	US-09-358-972-128
17	15	57.7	22	3	US-09-406-064-97
18	15	57.7	22	3	US-09-406-064-98
19	15	57.7	22	4	US-09-788-847-97
20	15	57.7	22	4	US-09-788-847-98
21	15	57.7	783	4	US-09-540-236-674
22	15	57.7	5183	1	US-08-459-568-3
23	15	57.7	5183	2	US-08-399-411-3
24	15	57.7	5868	3	US-08-516-859A-3
25	15	57.7	5868	4	US-09-586-472-3
26	15	57.7	5868	4	US-09-528-706-3
27	15	57.7	96109	4	US-09-596-002-35

c 28 14 53.8 294 3 US-09-172-108-26 Sequence 26, Appl  
c 29 14 53.8 294 3 US-09-172-711-23 Sequence 23, Appl  
c 30 14 53.8 984 4 US-09-540-236-670 Sequence 670, App  
c 31 14 53.8 1466 3 US-09-130-242-8 Sequence 8, Appl  
c 32 14 53.8 1535 4 US-09-848-295-1 Sequence 1, Appl  
c 33 14 53.8 1824 4 US-09-252-991A-16072 Sequence 16072, A  
c 34 14 53.8 2031 4 US-09-634-238-129 Sequence 129, App  
c 35 14 53.8 2040 1 US-08-393-985-17 Sequence 17, Appl  
c 36 14 53.8 2412 4 US-09-620-312D-881 Sequence 881, App  
c 37 14 53.8 3773 3 US-09-130-242-1 Sequence 1, Appl  
c 38 14 53.8 4832 4 US-08-851-567B-58 Sequence 58, Appl  
c 39 14 53.8 9495 1 US-08-271-829-1 Sequence 1, Appl  
c 40 14 53.8 9495 5 PCT-US93-01544-1 Sequence 1, Appl  
c 41 14 53.8 12225 2 US-08-822-445-11 Sequence 11, Appl  
c 42 14 53.8 12225 4 US-09-396-540-11 Sequence 11, Appl  
c 43 14 53.8 12616 2 US-08-822-445-9 Sequence 9, Appl  
c 44 14 53.8 12616 4 US-09-396-540-9 Sequence 9, Appl  
c 45 14 53.8 14042 3 US-08-652-877-85 Sequence 85, Appl

#### ALIGNMENTS

RESULT 1  
US-07-940-652-16  
; Sequence 16, Application US/07940652  
; Patent No. 542413  
; GENERAL INFORMATION:  
; APPLICANT: James J. Hogan et al.  
; TITLE OF INVENTION: BRANCHED NUCLEIC ACID PROBES  
; NUMBER OF SEQUENCES: 31  
; CORRESPONDENCE ADDRESS:  
; ADDRESSER: Lyon & Lyon  
; STREET: 611 West Sixth Street  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: USA  
; ZIP: 90017  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: IBM P.C. DOS Version 3.30  
; SOFTWARE: WordPerfect (Version 5.1)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/940,652  
; FILING DATE: 19920904  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/07/827,021  
; FILING DATE: 22-JAN-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Warburg, Richard J.  
; REGISTRATION NUMBER: 32,327  
; REFERENCE/DOCKET NUMBER: 199/201  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (213) 489-1600  
; TELEFAX: (213) 955-0440  
; TELEFAX: 67-3510  
; INFORMATION FOR SEQ ID NO: 16:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 56  
; TYPE: NUCLEIC ACID  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-07-940-652-16

Query Match 100.0%; Score 26; DB 1; Length 56;  
Best Local Similarity 100.0%; Pred. No. 2.3e-06;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CACTAGCCACTGGATTAAAGCAGAG 26

DB 10 CACTAGCCACTGGATTAAAGCAGAG 35

RESULT 2  
US-08-255-553-16  
; Sequence 16, Application US/08255553  
; Patent No. 5451503  
; GENERAL INFORMATION:  
; APPLICANT: James J. Hogan et al.  
; TITLE OF INVENTION: BRANCHED NUCLEIC ACID PROBES  
; NUMBER OF SEQUENCES: 31  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 611 West Sixth Street  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: USA  
; ZIP: 90017  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: IBM P.C. DOS Version 3.30  
; SOFTWARE: WordPerfect (Version 5.1)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/255,553  
; FILING DATE: 07-JUN-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/07/940,652  
; FILING DATE: 04-SEP-1992  
; APPLICATION NUMBER: US/07/827,021  
; FILING DATE: 22-JAN-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Warburg, Richard J.  
; REGISTRATION NUMBER: 32,327  
; REFERENCE/DOCKET NUMBER: 199/201  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (213) 489-1600  
; TELEFAX: (213) 955-0440  
; TELEX: 67-3510  
; INFORMATION FOR SEQ ID NO: 16:  
; LENGTH: 56  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-255-553-16

Query Match 100.0%; Score 26; DB 1; Length 56;  
Best Local Similarity 100.0%; Pred. No. 2.3e-06;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CACTAGCCACTGGATTAAAGCAGAG 26  
Db 10 CACTAGCCACTGGATTAAAGCAGAG 35

RESULT 3  
PCT-US93-06251-4  
; Sequence 4, Application PC/TUS9306251  
; GENERAL INFORMATION:  
; APPLICANT: Wickstrom, Eric and Rife, Jason P.  
; TITLE OF INVENTION: Trivalent Synthesis of Oligonucleotides Containing  
; Stereospecific Alkylphosphonates and Arylphosphonates  
; NUMBER OF SEQUENCES: 93  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER  
; STREET: 400 Garden City Plaza  
; CITY: Garden City  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 11530  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US93/06251  
; FILING DATE: 19930630  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Digiglio, Frank S.  
; REGISTRATION NUMBER: 31,346  
; REFERENCE/DOCKET NUMBER: 8586  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 516-742-4343  
; TELEFAX: 516-742-4366  
; TELEX: 230 901 SANS UR  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 90 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
PCT-US93-06251-4  
Query Match 100.0%; Score 26; DB 5; Length 90;  
Best Local Similarity 100.0%; Pred. No. 2.3e-06;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CACTAGCCACTGGATTAAAGCAGAG 26  
Db 45 CACTAGCCACTGGATTAAAGCAGAG 70  
RESULT 4  
US-08-152-621-4  
; Sequence 4, Application US/08152621  
; Patent No. 5652222  
; GENERAL INFORMATION:  
; APPLICANT: Calabretta, Bruno  
; TITLE OF INVENTION: Selective Inhibition of  
; Leukemic Cell Proliferation by bcr-abl  
; TITLE OF INVENTION: Antisense Oligonucleotides  
; NUMBER OF SEQUENCES: 34  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SEIDEL, GONDA, LAVORGNA  
; STREET: 1800 Two Penn Center  
; CITY: Philadelphia  
; STATE: Pennsylvania  
; COUNTRY: U.S.A.  
; ZIP: 19102  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb  
; COMPUTER: IBM PS/2  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: WordPerfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/152,621  
; FILING DATE: NO. 5652222ember 15, 1993  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/718,302  
; FILING DATE: June 18, 1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Monaco, Daniel A.  
; REGISTRATION NUMBER: 30,480  
; REFERENCE/DOCKET NUMBER: 6056-120 (CT.) 1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (215) 568-8383  
; TELEFAX: (215) 568-5549  
; TELEX: NO. 5652222e  
; INFORMATION FOR SEQ ID NO: 4:

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 266 Nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single stranded
; TOPOLOGY: linear
US-08-152-621-4
Query Match 100.0%; Score 26; DB 1; Length 266;
Best Local Similarity 100.0%; Pred. No. 2.4e-06;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CACTCAGCCACTGGATTAAAGCAGAG 26
Db 10 CACTCAGCCACTGGATTAAAGCAGAG 35

RESULT 5
US-08-306-691B-37
; Sequence 37, Application US/08306691B
; Patent No. 5734039
; GENERAL INFORMATION:
; APPLICANT: Calabretta, Bruno
; APPLICANT: Skorski, Tomasz
; TITLE OF INVENTION: ANTISENSE
; TITLE OF INVENTION: OLIGONUCLEOTIDES TARGETING COOPERATING ONCOGENES
; NUMBER OF SEQUENCES: 55
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seidel, Gonda, Lavorgna & Monaco, P.C.
; STREET: Two Penn Center, Suite 1800
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: U.S.A.
; ZIP: 19102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: 08/306,691B
; FILING DATE: September 15, 1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Monaco, Daniel A.
; REGISTRATION NUMBER: 30,480
; REFERENCE/DOCKET NUMBER: 8321-8
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-8383
; TELEFAX: (215) 568-5549
; TELEX: No. 5734039e
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 266 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-306-691B-37
Query Match 100.0%; Score 26; DB 1; Length 266;
Best Local Similarity 100.0%; Pred. No. 2.4e-06;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CACTCAGCCACTGGATTAAAGCAGAG 26
Db 10 CACTCAGCCACTGGATTAAAGCAGAG 35

RESULT 6
PCT-US92-05035-4
; Sequence 4, Application PC/TUS9205035

```

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; GENERAL INFORMATION:
; APPLICANT: Calabretta, Bruno
; APPLICANT: Gewirtz, Alan M.
; TITLE OF INVENTION: Selective Inhibition of
; TITLE OF INVENTION: Leukemic Cell Proliferation by bcr-abl
; TITLE OF INVENTION: Antisense Oligonucleotides
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Temple University - Of The Common-
; ADDRESSEE: wealth System of Higher Education
; STREET: 406 University Services Building
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: U.S.A.
; ZIP: 19122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/05035
; FILING DATE: 19920615
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/718,302
; FILING DATE: June 18, 1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/869,911
; FILING DATE: April 14, 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Monaco, Daniel A.
; REGISTRATION NUMBER: 30,480
; REFERENCE/DOCKET NUMBER: 6056-120 (CIP) 1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-8383
; TELEFAX: (215) 568-5549
; TELEX: None
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 266 Nucleotides
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single stranded
; TOPOLOGY: linear
PCT-US92-05035-4
Query Match 100.0%; Score 26; DB 5; Length 266;
Best Local Similarity 100.0%; Pred. No. 2.4e-06;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CACTCAGCCACTGGATTAAAGCAGAG 26
Db 10 CACTCAGCCACTGGATTAAAGCAGAG 35

RESULT 7
US-09-310-842-1
; Sequence 1, Application US/09310842A
; Patent No. 6451593
; GENERAL INFORMATION:
; APPLICANT: Wittig, Prof. Burghardt
; APPLICANT: Junghans, Claas
; TITLE OF INVENTION: Design Principle for Constructing Expression Constructs for Gene
; TITLE OF INVENTION: Therapy
; FILE REFERENCE: XI 597/99
; CURRENT APPLICATION NUMBER: US/09/310,842A
; CURRENT FILING DATE: 1999-05-12
; EARLIER APPLICATION NUMBER: DE 196 48 625.4
; EARLIER FILING DATE: 1996-11-13
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1078

```

TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
NAME/KEY: gene  
LOCATION: (1)..(1078)  
OTHER INFORMATION: bcr3=abl2; Oligo DNA Dumbbell  
FEATURE:  
NAME/KEY: misc binding  
LOCATION: (1)..(2)  
OTHER INFORMATION: intramolecular binding site; the T-nucleotides at position 1 to  
OTHER INFORMATION: 2 can be modified with amino or caroxy features  
FEATURE:  
NAME/KEY: misc binding  
LOCATION: (1077)..(1078)  
OTHER INFORMATION: intramolecular binding site; the T-nucleotides at position 1077  
OTHER INFORMATION: to 1078 can be modified with amino or caroxy features  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Strandness: both; nucleic  
OTHER INFORMATION: acid (linear), hypothetical: No. 6451593 anti-sense: No  
US-09-310-842-1

Query Match 100.0%; Score 26; DB 4; Length 1078;  
Best Local Similarity 100.0%; Pred. No. 2.5e-06;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CACTCAGCCACTGGATTAAAGCAGAG 26  
Db 744 CACTCAGCCACTGGATTAAAGCAGAG 769

RESULT 8  
US-09-358-972-125/c  
Sequence 125, Application US/09358972  
Patent No. 6235480  
GENERAL INFORMATION:  
APPLICANT: Shultz, John W.  
APPLICANT: Lewis, Martin K.  
APPLICANT: Lieppe, Donna  
APPLICANT: Mandrekar, Michelle  
APPLICANT: Kephart, Daniel  
APPLICANT: Rhodes, Richard B.  
APPLICANT: Andrews, Christine A.  
APPLICANT: Hartnett, James R.  
APPLICANT: Gu, Trent  
APPLICANT: Olson, Ryan J.  
APPLICANT: Wood, Keith W.  
TITLE OF INVENTION: Nucleic Acid Detection  
FILE REFERENCE: Pro-103 6868/75528  
CURRENT FILING DATE: 1999-07-22  
EARLIER APPLICATION NUMBER: 09/252,436  
EARLIER FILING DATE: 1999-02-18  
EARLIER APPLICATION NUMBER: 09/042,287  
EARLIER FILING DATE: 1998-03-13  
NUMBER OF SEQ ID NOS: 290  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 125  
LENGTH: 40  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: native bcr  
US-09-358-972-125

Query Match 96.2%; Score 25; DB 3; Length 40;  
Best Local Similarity 100.0%; Pred. No. 8.7e-06;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ACTCAGCCACTGGATTAAAGCAGAG 26  
Db 40 ACTCAGCCACTGGATTAAAGCAGAG 16

RESULT 9  
US-09-358-972-126/c  
Sequence 126, Application US/09358972  
Patent No. 6235480  
GENERAL INFORMATION:  
APPLICANT: Shultz, John W.  
APPLICANT: Lewis, Martin K.  
APPLICANT: Lieppe, Donna  
APPLICANT: Mandrekar, Michelle  
APPLICANT: Kephart, Daniel  
APPLICANT: Rhodes, Richard B.  
APPLICANT: Andrews, Christine A.  
APPLICANT: Hartnett, James R.  
APPLICANT: Gu, Trent  
APPLICANT: Olson, Ryan J.  
APPLICANT: Wood, Keith W.  
APPLICANT: Welch, Roy  
TITLE OF INVENTION: Nucleic Acid Detection  
FILE REFERENCE: Pro-103 6868/75528  
CURRENT FILING DATE: 1999-07-22  
EARLIER APPLICATION NUMBER: 09/252,436  
EARLIER FILING DATE: 1999-02-18  
EARLIER APPLICATION NUMBER: 09/042,287  
EARLIER FILING DATE: 1998-03-13  
NUMBER OF SEQ ID NOS: 290  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 126  
LENGTH: 41  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: bcr/abl translocation  
US-09-358-972-126

Query Match 96.2%; Score 25; DB 3; Length 41;  
Best Local Similarity 100.0%; Pred. No. 8.7e-06;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ACTCAGCCACTGGATTAAAGCAGAG 26  
Db 41 ACTCAGCCACTGGATTAAAGCAGAG 17

RESULT 10  
US-07-940-652-13/c  
Sequence 13, Application US/07940652  
Patent No. 5424413  
GENERAL INFORMATION:  
APPLICANT: James J. Hogan et al.  
TITLE OF INVENTION: BRANCHED NUCLEIC ACID PROBES  
NUMBER OF SEQUENCES: 31  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 611 West Sixth Street  
CITY: Los Angeles  
STATE: California  
COUNTRY: USA  
ZIP: 90017  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS Version 3.30  
SOFTWARE: WordPerfect (Version 5.1)  
CURRENT APPLICATION DATA:  
FILING DATE: 19920904  
APPLICATION NUMBER: US/07/940,652  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/827,021  
FILING DATE: 22-JAN-1992  
ATTORNEY/AGENT INFORMATION:



NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 199/201  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 66  
TYPE: NUCLEIC ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-07-940-652-13

Query Match 96.2%; Score 25; DB 1; Length 66;  
Best Local Similarity 100.0%; Pred. No. 8.8e-06;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ACTGAGCCACTGGATTAAAGCAGAG 26  
DB 66 ACTGAGCCACTGGATTAAAGCAGAG 42

RESULT 11  
US-08-255-553-13/c  
Sequence 13, Application US/08255553  
Patent No. 5451503  
GENERAL INFORMATION:  
APPLICANT: James J. Hogan et al.  
TITLE OF INVENTION: BRANCHED NUCLEIC ACID PROBES  
NUMBER OF SEQUENCES: 31  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 611 West Sixth Street  
CITY: Los Angeles  
STATE: California  
COUNTRY: USA  
ZIP: 90017  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS Version 3.30  
SOFTWARE: WordPerfect (Version 5.1)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/255,553  
FILING DATE: 07-JUN-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/940,652  
FILING DATE: 04-SEP-1992  
APPLICATION NUMBER: US/07/827,021  
FILING DATE: 22-JAN-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 199/201  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 66  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-255-553-13

Query Match 96.2%; Score 25; DB 1; Length 66;  
Best Local Similarity 100.0%; Pred. No. 8.8e-06;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ACTGAGCCACTGGATTAAAGCAGAG 26  
DB 66 ACTGAGCCACTGGATTAAAGCAGAG 42

RESULT 12  
US-08-761-131-2  
Sequence 2, Application US/08761131  
Patent No. 5804384  
GENERAL INFORMATION:  
APPLICANT: M ller, Uwe R. et al.  
TITLE OF INVENTION: DEVICES AND METHODS FOR DETECTING  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Vysis, Inc.  
STREET: 3100 Woodcreek Drive  
CITY: Downers Grove  
STATE: Illinois  
COUNTRY: U.S.A.  
ZIP: 60515  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/761,131  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Galloway, No. 5804384val B.  
REGISTRATION NUMBER: 33,595  
REFERENCE/DOCKET NUMBER: 01886/064001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 708-271-7417  
TELEFAX: 708-271-7048  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 40 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Genomic DNA  
US-08-761-131-2

Query Match 76.9%; Score 20; DB 1; Length 40;  
Best Local Similarity 100.0%; Pred. No. 0.0071;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ACTGAGCCACTGGATTAAAG 21  
DB 1 ACTGAGCCACTGGATTAAAG 20

RESULT 13  
US-08-761-131-4/c  
Sequence 4, Application US/08761131  
Patent No. 5804384  
GENERAL INFORMATION:  
APPLICANT: M ller, Uwe R. et al.  
TITLE OF INVENTION: DEVICES AND METHODS FOR DETECTING  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Vysis, Inc.  
STREET: 3100 Woodcreek Drive  
CITY: Downers Grove  
STATE: Illinois

```
/ COUNTRY: U.S.A.
/ ZIP: 60515
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: DOS
/ SOFTWARE: FastSeq Version 2.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/761,131
/ FILING DATE:
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER:
/ FILING DATE:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Galloway, No. 5804384val B.
/ REGISTRATION NUMBER: 33,595
/ REFERENCE/DOCKET NUMBER: 01886/064001
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 708-271-7417
/ TELEFAX: 708-271-7048
/ TELEX: 200154
/ INFORMATION FOR SEQ ID NO: 4:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 18 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: Genomic DNA
/ US-08-761-131-4

; Sequence 127, Application US/09358972
; Patent No. 6235480
; GENERAL INFORMATION:
; APPLICANT: Shultz, John W
; APPLICANT: Lewis, Martin K.
; APPLICANT: Lieppe, Donna
; APPLICANT: Mandrekar, Michelle
; APPLICANT: Kephart, Daniel
; APPLICANT: Rhodes, Richard B.
; APPLICANT: Andrews, Christine A.
; APPLICANT: Hartnett, James R.
; APPLICANT: Gu, Trent
; APPLICANT: Olson, Ryan J.
; APPLICANT: Wood, Keith W.
; APPLICANT: Welch, Roy
; TITLE OF INVENTION: Nucleic Acid Detection
; FILE REFERENCE: Pro-103 6868/75528
; CURRENT APPLICATION NUMBER: US/09/358,972
; CURRENT FILING DATE: 1999-07-22
; EARLIER APPLICATION NUMBER: 09/252,436
; EARLIER FILING DATE: 1999-02-18
; EARLIER APPLICATION NUMBER: 09/042,287
; EARLIER FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 290
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 127
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: probe for native bcr
US-09-358-972-127
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Query Match 69.2%; Score 18; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 0.1;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 2 ACTCAGCCACTGGATTTA 19
Db 18 ACTCAGCCACTGGATTTA 1
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RESULT 14
US-09-497-855A-38/c
; Sequence 38, Application US/09497855A
; Patent No. 6605432
; GENERAL INFORMATION:
; APPLICANT: Huang, Tim
; TITLE OF INVENTION: HIGH-THROUGHPUT METHODS FOR DETECTING DNA METHYLATION
; FILE REFERENCE: UMO1523
; CURRENT APPLICATION NUMBER: US/09/497,855A
; CURRENT FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: 60/120,592
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: 60/118,760
; PRIOR FILING DATE: 1999-02-05
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 38
; LENGTH: 128779
; TYPE: DNA
; ORGANISM: Homo sapiens;
US-09-497-855A-38
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Query Match 61.5%; Score 16; DB 4; Length 128779;  
Best Local Similarity 100.0%; Pred. No. 2;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 11 CTGGATTTAAGCAGAG 26
Db 47398 CTGGATTTAAGCAGAG 47383
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RESULT 15  
US-09-358-972-127

Query Match 57.7%; Score 15; DB 3; Length 22;  
Best Local Similarity 100.0%; Pred. No. 5.7;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 TGGATTTAAGCAGAG 15
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Search completed: May 27, 2004, 12:08:04  
Job time : 34.15 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: May 27, 2004, 14:58:36 ; Search time 151.125 Seconds  
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Title: US-09-121-239-27

Perfect score: 26

Sequence: 1 CACTCAGCCACTGGATTAAAGCAGAG 26

Scoring table: OLIGO NUC

Gapop 60.0 , Gapext 60.0

Searched: 2960401 seqs, 2274450654 residues

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Minimum DB seq length: 0

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Post-processing: Listing first 45 summaries

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- 10: /cgn2\_6/ptodata/2/pubpna/US09B\_PUBCOMB.seq.\*
- 11: /cgn2\_6/ptodata/2/pubpna/US09C\_PUBCOMB.seq.\*
- 12: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq.\*
- 13: /cgn2\_6/ptodata/2/pubpna/US10A\_PUBCOMB.seq.\*
- 14: /cgn2\_6/ptodata/2/pubpna/US10B\_PUBCOMB.seq.\*
- 15: /cgn2\_6/ptodata/2/pubpna/US10C\_PUBCOMB.seq.\*
- 16: /cgn2\_6/ptodata/2/pubpna/US10\_PUB.seq.\*
- 17: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq.\*
- 18: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq.\*
- 19: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	26	100.0	102	13	US-09-742-675-1
C 2	26	100.0	504	10	US-09-918-995-25454
C 3	26	100.0	542	9	US-09-796-692-8117
C 4	26	100.0	542	15	US-10-040-862-8117
C 5	26	100.0	542	16	US-10-057-475B-8117
C 6	26	100.0	542	16	US-10-154-884B-8117
C 7	26	100.0	1078	15	US-10-228-811-1
C 8	26	100.0	4739	9	US-09-954-531-586
C 9	26	100.0	4739	13	US-10-193-651-22
C 10	25	96.2	40	9	US-09-790-417-125
C 11	25	96.2	41	9	US-09-790-417-126
C 12	19	73.1	596	9	US-09-796-692-8967
C 13	19	73.1	596	15	US-10-040-862-8967
C 14	19	73.1	596	16	US-10-057-475B-8967

15	19	73.1	596	16	US-10-154-884B-8967	Sequence 8967, Ap
C 16	16	61.5	403	10	US-09-873-367C-524	Sequence 524, App
C 17	16	61.5	463	15	US-10-060-036-1266	Sequence 1266, Ap
C 18	16	61.5	476	9	US-09-864-761-10674	Sequence 10674, A
C 19	16	61.5	531	13	US-10-240-425-1354	Sequence 1354, Ap
C 20	16	61.5	982	13	US-10-027-632-263225	Sequence 263225,
C 21	16	61.5	982	16	US-10-027-632-263225	Sequence 263225,
C 22	16	61.5	1357	9	US-09-799-777-87	Sequence 87, Appl
C 23	16	61.5	1769	16	US-10-398-221-1846	Sequence 1846, Ap
C 24	16	61.5	5296	16	US-10-398-221-3744	Sequence 3744, Ap
C 25	16	61.5	128779	15	US-10-081-327-38	Sequence 38, Appl
C 26	16	61.5	133760	13	US-10-240-425-1101	Sequence 1101, Ap
C 27	15	57.7	22	9	US-09-790-417-127	Sequence 127, App
C 28	15	57.7	22	9	US-09-790-417-128	Sequence 128, App
C 29	15	57.7	22	10	US-09-788-847-97	Sequence 97, Appl
C 30	15	57.7	22	10	US-09-788-847-98	Sequence 98, Appl
C 31	15	57.7	40	13	US-10-382-634-15	Sequence 15, Appl
C 32	15	57.7	40	15	US-10-349-320-14	Sequence 14, Appl
C 33	15	57.7	480	13	US-10-335-977-276	Sequence 276, App
C 34	15	57.7	490	13	US-10-027-632-79686	Sequence 79686, A
C 35	15	57.7	490	16	US-10-027-632-79686	Sequence 79686, A
C 36	15	57.7	675	16	US-10-341-961A-45	Sequence 45, Appl
C 37	15	57.7	882	13	US-10-335-977-277	Sequence 277, App
C 38	15	57.7	882	13	US-10-335-977-278	Sequence 278, App
C 39	15	57.7	1095	13	US-10-424-599-57246	Sequence 57246, A
C 40	15	57.7	1488	16	US-10-369-493-31592	Sequence 31592, A
C 41	15	57.7	1963	13	US-10-170-385-104	Sequence 104, App
C 42	15	57.7	1963	16	US-10-094-749-797	Sequence 797, App
C 43	15	57.7	1991	9	US-09-864-761-4800	Sequence 4800, Ap
C 44	15	57.7	2335	9	US-09-917-800A-1569	Sequence 1569, Ap
C 45	15	57.7	2335	12	US-10-152-319A-1538	Sequence 1538, Ap

ALIGNMENTS

RESULT 1  
US-09-742-675-1/c  
; Sequence 1, Application US/09742675  
; Publication No. US20020049174A1  
; GENERAL INFORMATION:  
; APPLICANT: Stocks, Martin  
; APPLICANT: Rabbitts, Terrence  
; TITLE OF INVENTION: Structured Antisense Nucleic Acid Molecules  
; FILE REFERENCE: 18396/1490  
; CURRENT APPLICATION NUMBER: US/09/742,675  
; CURRENT FILING DATE: 2003-02-14  
; PRIOR APPLICATION NUMBER: PCT/GB99/01956  
; PRIOR FILING DATE: 1999-06-23  
; PRIOR APPLICATION NUMBER: US 60/090867  
; PRIOR FILING DATE: 1998-06-23  
; PRIOR APPLICATION NUMBER: GB 9813531 2  
; PRIOR FILING DATE: 1998-06-23  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; LENGTH: 102  
; TYPE: RNA  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: has210 antisense RNA  
US-09-742-675-1

Query Match 100.0%; Score 26; DB 13; Length 102;  
Best Local Similarity 100.0%; Pred No. 1.9e-05;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CACTCAGCCACTGGATTAAAGCAGAG 26

Db 56 CACTCAGCCACTGGATTAAAGCAGAG 31

RESULT 2

US-09-918-995-25454  
; Sequence 25454, Application US/09918995  
; Publication No. US20030073623A1  
; GENERAL INFORMATION:  
; APPLICANT: Hyseq, Inc.  
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED  
; FILE REFERENCE: 20411-756  
; CURRENT APPLICATION NUMBER: US/09/918,995  
; CURRENT FILING DATE: 2001-07-30  
; PRIOR APPLICATION NUMBER: US/09/235,076  
; PRIOR FILING DATE: 1999-01-20  
; NUMBER OF SEQ ID NOS: 38054  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 25454  
; LENGTH: 504  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1)...(504)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-918-995-25454

Query Match 100.0%; Score 26; DB 10; Length 504;  
Best Local Similarity 100.0%; Pred. No. 1.9e-05;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CACTAGCCCACTGGATTAAAGCAGAG 26  
Db 321 CACTAGCCCACTGGATTAAAGCAGAG 346

RESULT 3  
US-09-796-692-8117  
; Sequence 8117, Application US/09796692  
; Publication No. US20020198362A1  
; GENERAL INFORMATION:  
; APPLICANT: Gaiger, Alexander  
; APPLICANT: Algate, Paul A.  
; APPLICANT: Mannion, Jane  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY  
; FILE REFERENCE: 2077.001200  
; CURRENT APPLICATION NUMBER: US/09/796,692  
; CURRENT FILING DATE: 2001-03-01  
; PRIOR APPLICATION NUMBER: 60/186,126  
; PRIOR FILING DATE: 2000-03-01  
; PRIOR APPLICATION NUMBER: 60/190,479  
; PRIOR FILING DATE: 2000-03-17  
; PRIOR APPLICATION NUMBER: 60/200,545  
; PRIOR FILING DATE: 2000-04-27  
; PRIOR APPLICATION NUMBER: 60/200,303  
; PRIOR FILING DATE: 2000-04-28  
; PRIOR APPLICATION NUMBER: 60/200,779  
; PRIOR FILING DATE: 2000-04-28  
; PRIOR APPLICATION NUMBER: 60/200,999  
; PRIOR FILING DATE: 2000-05-01  
; PRIOR APPLICATION NUMBER: 60/202,084  
; PRIOR FILING DATE: 2000-05-04  
; PRIOR APPLICATION NUMBER: 60/206,201  
; PRIOR FILING DATE: 2000-05-22  
; PRIOR APPLICATION NUMBER: 60/218,950  
; PRIOR FILING DATE: 2000-07-14  
; PRIOR APPLICATION NUMBER: 60/222,903  
; PRIOR FILING DATE: 2000-08-03  
; PRIOR APPLICATION NUMBER: 60/223,416  
; PRIOR FILING DATE: 2000-08-04  
; PRIOR APPLICATION NUMBER: 60/223,378  
; PRIOR FILING DATE: 2000-08-07  
; NUMBER OF SEQ ID NOS: 9597  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 8117

; LENGTH: 542  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-796-692-8117

Query Match 100.0%; Score 26; DB 9; Length 542;  
Best Local Similarity 100.0%; Pred. No. 1.9e-05;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CACTAGCCCACTGGATTAAAGCAGAG 26  
Db 515 CACTAGCCCACTGGATTAAAGCAGAG 540

RESULT 4  
US-10-040-862-8117  
; Sequence 8117, Application US/10040862  
; Publication No. US20030078396A1  
; GENERAL INFORMATION:  
; APPLICANT: Gaiger, Alexander  
; APPLICANT: Algate, Paul A.  
; APPLICANT: Mannion, Jane  
; APPLICANT: Retter, Marc  
; APPLICANT: Corixa Corporation  
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy  
; FILE REFERENCE: 014058-013520US  
; CURRENT APPLICATION NUMBER: US/10/040,862  
; CURRENT FILING DATE: 2001-11-06  
; PRIOR APPLICATION NUMBER: US 60/186,126  
; PRIOR FILING DATE: 2000-03-01  
; PRIOR APPLICATION NUMBER: US 60/190,479  
; PRIOR FILING DATE: 2000-03-17  
; PRIOR APPLICATION NUMBER: US 60/200,545  
; PRIOR FILING DATE: 2000-04-27  
; PRIOR APPLICATION NUMBER: US 60/200,303  
; PRIOR FILING DATE: 2000-04-28  
; PRIOR APPLICATION NUMBER: US 60/200,779  
; PRIOR FILING DATE: 2000-04-28  
; PRIOR APPLICATION NUMBER: US 60/200,999  
; PRIOR FILING DATE: 2000-05-01  
; PRIOR APPLICATION NUMBER: US 60/202,084  
; PRIOR FILING DATE: 2000-05-04  
; PRIOR APPLICATION NUMBER: US 60/206,201  
; PRIOR FILING DATE: 2000-05-22  
; PRIOR APPLICATION NUMBER: US 60/218,950  
; PRIOR FILING DATE: 2000-07-14  
; PRIOR APPLICATION NUMBER: US 60/222,903  
; PRIOR FILING DATE: 2000-08-03  
; PRIOR APPLICATION NUMBER: US 60/223,416  
; PRIOR FILING DATE: 2000-08-04  
; PRIOR APPLICATION NUMBER: US 60/223,378  
; PRIOR FILING DATE: 2000-08-07  
; PRIOR APPLICATION NUMBER: US 09/796,692  
; PRIOR FILING DATE: 2001-03-01  
; NUMBER OF SEQ ID NOS: 10467  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 8117  
; LENGTH: 542  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-040-862-8117

Query Match 100.0%; Score 26; DB 15; Length 542;  
Best Local Similarity 100.0%; Pred. No. 1.9e-05;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CACTAGCCCACTGGATTAAAGCAGAG 26  
Db 515 CACTAGCCCACTGGATTAAAGCAGAG 540

RESULT 5

US-10-057-475B-8117  
; Sequence 8117, Application US/10057475B  
; Publication No. US2004002068A1  
; GENERAL INFORMATION:  
; APPLICANT: Gaiger, Alexander  
; APPLICANT: Algate, Paul A.  
; APPLICANT: Mannion, Jane  
; APPLICANT: Clapper, Jonathan David  
; APPLICANT: Wang, Aijun  
; APPLICANT: Ordonez, Nadia  
; APPLICANT: Carter, Lauren  
; APPLICANT: McNeill, Patricia Dianne  
; APPLICANT: Corixa Corporation  
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy  
; FILE REFERENCE: 014058-014402US  
; CURRENT APPLICATION NUMBER: US/10/057,475B  
; CURRENT FILING DATE: 2002-01-22  
; PRIOR APPLICATION NUMBER: US 60/186,126  
; PRIOR FILING DATE: 2000-03-01  
; PRIOR APPLICATION NUMBER: US 60/190,479  
; PRIOR FILING DATE: 2000-03-17  
; PRIOR APPLICATION NUMBER: US 60/200,545  
; PRIOR FILING DATE: 2000-04-27  
; PRIOR APPLICATION NUMBER: US 60/200,303  
; PRIOR FILING DATE: 2000-04-28  
; PRIOR APPLICATION NUMBER: US 60/200,779  
; PRIOR FILING DATE: 2000-04-28  
; PRIOR APPLICATION NUMBER: US 60/200,999  
; PRIOR FILING DATE: 2000-05-01  
; PRIOR APPLICATION NUMBER: US 60/202,084  
; PRIOR FILING DATE: 2000-05-04  
; PRIOR APPLICATION NUMBER: US 60/206,201  
; PRIOR FILING DATE: 2000-05-22  
; PRIOR APPLICATION NUMBER: US 60/218,950  
; PRIOR FILING DATE: 2000-07-14  
; PRIOR APPLICATION NUMBER: US 60/222,903  
; PRIOR FILING DATE: 2000-08-03  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 10979  
; SOFTWARE: FastSeq For Windows Version 3.0  
; SEQ ID NO 8117  
; LENGTH: 542  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-057-475B-8117

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Best Local Similarity 100.0%; Pred. No. 1.9e-05;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 515 CACTCAGCCACTGGATTAAAGCAGAG 540

## RESULT 6

US-10-154-884B-8117  
; Sequence 8117, Application US/10154884B  
; Publication No. US20040005561A1  
; GENERAL INFORMATION:  
; APPLICANT: Gaiger, Alexander  
; APPLICANT: Algate, Paul A.  
; APPLICANT: Mannion, Jane  
; APPLICANT: Retter, Marc W.  
; APPLICANT: Corixa Corporation  
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy  
; FILE REFERENCE: 014058-013521US  
; CURRENT APPLICATION NUMBER: US/10/154,884B  
; CURRENT FILING DATE: 2002-05-23  
; PRIOR APPLICATION NUMBER: US 60/186,126  
; PRIOR FILING DATE: 2000-03-01

; PRIOR APPLICATION NUMBER: US 60/190,479  
; PRIOR FILING DATE: 2000-03-17  
; PRIOR APPLICATION NUMBER: US 60/200,545  
; PRIOR FILING DATE: 2000-04-27  
; PRIOR APPLICATION NUMBER: US 60/200,303  
; PRIOR FILING DATE: 2000-04-28  
; PRIOR APPLICATION NUMBER: US 60/200,779  
; PRIOR FILING DATE: 2000-04-28  
; PRIOR APPLICATION NUMBER: US 60/200,999  
; PRIOR FILING DATE: 2000-05-01  
; PRIOR APPLICATION NUMBER: US 60/202,084  
; PRIOR FILING DATE: 2000-05-04  
; PRIOR APPLICATION NUMBER: US 60/206,201  
; PRIOR FILING DATE: 2000-05-22  
; PRIOR APPLICATION NUMBER: US 60/218,950  
; PRIOR FILING DATE: 2000-07-14  
; PRIOR APPLICATION NUMBER: US 60/222,903  
; PRIOR FILING DATE: 2000-08-03  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 11290  
; SOFTWARE: FastSeq For Windows Version 3.0  
; SEQ ID NO 8117  
; LENGTH: 542  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-154-884B-8117

Query Match 100.0%; Score 26; DB 16; Length 542;  
Best Local Similarity 100.0%; Pred. No. 1.9e-05;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CACTCAGCCACTGGATTAAAGCAGAG 26  
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DB 515 CACTCAGCCACTGGATTAAAGCAGAG 540

## RESULT 7

US-10-228-811-1  
; Sequence 1, Application US/10228811  
; Publication No. US20030054392A1  
; GENERAL INFORMATION:  
; APPLICANT: Wittig, Prof. Burghardt  
; APPLICANT: Junghans, Claas  
; TITLE OF INVENTION: Design Principle for Constructing Expression Constructs for Gene  
; FILE REFERENCE: XI 597/99  
; CURRENT APPLICATION NUMBER: US/10/228,811  
; CURRENT FILING DATE: 2002-08-27  
; PRIOR APPLICATION NUMBER: DE 196 48 625.4  
; PRIOR FILING DATE: 1996-11-13  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 1078  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; NAME/KEY: gene  
; LOCATION: (1)..(1078)  
; OTHER INFORMATION: bcr3=abl2; Oligo DNA Dumbbell  
; FEATURE:  
; NAME/KEY: misc\_binding  
; LOCATION: (1)..(2)  
; OTHER INFORMATION: intramolecular binding site; the T-nucleotides at position 1 to  
; FEATURE:  
; NAME/KEY: misc\_binding  
; LOCATION: (1077)..(1078)  
; OTHER INFORMATION: intramolecular binding site; the T-nucleotides at position 1077  
; OTHER INFORMATION: to 1078 can be modified with amino or caroxy features  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Strandness: both; nucleic  
; OTHER INFORMATION: acid (linear); hypothetical: No. US20030054392A1 anti-sense: No

US-10-228-811-1

Query Match 100.0%; Score 26; DB 15; Length 1078;  
Best Local Similarity 100.0%; Pred. No. 1.9e-05;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CACTAGCCCACTGGATTAAAGCAG 26  
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Db 744 CACTAGCCCACTGGATTAAAGCAG 769

RESULT 8

US-09-954-531-586  
; Sequence 586, Application US/09954531  
; Patent No. US20020165180A1  
; GENERAL INFORMATION:  
; APPLICANT: Weaver, Zoe  
; TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Cand  
; FILE REFERENCE: 689290-77  
; CURRENT APPLICATION NUMBER: US/09/954,531  
; CURRENT FILING DATE: 2002-05-02  
; PRIOR APPLICATION NUMBER: US/60/233,133  
; PRIOR FILING DATE: 2000-09-18  
; PRIOR APPLICATION NUMBER: US/60/234,009  
; PRIOR FILING DATE: 2000-09-20  
; PRIOR APPLICATION NUMBER: US/60/234,034  
; PRIOR FILING DATE: 2000-09-20  
; PRIOR APPLICATION NUMBER: US/60/234,509  
; PRIOR FILING DATE: 2000-09-22  
; PRIOR APPLICATION NUMBER: US/60/234,567  
; PRIOR FILING DATE: 2000-09-22  
; NUMBER OF SEQ ID NOS: 1392  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 586  
; LENGTH: 4739  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-954-531-586

Query Match 100.0%; Score 26; DB 9; Length 4739;  
Best Local Similarity 100.0%; Pred. No. 1.9e-05;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CACTAGCCCACTGGATTAAAGCAG 26  
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Db 3240 CACTAGCCCACTGGATTAAAGCAG 3265

RESULT 9

US-10-193-651-22  
; Sequence 22, Application US/10193651  
; Publication No. US20030064061A1  
; GENERAL INFORMATION:  
; APPLICANT: Zhao, Xun  
; APPLICANT: Ghaffari, Saghi  
; APPLICANT: Lodish, Harvey P.  
; APPLICANT: Malashkevich, Vladimir N.  
; APPLICANT: Kim, Peter S.  
; TITLE OF INVENTION: Bcr-Abl Oligomerization Domain  
; FILE REFERENCE: 0399.2031-001  
; CURRENT APPLICATION NUMBER: US/10/193,651  
; CURRENT FILING DATE: 2002-11-19  
; PRIOR APPLICATION NUMBER: US 60/303,857  
; PRIOR FILING DATE: 2001-07-09  
; NUMBER OF SEQ ID NOS: 22  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 22  
; LENGTH: 4739  
; TYPE: DNA  
; ORGANISM: Homo Sapiens  
; FEATURE:

; OTHER INFORMATION: Bcr nucleic acid  
US-10-193-651-22

Query Match 100.0%; Score 26; DB 13; Length 4739;  
Best Local Similarity 100.0%; Pred. No. 1.9e-05;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CACTAGCCCACTGGATTAAAGCAG 26  
|||||  
Db 3240 CACTAGCCCACTGGATTAAAGCAG 3265

RESULT 10

US-09-790-417-125/c  
; Sequence 125, Application US/09790417  
; Patent No. US20010031470A1  
; GENERAL INFORMATION:  
; APPLICANT: Shultz, John W  
; APPLICANT: Lewis, Martin K.  
; APPLICANT: Lieppe, Donna  
; APPLICANT: Mandrekar, Michelle  
; APPLICANT: Kephart, Daniel  
; APPLICANT: Rhodes, Richard B.  
; APPLICANT: Andrews, Christine A.  
; APPLICANT: Hartnett, James R.  
; APPLICANT: Gu, Trent  
; APPLICANT: Olson, Ryan J.  
; APPLICANT: Wood, Keith W.  
; APPLICANT: Welch, Roy  
; TITLE OF INVENTION: Nucleic Acid Detection  
; FILE REFERENCE: Pro-103 6868/75528  
; CURRENT APPLICATION NUMBER: US/09/790,417  
; CURRENT FILING DATE: 2001-02-22  
; PRIOR APPLICATION NUMBER: 09/358,972  
; PRIOR FILING DATE: 1999-07-21  
; PRIOR APPLICATION NUMBER: 09/042,287  
; PRIOR FILING DATE: 1998-03-13  
; NUMBER OF SEQ ID NOS: 290  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 125  
; LENGTH: 40  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: native bcr  
US-09-790-417-125

Query Match 96.2%; Score 25; DB 9; Length 40;  
Best Local Similarity 100.0%; Pred. No. 7.4e-05;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ACTAGCCCACTGGATTAAAGCAG 26  
|||||  
Db 40 ACTAGCCCACTGGATTAAAGCAG 16

RESULT 11

US-09-790-417-126/c  
; Sequence 126, Application US/09790417  
; Patent No. US20010031470A1  
; GENERAL INFORMATION:  
; APPLICANT: Shultz, John W  
; APPLICANT: Lieppe, Donna  
; APPLICANT: Mandrekar, Michelle  
; APPLICANT: Kephart, Daniel  
; APPLICANT: Rhodes, Richard B.  
; APPLICANT: Andrews, Christine A.  
; APPLICANT: Hartnett, James R.  
; APPLICANT: Gu, Trent  
; APPLICANT: Olson, Ryan J.  
; APPLICANT: Wood, Keith W.  
; APPLICANT: Welch, Roy

; TITLE OF INVENTION: Nucleic Acid Detection  
 ; FILE REFERENCE: Pro-103 6868/75528  
 ; CURRENT APPLICATION NUMBER: US/09/790,417  
 ; PRIOR FILING DATE: 2001-02-22  
 ; PRIOR APPLICATION NUMBER: 09/358,972  
 ; PRIOR FILING DATE: 1999-07-21  
 ; PRIOR APPLICATION NUMBER: 09/042,287  
 ; PRIOR FILING DATE: 1998-03-13  
 ; NUMBER OF SEQ ID NOS: 290  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 126  
 ; LENGTH: 41  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; OTHER INFORMATION: bcr/abl translocation  
 US-09-790-417-126

Query Match 96.2%; Score 25; DB 9; Length 41;  
 Best Local Similarity 100.0%; Pred. No. 7.4e-05;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ACTCAGCCACTGGATTAAAGCAG 26  
 Db 41 ACTCAGCCACTGGATTAAAGCAG 17

RESULT 12  
 US-09-796-692-8967  
 ; Sequence 8967, Application US/09796692  
 ; Publication No. US20020198362A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Gaiger, Alexander  
 ; APPLICANT: Algate, Paul A.  
 ; APPLICANT: Mannion, Jane  
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY  
 ; TITLE OF INVENTION: HEMATOLOGICAL MALIGNANCIES  
 ; FILE REFERENCE: 2077.001200  
 ; CURRENT APPLICATION NUMBER: US/09/796,692  
 ; CURRENT FILING DATE: 2001-03-01  
 ; PRIOR APPLICATION NUMBER: 60/186,126  
 ; PRIOR FILING DATE: 2000-03-01  
 ; PRIOR APPLICATION NUMBER: 60/190,479  
 ; PRIOR FILING DATE: 2000-03-17  
 ; PRIOR APPLICATION NUMBER: 60/200,545  
 ; PRIOR FILING DATE: 2000-04-27  
 ; PRIOR APPLICATION NUMBER: 60/200,303  
 ; PRIOR FILING DATE: 2000-04-28  
 ; PRIOR APPLICATION NUMBER: 60/200,779  
 ; PRIOR FILING DATE: 2000-04-28  
 ; PRIOR APPLICATION NUMBER: 60/200,999  
 ; PRIOR FILING DATE: 2000-05-01  
 ; PRIOR APPLICATION NUMBER: 60/202,084  
 ; PRIOR FILING DATE: 2000-05-04  
 ; PRIOR APPLICATION NUMBER: 60/206,201  
 ; PRIOR FILING DATE: 2000-05-22  
 ; PRIOR APPLICATION NUMBER: 60/218,950  
 ; PRIOR FILING DATE: 2000-07-14  
 ; PRIOR APPLICATION NUMBER: 60/222,903  
 ; PRIOR FILING DATE: 2000-08-03  
 ; PRIOR APPLICATION NUMBER: 60/223,416  
 ; PRIOR FILING DATE: 2000-08-04  
 ; PRIOR APPLICATION NUMBER: 60/223,378  
 ; PRIOR FILING DATE: 2000-08-07  
 ; NUMBER OF SEQ ID NOS: 9597  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 8967  
 ; LENGTH: 596  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
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 ; LOCATION: (551)  
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 US-09-796-692-8967

Query Match 73.1%; Score 19; DB 9; Length 596;  
 Best Local Similarity 100.0%; Pred. No. 0.24;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CCACTGGATTAAAGCAG 26  
 Db 522 CCACTGGATTAAAGCAG 540

RESULT 13  
 US-10-040-862-8967  
 ; Sequence 8967, Application US/10040862  
 ; Publication No. US20030078396A1

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; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; FILE REFERENCE: 014058-013520US
; CURRENT APPLICATION NUMBER: US/10/040,862
; CURRENT FILING DATE: 2001-11-06
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: US 60/223,416
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: US 60/223,378
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: US 09/796,692
; PRIOR FILING DATE: 2001-03-01
; NUMBER OF SEQ ID NOS: 10467
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8967
; LENGTH: 596
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (13)
; OTHER INFORMATION: n=A,T,C or G
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (47)
; OTHER INFORMATION: n=A,T,C or G
; FEATURE:
; NAME/KEY: unsure
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; OTHER INFORMATION: n=A,T,C or G
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (155)
; OTHER INFORMATION: n=A,T,C or G
; FEATURE:
; NAME/KEY: unsure

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; LOCATION: (196)
; OTHER INFORMATION: n=A,T,C or G
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; NAME/KEY: unsure
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; NAME/KEY: unsure
; LOCATION: (281)
; OTHER INFORMATION: n=A,T,C or G
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (282)
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; US-10-040-862-8967

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Query Match 73.1%; Score 19; DB 15; Length 596;  
 Best Local Similarity 100.0%; Pred. No. 0.24;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      8 CCACTGCGATTTAAGCAGAG 26
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Db      522 CCACTGCGATTTAAGCAGAG 540

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RESULT 14
US-10-057-475B-8967
; Sequence 8967, Application US/10057475B
; Publication No. US20040002068A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Clapper, Jonathan David
; APPLICANT: Wang, Aijun
; APPLICANT: Ordonez, Nadia
; APPLICANT: Carter, Lauren

```



; APPLICANT: McNeill, Patricia Dianne  
 ; APPLICANT: Corixa Corporation  
 ; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy  
 ; TITLE OF INVENTION: Hematological Malignancies  
 ; FILE REFERENCE: 014058-014402US  
 ; CURRENT APPLICATION NUMBER: US/10/057,475B  
 ; CURRENT FILING DATE: 2002-01-22  
 ; PRIOR APPLICATION NUMBER: US 60/186,126  
 ; PRIOR FILING DATE: 2000-03-01  
 ; PRIOR APPLICATION NUMBER: US 60/190,479  
 ; PRIOR FILING DATE: 2000-03-17  
 ; PRIOR APPLICATION NUMBER: US 60/200,545  
 ; PRIOR FILING DATE: 2000-04-27  
 ; PRIOR APPLICATION NUMBER: US 60/200,303  
 ; PRIOR FILING DATE: 2000-04-28  
 ; PRIOR APPLICATION NUMBER: US 60/200,779  
 ; PRIOR FILING DATE: 2000-04-28  
 ; PRIOR APPLICATION NUMBER: US 60/200,999  
 ; PRIOR FILING DATE: 2000-05-01  
 ; PRIOR APPLICATION NUMBER: US 60/202,084  
 ; PRIOR FILING DATE: 2000-05-04  
 ; PRIOR APPLICATION NUMBER: US 60/206,201  
 ; PRIOR FILING DATE: 2000-05-22  
 ; PRIOR APPLICATION NUMBER: US 60/218,950  
 ; PRIOR FILING DATE: 2000-07-14  
 ; PRIOR APPLICATION NUMBER: US 60/222,903  
 ; PRIOR FILING DATE: 2000-08-03  
 ; Remaining Prior Application data removed - See File Wrapper or PALM.  
 ; NUMBER OF SEQ ID NOS: 10979  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 8967  
 ; LENGTH: 596  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: misc\_feature  
 ; LOCATION: (1)...(596)  
 ; OTHER INFORMATION: n = g, a, c or t  
 US-10-057-475B-8967

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 Matches 19; Conservative 0; Mismatches 0;

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 Db 522 CCACTGGATTAAAGCAGAG 540

RESULT 15  
 US-10-154-884B-8967  
 ; Sequence 8967, Application US/10154884B  
 ; Publication No. US20040005561A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Gaiger, Alexander  
 ; APPLICANT: Algate, Paul A.  
 ; APPLICANT: Mannion, Jane  
 ; APPLICANT: Retter, Marc W.  
 ; APPLICANT: Corixa Corporation  
 ; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy  
 ; TITLE OF INVENTION: Hematological Malignancies  
 ; FILE REFERENCE: 014058-013521US  
 ; CURRENT APPLICATION NUMBER: US/10/154,884B  
 ; CURRENT FILING DATE: 2002-05-23  
 ; PRIOR APPLICATION NUMBER: US 60/186,126  
 ; PRIOR FILING DATE: 2000-03-01  
 ; PRIOR APPLICATION NUMBER: US 60/190,479  
 ; PRIOR FILING DATE: 2000-03-17  
 ; PRIOR APPLICATION NUMBER: US 60/200,545  
 ; PRIOR FILING DATE: 2000-04-27  
 ; PRIOR APPLICATION NUMBER: US 60/200,303  
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 ; PRIOR APPLICATION NUMBER: US 60/200,779

; PRIOR FILING DATE: 2000-04-28  
 ; PRIOR APPLICATION NUMBER: US 60/200,999  
 ; PRIOR FILING DATE: 2000-05-01  
 ; PRIOR APPLICATION NUMBER: US 60/202,084  
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 ; PRIOR APPLICATION NUMBER: US 60/218,950  
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 ; PRIOR APPLICATION NUMBER: US 60/222,903  
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 ; Remaining Prior Application data removed - See File Wrapper or PALM.  
 ; NUMBER OF SEQ ID NOS: 11290  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 8967  
 ; LENGTH: 596  
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 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
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 ; OTHER INFORMATION: n = g, a, c or t  
 US-10-154-884B-8967

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 Best Local Similarity 100.0%; Pred. No. 0.24; Indels 0; Gaps 0;  
 Matches 19; Conservative 0; Mismatches 0;

QY 8 CCACTGGATTAAAGCAGAG 26  
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 Db 522 CCACTGGATTAAAGCAGAG 540

Search completed: May 27, 2004, 18:33:25  
 Job time : 153.125 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 26, 2004, 22:44:40 ; Search time 1349.08 Seconds  
(without alignments)  
575.518 Million cell updates/sec

Title: US-09-121-239-27

Perfect score: 26

Sequence: 1 CACTCAGCCACTGGATTAAAGCAGAG 26

Scoring table: OLIGO NUC  
Gapop 60.0 , Gapext 60.0

Searched: 27513289 seqs, 14931090276 residues

Word size : 0

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

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7: em\_estro:\*  
8: em\_htc:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_htc:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
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16: em\_estom:\*  
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18: em\_gss\_inv:\*  
19: em\_gss\_pin:\*  
20: em\_gss\_vrt:\*  
21: em\_gss\_fun:\*  
22: em\_gss\_mam:\*  
23: em\_gss\_mus:\*  
24: em\_gss\_pro:\*  
25: em\_gss\_rod:\*  
26: em\_gss\_pbg:\*  
27: em\_gss\_vrl:\*  
28: gb\_gss1:\*  
29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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3	26	100.0	314	9	AA38025 EST42869
4	26	100.0	377	10	BF800308 CM4-C1006

c	5	26	100.0	417	10	BF512134	UI-H-B13-
c	6	26	100.0	437	10	BF873838	IL3-ET011
	7	26	100.0	549	12	BM854793	K-EST0137
	8	26	100.0	550	12	BM824089	K-EST0095
	9	26	100.0	590	10	BF953848	MRO-NN117
	10	26	100.0	605	10	AW961897	EST373970
	11	26	100.0	621	10	BE267891	601125452
	12	26	100.0	642	10	BE019411	bb55b12.y
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	14	26	100.0	655	10	BE514596	601316940
	15	26	100.0	684	10	BF530440	602071562
	16	26	100.0	712	10	BE397695	601289802
	17	26	100.0	734	10	BE513555	601315079
	18	26	100.0	741	10	BE265121	601193661
	19	26	100.0	751	12	BM716187	UI-E-C11-
	20	26	100.0	777	13	BU597369	AGENCOURT
	21	26	100.0	796	10	BE743192	601573879
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	23	26	100.0	844	14	CD652568	AGENCOURT
	24	26	100.0	853	13	BQ227532	AGENCOURT
	25	26	100.0	875	10	BF241073	601880612
	26	26	100.0	878	10	BF338795	602036226
	27	26	100.0	880	13	BQ422888	AGENCOURT
	28	26	100.0	880	13	BU539742	AGENCOURT
	29	26	100.0	888	13	BU540933	AGENCOURT
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	31	26	100.0	903	13	BQ441890	AGENCOURT
	32	26	100.0	918	13	BQ212925	AGENCOURT
	33	26	100.0	955	13	BQ945725	AGENCOURT
	34	26	100.0	965	12	BQ770328	602742351
	35	26	100.0	975	12	BG392048	602410011
	36	26	100.0	981	12	BG119450	602349240
	37	26	100.0	1001	13	BQ946606	AGENCOURT
	38	26	100.0	1021	13	BQ896733	AGENCOURT
	39	26	100.0	1503	14	CD245822	AGENCOURT
	40	23	88.5	637	14	CB267185	1006091 H
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#### ALIGNMENTS

RESULT 1  
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DEFINITION  
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H55528.1 GI:1108394  
VERSION  
EST.  
KEYWORDS  
SOURCE  
ORGANISM  
Homo sapiens (human)  
Homo sapiens  
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE  
1 (bases 1 to 75)  
Trotter, J.A., Long, K.R., Murrell, J.R., Stotler, C.J., Gusella, J.F.  
and Buckler, A.J.  
An expression-independent catalog of genes from human chromosome 22  
Genome Res. 5 (3), 214-224 (1995)  
JOURNAL  
MEDLINE  
PUBMED  
COMMENT  
Contact: Buckler AJ  
Molecular Neurogenetics Unit  
Massachusetts General Hospital  
Building 149, 13th St., Charlestown MA 02129  
Tel: 6177249616  
Fax: 6177265736  
Email: buckler@helix.mgh.harvard.edu  
Seq primer: T3.

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FEATURES
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  /lab_host="E. coli DH5a"
  /notes="Vector: pBluescriptIIKS+; Site_1: Sal I; Site_2:
  Bam HI (destroyed); Exons were isolated from human
  chromosome 22 specific cosmids using a modification of
  the method of exon amplification (Proc. Natl. Acad. Sci.
  USA 88:4005-4009, 1991). Amplified exons were digested
  with Sal I and Bgl II and subsequently cloned into
  pBluescriptIIKS+ at the Sal I and Bam HI sites."

ORIGIN
Query Match      100.0%; Score 26; DB 14; Length 75;
Best Local Similarity 100.0%; Pred. No. 0.0001;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CACTGAGCCACTGGATTAAAGCAGAG 26
    |||||||
Db 45 CACTGAGCCACTGGATTAAAGCAGAG 70

RESULT 2
AA371833 277 bp mRNA linear EST 21-APR-1997
LOCUS EST83693 Pituitary gland, subtracted (prolactin/growth hormone) II
DEFINITION Homo sapiens cDNA 5' end similar to breakpoint cluster region, mRNA
sequence.
ACCESSION AA371833.1 GI:2024183
VERSION EST.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 277)
Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A.,
Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D.,
White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C.,
Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D.,
Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S.,
Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S.Jr.,
Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M.,
Moreno-Palauques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,
Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R.,
Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y.,
Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,G.A.,
Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A.,
He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K.,
Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Meissner,P.S., Olsen,H.,
Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M.,
Dillion,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C.,
Fraser,C.M. and Venter,J.C.
Initial assessment of human gene diversity and expression patterns
based upon 83 million nucleotides of cDNA sequence
NATURE 377 (6547 Suppl), 3-174 (1995)
JOURNAL MEDLINE
PUBMED 7566098
COMMENT Other ESTs: THCI166164
Contact: Kerlavage, AR
Bioinformatics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
Fax: 3018699423
Email: arkerlav@tigr.org
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index, (http://www.tigr.org/tdb/hgi/hgi.html)

FEATURES
source
  Location/Qualifiers
  1..314
  /organism="Homo sapiens"

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/mol_type="mRNA"
/db_xref="AYCC (inhost):139826"
/db_xref="taxon:9606"
/sex="female"
/dev_stage="adult"
/clone_lib="Endometrial tumor"
/note="Organ: endometrium; Vector: pBluescript SK-;
Site_1: EcoRI; Site_2: XhoI"

ORIGIN
Query Match      100.0%; Score 26; DB 9; Length 314;
Best Local Similarity 100.0%; Pred. No. 0.00015;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CACTCAGCCACTGGATTAAAGCAGAG 26
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Db 74 CACTCAGCCACTGGATTAAAGCAGAG 99
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RESULT 4
BF800308
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, P.F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,
Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V.,
O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
10737800
COMMENT
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CM4&t2=CM4-CI0062-
181000-370-b1&t3=2000-10-18&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 18
High quality sequence stop: 377.
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="CI0062"
/note="Organ: colon ins; Vector: puc18; Site 1: SmaI;
Site 2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

ORIGIN
Query Match      100.0%; Score 26; DB 9; Length 314;
Best Local Similarity 100.0%; Pred. No. 0.00015;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CACTCAGCCACTGGATTAAAGCAGAG 26
    |||||||
Db 74 CACTCAGCCACTGGATTAAAGCAGAG 99
    |||||||

RESULT 4
BF800308
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, P.F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,
Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V.,
O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
10737800
COMMENT
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CM4&t2=CM4-CI0062-
181000-370-b1&t3=2000-10-18&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 18
High quality sequence stop: 377.
Location/Qualifiers
1..377
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="CI0062"
/note="Organ: colon ins; Vector: puc18; Site 1: SmaI;
Site 2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

ORIGIN
Query Match      100.0%; Score 26; DB 10; Length 377;
Best Local Similarity 100.0%; Pred. No. 0.00016;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CACTCAGCCACTGGATTAAAGCAGAG 26
    |||||||
Db 332 CACTCAGCCACTGGATTAAAGCAGAG 357
    |||||||

RESULT 5
BF512134/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
The sequence contained an oligo-dT track that was present in the
oligonucleotide that was used to prime the synthesis of first
strand cDNA and therefore this may represent a bonafide poly A
tail. cDNA Library Preparation: M.B. Soares Lab Clone distribution:
NCI-CGAP clone distribution information can be found through the
I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/bbrp/image/image.html
Seq primer: M13 Forward
POLYA=yes.
Location/Qualifiers
1..417
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3068112"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI CGAP Subs"
/note="Vector: pTV73D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; NCI CGAP Subs
is a subtracted library derived from NCI CGAP Sub4. The
NCI CGAP Subs library had 3 million recombinants. A
single-stranded DNA preparation of NCI CGAP Sub4 was used
as a tracer in a subtractive hybridization with a driver
comprising the IMAGE pool (NCI CGAP kid3 pool 1 LLAM
3334-3337, 3682-3683, 3798-3803 (IMAGE Clones)
132376-132391, 145608-145675, 1500552-1502855);
NCI CGAP Kid5 pool 1 LLAM 3338-3342, 3722-3725, 3776-3778
(IMAGE Clones) 1323912-1325831, 1471368-1472903,
1492104-1493255); NCI CGAP Lu5 pool 1 LLAM 3575-3582,
3851-3854 (IMAGE Clones)
1414920-1417991, 1520904-1522439); NCI CGAP GC4 pool 1 LLAM
3164-3167, 3716-3720, 3733-3735 (IMAGE Clones)
1257096-1258631, 1469064-1470983, 1475592-1476743);
NCI CGAP Pr22 pool 1 LLAM 2457-2459, 2758-2759, 3062-3068
(IMAGE Clones) 985608-986759, 1101192-1101959,
1217928-1220615); NCI CGAP Co10 pool 1 LLAM 2644-2653,
2871-2872 (IMAGE Clones)
1057416-1061255, 1144584-1145351). (10% of the driver
population), plus a pool of 3,840 arrayed clones from
NCI CGAP Sub1 (IMAGE Clones) 2708616-2710535) and
NCI CGAP Sub2 (IMAGE Clones) 2710536-2712455) (10% of
the driver population), plus a pool of 11,136 clones from
NCI CGAP Sub3 (IMAGE Clones) 2712456-2723591) (10% of the
driver population), plus a pool of 5,472 clones from
NCI CGAP Sub4 (IMAGE Clones) 2723592-2728969) (70% of the

```

driver population). Subtraction was performed as previously described [Bonaldo, Lennon & Soares (1996): Normalization and Subtraction: Two Approaches To Facilitate Gene Discovery. Genome Research 6, 791-806. TAG TISSUE=colon TAG LIB=NCI CGAP\_Colo TAG\_SEQ=AAACG"]

## ORIGIN

Query Match 100.0%; Score 26; DB 10; Length 417;  
Best Local Similarity 100.0%; Pred. No. 0.00017;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CACTAGCCACTGGATTAAAGCAGAG 26  
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Db 356 CACTAGCCACTGGATTAAAGCAGAG 331

## RESULT 6

LOCUS BF873838/c 437 bp mRNA linear EST 17-JAN-2001  
DEFINITION IL3-ET0114-071100-338-C02 ET0114 Homo sapiens cDNA, mRNA sequence.  
ACCESSION BF873838  
VERSION BF873838.1 GI:12264007  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 437)

AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F., Goldman,G.H., Carvalho,A.P., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,D.F., de Souza,S.J. and Simpson,A.J.  
TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags

JOURNAL PROC. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
MEDLINE 20202663  
PUBMED 10737800

COMMENT Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL  
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=IL3&t2=IL3-ET0114-071100-338-C02&t3=2000-11-07&t4=1)  
Seq primer: puc 18 forward  
High quality sequence stop: 390.

## FEATURES

Location/Qualifiers  
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/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/dev\_stage="Adult"  
/clone\_lib="ET0114"

/notes="Organ: lung tumor; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

## ORIGIN

Query Match 100.0%; Score 26; DB 10; Length 437;  
Best Local Similarity 100.0%; Pred. No. 0.00017;

Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CACTAGCCACTGGATTAAAGCAGAG 26  
|||||  
Db 236 CACTAGCCACTGGATTAAAGCAGAG 211

## RESULT 7

LOCUS BM854793 549 bp mRNA linear EST 06-MAR-2002  
DEFINITION K-EST0137456 S22SNU16n1 Homo sapiens cDNA clone S22SNU16n1-148-F10 5', mRNA sequence.

ACCESSION BM854793  
VERSION BM854793.1 GI:19211192  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 549)

AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Kim,Y.S.  
TITLE 21C Frontier Korean EST Project 2001  
JOURNAL Unpublished (2002)  
COMMENT Contact: Kim YS  
Genome Research Center  
Korea Research Institute of Bioscience & Biotechnology  
52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea  
Tel: +82-42-860-4470  
Fax: +82-42-860-4409  
Email: yongsung@mail.kribb.re.kr  
Plate: 148 row: F column: 10  
High quality sequence stop: 549.

Location/Qualifiers  
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/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="S22SNU16n1-148-F10"

/sex="F"  
/tissue\_type="Ascites"  
/cell\_type="Lymphoblast-like"  
/cell\_line="SNU-16"  
/lab\_host="DH10B"  
/clone\_lib="S22SNU16n1"  
/note="Organ: Stomach; Vector: pT7T3-Pac; Site 1: EcoRI; Site 2: NotI; The S22SNU16 library was contributed by the Soares laboratory and it was constructed as described by Bonaldo, M.F., Lennon, G. and Soares, M.B. (1996), Genome Research 6(9): 791-806. RNA was prepared from harvested cells of SNU-16 culture. SNU-16 cell was obtained from Korean Cell Line Bank (KCLB). SNU-16 was established from ascitic fluids of Korean patients by Park J.G. et al. (1990), Cancer Res 50: 2773-2780."

FEATURES  
Source  
Location/Qualifiers  
1..549  
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/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="S22SNU16n1-148-F10"

/sex="F"  
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/cell\_type="Lymphoblast-like"  
/cell\_line="SNU-16"  
/lab\_host="DH10B"  
/clone\_lib="S22SNU16n1"  
/note="Organ: Stomach; Vector: pT7T3-Pac; Site 1: EcoRI; Site 2: NotI; The S22SNU16 library was contributed by the Soares laboratory and it was constructed as described by Bonaldo, M.F., Lennon, G. and Soares, M.B. (1996), Genome Research 6(9): 791-806. RNA was prepared from harvested cells of SNU-16 culture. SNU-16 cell was obtained from Korean Cell Line Bank (KCLB). SNU-16 was established from ascitic fluids of Korean patients by Park J.G. et al. (1990), Cancer Res 50: 2773-2780."

## source

Location/Qualifiers  
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/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="S22SNU16n1-148-F10"

/sex="F"  
/tissue\_type="Ascites"  
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/cell\_line="SNU-16"  
/lab\_host="DH10B"  
/clone\_lib="S22SNU16n1"  
/note="Organ: Stomach; Vector: pT7T3-Pac; Site 1: EcoRI; Site 2: NotI; The S22SNU16 library was contributed by the Soares laboratory and it was constructed as described by Bonaldo, M.F., Lennon, G. and Soares, M.B. (1996), Genome Research 6(9): 791-806. RNA was prepared from harvested cells of SNU-16 culture. SNU-16 cell was obtained from Korean Cell Line Bank (KCLB). SNU-16 was established from ascitic fluids of Korean patients by Park J.G. et al. (1990), Cancer Res 50: 2773-2780."

FEATURES  
Source  
Location/Qualifiers  
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/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="S22SNU16n1-148-F10"

/sex="F"  
/tissue\_type="Ascites"  
/cell\_type="Lymphoblast-like"  
/cell\_line="SNU-16"  
/lab\_host="DH10B"  
/clone\_lib="S22SNU16n1"  
/note="Organ: Stomach; Vector: pT7T3-Pac; Site 1: EcoRI; Site 2: NotI; The S22SNU16 library was contributed by the Soares laboratory and it was constructed as described by Bonaldo, M.F., Lennon, G. and Soares, M.B. (1996), Genome Research 6(9): 791-806. RNA was prepared from harvested cells of SNU-16 culture. SNU-16 cell was obtained from Korean Cell Line Bank (KCLB). SNU-16 was established from ascitic fluids of Korean patients by Park J.G. et al. (1990), Cancer Res 50: 2773-2780."

## ORIGIN

Query Match 100.0%; Score 26; DB 12; Length 549;  
Best Local Similarity 100.0%; Pred. No. 0.00018;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CACTAGCCACTGGATTAAAGCAGAG 26  
|||||  
Db 39 CACTAGCCACTGGATTAAAGCAGAG 64

## RESULT 8

LOCUS BM824089 550 bp mRNA linear EST 06-MAR-2002  
DEFINITION K-EST0095497 S22SNU16n1 Homo sapiens cDNA clone S22SNU16n1-90-G09 5', mRNA sequence.

ACCESSION BM824089  
VERSION BM824089.1 GI:19180502

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KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 550)
AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
Kim,Y.S.
TITLE 21C Frontier Korean EST Project 2001
JOURNAL Unpublished (2002)
COMMENT Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 90 row: G column: 09
High quality sequence stop: 550.
Location/Qualifiers
FEATURES
source
1..550
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="S22SNU16n1-90-G09"
/sex="F"
/tissue_type="Ascites"
/cell_type="lymphoblast-like"
/cell_line="SNU-16"
/lab_host="DH10B"
/clone_lib="S22SNU16n1"
/Note="Organ: Stomach; Vector: pT7T3-Pac; Site 1: EcoRI;
Site 2: NotI; The S22SNU16 library was contributed by the
Soares laboratory and it was constructed as described by
Bonaldi, M.F., Lennon, G. and Soares, M.B. (1996), Genome
Research 6(9): 791-806. RNA was prepared from harvested
cells of SNU-16 culture. SNU-16 cell was obtained from
Korean Cell Line Bank (KCLB). SNU-16 was established from
ascitic fluids of Korean patients by Park J.G. et al.
(1990), Cancer Res 50: 2773-2780."
ORIGIN
Query Match 100.0%; Score 26; DB 12; Length 550;
Best Local Similarity 100.0%; Pred. No. 0.00018;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CACTGAGCCACTGGATTGAAGCAGAG 26
Db 67 CACTGAGCCACTGGATTGAAGCAGAG 92
RESULT 9
BF953848
LOCUS MRO-NN1170-131100-302-f01 NN1170 Homo sapiens cDNA, mRNA sequence.
DEFINITION BF953848
ACCESSION BF953848
VERSION BF953848.1 GI:12371149
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 590)
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
PUBMED 10737800
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?ci=MR0&t2=MR0-NN1170-
131100-302-f01&t3=2000-11-13&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 31
High quality sequence stop: 569.
Location/Qualifiers
FEATURES
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1..590
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="NN1170"
/Note="Organ: nervous normal; Vector: puc18; Site 1: SmaI;
Site 2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
ORIGIN
Query Match 100.0%; Score 26; DB 10; Length 590;
Best Local Similarity 100.0%; Pred. No. 0.00018;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CACTGAGCCACTGGATTGAAGCAGAG 26
Db 270 CACTGAGCCACTGGATTGAAGCAGAG 295
RESULT 10
AW961897
LOCUS EST373970 MAGE resequences, MAGG Homo sapiens cDNA, mRNA sequence.
DEFINITION AW961897
ACCESSION AW961897
VERSION AW961897.1 GI:8151583
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 605)
AUTHORS Hegde,P., Qi,R., Abernathy,K., Dharap,S., Gaspard,R., Gay,C.,
Holt,I.E., Saeed,A.I., Sharov,V., Lee,N.H., Yeatman,T.J. and
Quackenbush,J.
TITLE Assessment of gene expression patterns in a model of colon tumor
metastasis using a 19,200 element cDNA microarray
JOURNAL Unpublished (2000)
COMMENT Contact: John Quackenbush
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 3528
Fax: 301 838 0208
Email: johnq@tigr.org
Plate: 167
Seq primer: Reverse.
Location/Qualifiers
FEATURES
source
1..605
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"

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ORIGIN
/clone lib="MAGE resequences, MAGG"
/note="Vector: pBluescriptSkm"

Query Match      100.0%; Score 26; DB 10; Length 605;
Best Local Similarity 100.0%; Pred. No. 0.00019;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CACTCAGCCACTGGATTAAAGCAGAG 26
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Db 495 CACTCAGCCACTGGATTAAAGCAGAG 520

RESULT 11
BE267891
LOCUS
DEFINITION
601125452F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3345084 5',
mRNA sequence.
ACCESSION
BE267891
VERSION
BE267891.1 GI:9141488
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 621)
AUTHORS
NIH-MGC http://mgc.nci.nih.gov/
TITLE
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL
Unpublished (1999)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
image.llnl.gov/image/html/iresources.shtml
Seq primer: -40RP from Gibco
High quality sequence stop: 619.
Location/Qualifiers
1..621
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3345084"
/tissue_type="Burkitt lymphoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 8"
/note="Organ: lymph; Vector: pOTB7; Site 1: XhoI; Site 2:
ECORI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5',
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."

FEATURES
source
1..621
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3345084"
/tissue_type="Burkitt lymphoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 8"
/note="Organ: lymph; Vector: pOTB7; Site 1: XhoI; Site 2:
ECORI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5',
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."

ORIGIN
Query Match      100.0%; Score 26; DB 10; Length 621;
Best Local Similarity 100.0%; Pred. No. 0.00019;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CACTCAGCCACTGGATTAAAGCAGAG 26
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Db 266 CACTCAGCCACTGGATTAAAGCAGAG 291

RESULT 12
BE019411
LOCUS
DEFINITION
BE555b12.y1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3010559 5',
similar to gb:U01147 BREAKPOINT CLUSTER REGION PROTEIN (HUMAN);,
mRNA sequence.

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ACCESSION
BE019411
VERSION
BE019411.1 GI:8279481
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 642)
AUTHORS
NIH-MGC http://mgc.nci.nih.gov/
TITLE
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL
Unpublished (1999)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
image.llnl.gov/image/html/iresources.shtml
Seq primer: -40RP from Gibco
High quality sequence stop: 509.
Location/Qualifiers
1..642
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3010559"
/tissue_type="rhabdomyosarcoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 17"
/note="Organ: muscle; Vector: pOTB7; Site 1: EcoRI;
Site 2: XhoI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."

ORIGIN
Query Match      100.0%; Score 26; DB 10; Length 642;
Best Local Similarity 100.0%; Pred. No. 0.00019;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CACTCAGCCACTGGATTAAAGCAGAG 26
|||||
Db 570 CACTCAGCCACTGGATTAAAGCAGAG 595

RESULT 13
BG829045
LOCUS
DEFINITION
602753375F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4905979 5',
mRNA sequence.
ACCESSION
BG829045
VERSION
BG829045.1 GI:14176632
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 653)
AUTHORS
NIH-MGC http://mgc.nci.nih.gov/
TITLE
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL
Unpublished (1999)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be

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found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LLCM1808 row: e column: 20  
High quality sequence stop: 653.

#### FEATURES source

Location/Qualifiers  
1. 653  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:4905979"  
/tissue\_type="rhabdomyosarcoma"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH\_MGC\_17"

/note="Organ: muscle; Vector: pOTB7; Site\_1: EcoRI; Site\_2: XhoI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

#### ORIGIN

Query Match 100.0%; Score 26; DB 12; Length 653;  
Best Local Similarity 100.0%; Pred. No. 0.00019;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CACTAGCCACTGGATTAAAGCAGAG 26  
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Db 573 CACTAGCCACTGGATTAAAGCAGAG 598

#### RESULT 14

BE514596  
LOCUS 601316940F1 NIH\_MGC\_9 Homo sapiens cDNA clone IMAGE:3633656 5',  
DEFINITION mRNA sequence.  
ACCESSION BE514596  
VERSION BE514596.1 GI:9721810  
KEYWORDS EST.  
SOURCE Homo sapiens (human)

#### ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 653)

AUTHORS NIH-MGC http://mgc.nci.nih.gov/  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: DCTD/DTF

cDNA Library Preparation: Ling Hong/Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov  
Plate: LLCM326 row: p column: 09  
High quality sequence stop: 662.

#### FEATURES source

Location/Qualifiers  
1. 665  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:3633656"  
/tissue\_type="adenocarcinoma cell line"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH\_MGC\_9"

/note="Organ: ovary; Vector: pOTB7; Site\_1: XhoI; Site\_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of

#### ORIGIN

Query Match 100.0%; Score 26; DB 10; Length 665;  
Best Local Similarity 100.0%; Pred. No. 0.00019;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CACTAGCCACTGGATTAAAGCAGAG 26  
|||||  
Db 298 CACTAGCCACTGGATTAAAGCAGAG 323

#### RESULT 15

BF530440  
LOCUS 602071562F1 NCI\_CGAP\_Brn67 Homo sapiens cDNA clone IMAGE:4214535  
DEFINITION 5' mRNA sequence.  
ACCESSION BF530440  
VERSION BF530440.1 GI:11617803  
KEYWORDS EST.  
SOURCE Homo sapiens (human)

#### ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 684)  
AUTHORS NIH-MGC http://mgc.nci.nih.gov/  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov

Tissue Procurement: David N. Louis, M.D.  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov  
Plate: LLCM9788 row: k column: 16  
High quality sequence stop: 684.

#### FEATURES source

Location/Qualifiers  
1. 684  
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/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:4214535"  
/tissue\_type="anaplastic oligodendroglioma with 1p/19q loss"  
/lab\_host="DH10B (T1 phage-resistant)"  
/clone\_lib="NCI\_CGAP\_Brn67"

/note="Organ: brain; Vector: pCMV-SPORT6; Site\_1: NotI; Site\_2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 2.3 kb. Constructed by Life Technologies. Note: this is a NCI\_CGAP Library."

#### ORIGIN

Query Match 100.0%; Score 26; DB 10; Length 684;  
Best Local Similarity 100.0%; Pred. No. 0.00019;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CACTAGCCACTGGATTAAAGCAGAG 26  
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Db 476 CACTAGCCACTGGATTAAAGCAGAG 501

Search completed: May 27, 2004, 11:30:41  
Job time : 1350.08 secs

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